

(12) INTERNATIONAL APPLICATION PUBLISHED UNDER THE PATENT COOPERATION TREATY (PCT)

(19) World Intellectual Property Organization
International Bureau



(43) International Publication Date
13 June 2002 (13.06.2002)

PCT

(10) International Publication Number
WO 02/46467 A2

(51) International Patent Classification⁷: C12Q 1/68

[FR/FR]; 971, chemin du Tardinaou, F-13190 Allauch (FR).

(21) International Application Number: PCT/IB01/02811

(74) Agents: **BREESE, Pierre** et al.; Breese-Majerowicz, 3, avenue de l'Opéra, F-75001 Paris (FR).

(22) International Filing Date: 7 December 2001 (07.12.2001)

(25) Filing Language: English

(81) Designated States (*national*): AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN, CO, CR, CU, CZ, DE, DK, DM, DZ, EC, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NO, NZ, PH, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, TZ, UA, UG, US, UZ, VN, YU, ZA, ZW.

(26) Publication Language: English

(30) Priority Data:

60/254,090 8 December 2000 (08.12.2000) US
10/007,926 7 December 2001 (07.12.2001) US

(71) Applicant (*for all designated States except US*): **IPSO-GEN** [FR/FR]; 232 Boulevard Sainte-Marguerite, F-13273 Marseille Cedex 09 (FR).

(84) Designated States (*regional*): ARIPO patent (GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZM, ZW), Eurasian patent (AM, AZ, BY, KG, KZ, MD, RU, TJ, TM), European patent (AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, TR), OAPI patent (BF, BJ, CF, CG, CI, CM, GA, GN, GQ, GW, ML, MR, NE, SN, TD, TG).

(72) Inventors; and

(75) Inventors/Applicants (*for US only*): **BERTUCCI, François** [FR/FR]; Le Sully, Parc de la Cadenelle, 122, rue du Commandant Rolland, F-13008 Marseille (FR). **HOULGATTE, Rémi** [FR/FR]; 31, Boulevard Lombard, F-13015 Marseille (FR). **BIRNBAUM, Daniel** [FR/FR]; 9, rue Baldacchini, La Croix-du-Sud, F-13009 Marseille (FR). **NGUYEN, Catherine** [FR/FR]; 8 Boulevard de la Kabylie, F-13016 Marseille (FR). **VIENS, Patrice** [FR/FR]; La Palmeraie Borely, Entrée A, 70, avenue d'Haïfa, F-13008 Marseille (FR). **FERT, Vincent**

Published:

— without international search report and to be republished upon receipt of that report

For two-letter codes and other abbreviations, refer to the "Guidance Notes on Codes and Abbreviations" appearing at the beginning of each regular issue of the PCT Gazette.

(54) Title: GENE EXPRESSION PROFILING OF PRIMARY BREAST CARCINOMAS USING ARRAYS OF CANDIDATE GENES

(57) Abstract: The invention relates to a polynucleotide library useful in the molecular characterization of a carcinoma, the library including a pool of polynucleotide sequences of subsequences thereof wherein the sequences of subsequences are overpressed in tumor cells, further wherein the sequences of subsequences correspond substantially to any of the polynucleotide sequences set forth in any of SEQ ID NOS: 1-468 or the complement thereof. The invention relates also to polynucleotide arrays useful to differentiate tumor cells from normal cells comprising combinations of selected immobilized polynucleotide sequences sets.

Best Available Copy

WO 02/46467 A2

GENE EXPRESSION PROFILING OF PRIMARY BREAST
CARCINOMAS USING ARRAYS OF CANDIDATE GENES

5 This invention relates to polynucleotide analysis
and, in particular, to polynucleotide expression profiling of
carcinomas using arrays of candidate polynucleotides.

10 Pathologists and clinicians in charge of the
management of breast cancer patients are facing two major
problems, namely the extensive heterogeneity of the disease
and the lack of factors - among conventional histological and
clinical features - predicting with reliability the evolution
of the disease and its sensitivity to cancer therapies.
Breast tumors of the same apparent prognostic type vary
widely in their responsiveness to therapy and consequent
15 survival of the patient. New prognostic and predictive
factors are needed to allow an individualization of therapy
for each patient.

20 Great hope is currently being placed on molecular
studies, which address the problem in a global fashion.
Methods such as cytogenetics, comparative genomic
hybridization, and whole-genome allelotyping have addressed
the issue at the genome level. Currently, the modifications
that take place in human tumors at the level of transcription
can also be studied in a large, unprecedented scale, using
25 new methods such as cDNA arrays that allow quantitative
measurement of the mRNA expression levels of many genes
simultaneously. Thus, it would be advantageous to provide a
means to assess the capacity of cDNA array testing in
clinical practice to better classify an heterogeneous cancer
30 into tumor subtypes with more homogeneous clinical outcomes,
and to identify new potential prognostic factors and
therapeutics targets.

The invention relates to a polynucleotide library useful in the molecular characterization of a carcinoma, the library including a pool of polynucleotide sequences or subsequences thereof wherein the sequences or subsequences are either underexpressed or overpressed in tumor cells, further wherein the sequences or subsequences correspond substantially to any of the polynucleotide sequences set forth in any of SEQ ID NOS: 1 - 468 or the complement thereof.

Fig. 1 shows an example of differential gene expression between normal breast tissue (NB) and breast tumor samples.

Fig. 2 is a representation of expression levels of 176 genes in normal breast tissue (NB) and 34 samples of breast carcinoma.

Fig. 3 is prognostic classification of breast cancer by gene expression profiling.

Fig. 4 shows the correlation of GATA3 expression with ER phenotype.

In the context of this disclosure, a number of terms shall be utilized.

The term "polynucleotide" refers to a polymer of RNA or DNA that is single-stranded, optionally containing synthetic, non-natural or altered nucleotide bases. A polynucleotide in the form of a polymer of DNA may be comprised of one or more segments of cDNA, genomic DNA or synthetic DNA.

The term "subsequence" refers to a sequence of nucleic acids that comprises a part of a longer sequence of nucleic acids.

The term "immobilized on a support" means bound directly or indirectly thereto including attachment by

covalent binding, hydrogen bonding, ionic interaction, hydrophobic interaction or otherwise.

Breast cancer is characterized by an important histoclinical heterogeneity that currently hampers the selection of the most appropriate treatment for each case. This problem could be solved by the identification of new parameters that better predict the natural history of the disease and its sensitivity to treatment. An important object of the present invention relates to a large-scale molecular characterization of breast cancer that could help in prediction, prognosis and cancer treatment.

An important aspect of the invention relates to the use of cDNA arrays, which allows to quantitative study mRNA expression levels of 188 candidate genes in 34 consecutive primary breast carcinomas along three directions: comparison of tumor samples, correlations of molecular data with conventional histoclinical prognostic features and gene correlations. The experimentation evidenced extensive heterogeneity of breast tumors at the transcriptional level. Hierarchical clustering algorithm identified two molecularly distinct subgroups of tumors characterized by a different clinical outcome after chemotherapy. This outcome could not have been predicted by the commonly used histoclinical parameters. No correlation was found with the age of patients, tumor size, histological type and grade. However, expression of genes was differential in tumors with lymph node metastasis and according to the estrogen receptor status; ERBB2 expression was strongly correlated with the lymph node status ($p \leq 0.0001$) and that of GATA3 with the presence of estrogen receptors ($p \leq 0.001$). Thus, experimental results identified new ways to group tumors according to outcome and new potential targets of carcinogenesis. They show that the systematic use of cDNA

array testing holds great promise to improve the classification of breast cancer in terms of prognosis and chemosensitivity and to provide new potential therapeutic targets.

5 DNA arrays consist of large numbers of DNA molecules spotted in a systematic order on a solid support or substrate such as a nylon membrane, glass slide, glass beads or a silicon chip. Depending on the size of each DNA spot on the array, DNA arrays can be categorized as microarrays (each
10 DNA spot has a diameter less than 250 microns) and macroarrays (spot diameter is greater than 300 microns). When the solid substrate used is small in size, arrays are also referred to as DNA chips. Depending on the spotting technique used, the number of spots on a glass microarray can
15 range from hundreds to thousands.

DNA microarrays have serve a variety of purposes, including, gene expression profiling, de novo gene sequencing, gene mutation analysis, gene mapping and genotyping. cDNA microarrays are printed with distinct cDNA
20 clones isolated from cDNA libraries. Therefore, each spot represents an expressed gene, since it is derived from a distinct mRNA.

Typically, a method of monitoring gene expression involves providing (1) providing a pool of sample
25 polynucleotides comprising RNA transcript(s) of one or more target gene(s) or nucleic acids derived from the RNA transcript(s); (2) reacting, such as hybridizing the sample polynucleotide to an array of probes (for example, polynucleotides obtained from a polynucleotide library)
30 (including control probes) and (3) detecting the reacted/hybridized polynucleotides. Detection can also involve calculating/quantifying a relative expression (transcription) level.

The present invention concerns a polynucleotide library useful in the molecular characterization of a carcinoma, said library comprising a pool of polynucleotide sequences or subsequences thereof wherein said sequences or subsequences are either underexpressed or overpressed in tumor cells, further wherein said sequences or subsequences correspond substantially to any of the polynucleotide sequences set forth in any of SEQ ID Nos: 1 - 468 in annex or the complement thereof.

Obviously, sequences having a great degree of homology with the above sequences could also been used to realize the molecular characterization of the invention, namely when those sequences present one or a few punctual mutations when compared with anyone of sequences SEQ ID Nos: 1 - 468.

The invention concerns a polynucleotide library useful in the molecular characterization of a carcinoma, said library comprising a pool of polynucleotide sequences or subsequences thereof wherein said sequences or subsequences are overpressed in tumor cells, further wherein said sequences or subsequences correspond substantially to any of the polynucleotide sequences set forth in any of SEQ ID NOS: 1 - 249 (Here, these SEQ ID N° refer to old SEQ ID N° 1-249 in priority document, the correlation table 10 allows to identify these sequences in the sequence listing of the present application in annex) or the complement thereof

Preferably the pool of polynucleotide sequences or subsequences correspond substantially to the polynucleotide sequences set forth in any of SEQ ID NOS: 1 - 247 (Here, these SEQ ID N° refer to old SEQ ID N° 1-247 in priority document, the correlation table 10 allows to identify these sequences in the sequence listing of the present application

in annex); further wherein said sequences are useful in differentiating a normal cell from a cancer cell.

5 The invention relates also to a polynucleotide library wherein the pool of polynucleotide sequences or subsequences correspond substantially to the polynucleotide sequences set forth in any of SEQ ID NOS: 1 - 242 (Here, these SEQ ID N° refer to old SEQ ID N° 1-242 in priority document, the correlation table 10 allows to identify these sequences in the sequence listing of the present application in annex);
10 wherein said sequences are useful in detecting a hormone sensitive tumor cell, or wherein said sequences are useful in differentiating a tumor with lymph nodes from a tumor without lymph nodes.

15 The invention relates also to a polynucleotide library wherein the pool of polynucleotide sequences or subsequences correspond substantially to the polynucleotide sequences set forth in any of SEQ ID NOS: 1 - 224; (Here, these SEQ ID N° refer to old SEQ ID N° 1-224 in priority document, the correlation table 10 allows to identify these sequences in the sequence listing of the present application in annex) wherein said sequences are useful in differentiating tetracycline-sensitive tumors from tetracycline-insensitive tumors.

25 The invention relates also to any polynucleotide library as previously described wherein said polynucleotides are immobilized on a solid support in order to form a polynucleotide array.

30 Preferably the support is selected from the group consisting of a nylon membrane, glass slide, glass beads, or a silicon chip.

The invention concerns also a method for detecting differentially expressed polynucleotide sequences which are correlated with a cancer, said method comprising:

- a) obtaining a polynucleotide sample from a patient; and
- 5 b) reacting the sample polynucleotide obtained in step (a) with a probe immobilized on a solid support wherein said probe comprises any of the polynucleotide sequences of the libraries previously described or an expression product encoded by any of the polynucleotide sequences of said
- 10 libraries and
- c) detecting the reaction product of step (b).

The invention relates also to a such method for detecting differentially expressed polynucleotide sequences

15 of the invention wherein the amount of reaction product of step (c) is compared to a control sample.

Preferably the polynucleotide sample isolated for, the sample is RNA or mRNA.

Preferably the polynucleotide sample is cDNA obtained by

20 reverse transcription of the mRNA.

In a preferred embodiment the method for detecting differentially expressed polynucleotide sequences, the step (b) comprises a hybridization of the sample RNA with the labeled probe.

25 The method for detecting differentially expressed polynucleotide sequences is used for detecting, diagnosing, staging, monitoring, prognosticating, preventing or treating conditions associated with cancer, and namely breast cancer.

30 The method for detecting differentially expressed polynucleotide sequences is particularly useful wherein the product encoded by any of the polynucleotide sequences or

subsequences is involved in a receptor-ligand reaction on which detection is based.

The invention relates also to a method for screening an anti-tumor agent comprising the method for detecting differentially expressed polynucleotide sequences previously described wherein the sample has been treated with the anti-tumor agent to be screened.

The label used to label polynucleotide samples is selected from the group consisting of radioactive, colorimetric, enzymatic, molecular amplification, bioluminescent or fluorescent label.

The invention also relates to a library of polynucleotides comprising a population of polynucleotide sequences overexpressed or underexpresses in cells derived from a tumor selected from SEQ ID NO :1 to SEQ ID NO :249 and their respective complements. (Here, these SEQ ID N° refer to old SEQ ID N° 1-249 in priority document, the correlation table 10 allows to identify these sequences in the sequence listing of the present application in annex).

In a particular embodiment the invention relates to polynucleotide sequences: SEQ ID No : 1 ; SEQ ID No : 5 ; SEQ ID No : 8 ; SEQ ID No : 9 ; SEQ ID No : 28 ; SEQ ID No : 29 ; SEQ ID No : 30 ; SEQ ID No : 31 ; SEQ ID No : 32 ; SEQ ID No : 45 ; SEQ ID No : 46 ; SEQ ID No : 52 ; SEQ ID No : 54 ; SEQ ID No : 63 ; SEQ ID No : 64 ; SEQ ID No : 81 ; SEQ ID No : 82 ; SEQ ID No : 87 ; SEQ ID No : 88 ; SEQ ID No : 101 ; SEQ ID No : 102 ; SEQ ID No : 103 ; SEQ ID No : 104 ; SEQ ID No : 105 ; SEQ ID No : 107 ; SEQ ID No : 113 ; SEQ ID No : 114 ; SEQ ID No : 115 ; SEQ ID No : 116 ; SEQ ID No : 127 ; SEQ ID No : 128 ; SEQ ID No : 131 ; SEQ ID No : 139 ; SEQ ID No : 140 ; SEQ ID No : 142 ; SEQ ID No : 150 ; SEQ ID No : 151 ; SEQ ID No : 154 ; SEQ ID No : 156 ; SEQ ID

No : 160 ; SEQ ID No : 161 ; SEQ ID No : 162 ; SEQ ID No : 177 ;
SEQ ID No : 178 ; SEQ ID No : 194 ; SEQ ID No : 195 ; SEQ ID No :
227 ; SEQ ID No : 228 ; SEQ ID No : 229 ; SEQ ID No : 231 ; SEQ ID
No : 233 ; SEQ ID No : 243 ; SEQ ID No : 244 ; SEQ ID No : 245 ;
5 SEQ ID No : 246 ; SEQ ID No : 247, (Here, these SEQ ID N° refer
to old SEQ ID N° presented on table 5 in priority document,
the correlation table 10 allows to identify these sequences
in the sequence listing of the present application in annex),
which distinguish a healthy person from a person with cancer.

10 Preferably the invention relates to
polynucleotide sequences: SEQ ID No : 1 ; SEQ ID No : 5 ; SEQ ID
No : 102 ; SEQ ID No : 103 ; SEQ ID No : 107 ; SEQ ID No : 229 ;
SEQ ID No : 45 ; SEQ ID No : 46 ; SEQ ID No : 243 ; SEQ ID No :
244 ; SEQ ID No : 245 ; SEQ ID No : 246 ; SEQ ID No : 247 (Here,
15 these SEQ ID N° refer to old SEQ ID N° presented on table 6
in priority document, the correlation table 10 allows to
identify these sequences in the sequence listing of the
present application in annex), which distinguish a healthy
person from a person with cancer.

20 In another particular embodiment the invention relates
to polynucleotide sequences: SEQ ID No : 2 ; SEQ ID No : 3 ;
SEQ ID No : 4 ; SEQ ID No : 5 ; SEQ ID No : 6 ; SEQ ID No : 7 ;
SEQ ID No : 8 ; SEQ ID No : 9 ; SEQ ID No : 10 ; SEQ ID No : 11 ;
25 SEQ ID No : 12 ; SEQ ID No : 13 ; SEQ ID No : 14 ; SEQ ID No : 15
; SEQ ID No : 16 ; SEQ ID No : 17 ; SEQ ID No : 18 ; SEQ ID No :
19 ; SEQ ID No : 20 ; SEQ ID No : 21 ; SEQ ID No : 22 ; SEQ ID No
: 23 ; ; SEQ ID No : 24 ; SEQ ID No : 25 ; SEQ ID No : 26 ; SEQ ID
No : 27 ; SEQ ID No : 221 ; SEQ ID No : 222 ; SEQ ID No : 223 ;
30 SEQ ID No : 241 ; SEQ ID No : 242 (Here, these SEQ ID N° refer
to old SEQ ID N° presented on table 7 in priority document,
the correlation table 10 allows to identify these sequences
in the sequence listing of the present application in annex)
which detect hormone sensitive tumors.

Preferably the invention relates to polynucleotide sequences SEQ ID No : 1; SEQ ID No : 2 SEQ ID No : 3; SEQ ID No : 4; SEQ ID No : 5; SEQ ID No : 221; SEQ ID No : 222 ; SEQ ID No : 15; SEQ ID No : 16; SEQ ID No : 17; SEQ ID No : 18 ; SEQ ID No : 19; SEQ ID No : 20 ; SEQ ID No : 21; SEQ ID No : 22 ; SEQ ID No : 241; SEQ ID No : 242 (Here, these SEQ ID N° refer to old SEQ ID N° presented on table 8 in priority document, the correlation table 10 allows to identify these sequences in the sequence listing of the present application in annex), which detect hormone sensitive tumors.

In another particular embodiment the invention relates to polynucleotide sequences: SEQ ID No : 1 ; SEQ ID No : 3 ; SEQ ID No : 4 ; SEQ ID No : 19 ; SEQ ID No : 20 ; SEQ ID No : 21; SEQ ID No : 22 ; SEQ ID No : 23 ; SEQ ID No : 26 ; SEQ ID No : 27 ; SEQ ID No : 28 ; SEQ ID No : 29 ; SEQ ID No : 30 ; SEQ ID No : 31 ; SEQ ID No : 32 ; SEQ ID No : 33 ; SEQ ID No : 34 ; SEQ ID No : 35 ; SEQ ID No : 36; SEQ ID No : 37; SEQ ID No : 38; SEQ ID No : 39; SEQ ID No : 40 ; SEQ ID No : 41 ; SEQ ID No : 42 ; SEQ ID No : 43 ; SEQ ID No : 44 ; SEQ ID No : 221 ; SEQ ID No : 222 ; SEQ ID No : 233 ; SEQ ID No : 241 ; SEQ ID No : 242 (Here, these SEQ ID N° refer to old SEQ ID N° presented on table 8 in priority document, the correlation table 10 allows to identify these sequences in the sequence listing of the present application in annex), which distinguish tumors with lymph node from tumors with no lymph node.

Preferably the invention relates to polynucleotide sequences : SEQ ID No : 1 ; SEQ ID No : 21 ; SEQ ID No : 22 ; SEQ ID No : 28; ; SEQ ID No : 29 ; SEQ ID No : 29 ; SEQ ID No : 31 ; SEQ ID No : 32 ; SEQ ID No : 19 ; SEQ ID No : 20 ; SEQ ID No : 26 ; SEQ ID No : 27 ; SEQ ID No : 37 ; SEQ ID No : 38 ; SEQ ID No : 39 ; SEQ ID No : 241 ; SEQ ID No : 241, (Here, these SEQ ID N° refer to old SEQ ID N° presented on table 8 in priority document, the correlation table 10 allows to

identify these sequences in the sequence listing of the present application in annex), which distinguish tumors with lymph node from tumors with no lymph node.

5 In another particular embodiment the invention relates to polynucleotide sequences: SEQ ID No : 1 ; SEQ ID No : 2 ;
SEQ ID No : 6 ; SEQ ID No : 7 ; SEQ ID No : 8 ; SEQ ID No : 9 ;
10 SEQ ID No : 10 ; SEQ ID No : 11 ; SEQ ID No : 13 ; SEQ ID No : 14 ;
SEQ ID No : 19 ; SEQ ID No : 20 ; SEQ ID No : 21 ; SEQ ID No :
22 ; SEQ ID No : 23 ; SEQ ID No : 35 ; SEQ ID No : 36 ; ; SEQ ID
No : 37 ; SEQ ID No : 56 ; SEQ ID No : 57 ; SEQ ID No : 74 ; SEQ
ID No : 75 ; SEQ ID No : 102 ; SEQ ID No : 104 ; SEQ ID No : 107
; SEQ ID No : 108 ; SEQ ID No : 109 ; SEQ ID No : 118 ; SEQ ID No
: 119 ; ; SEQ ID No : 136 ; SEQ ID No : 213 ; SEQ ID No : 214 ;
15 SEQ ID No : 215 ; SEQ ID No : 223 ; SEQ ID No : 224 (Here, these
SEQ ID N° refer to old SEQ ID N° presented on table 11 in
priority document, the correlation table 10 allows to
identify these sequences in the sequence listing of the
present application in annex) which distinguish tumors
20 sensitive to anthracycline from tumors unsensitive to
anthracycline.

25 The invention relates also to a method of detecting differentially expressed genes correlated with a cancer comprising detecting at least one library of polynucleotide sequences as above defined or of products encoded by said library in a sample obtained from a patient.

30 A particular embodiment of the invention relates to a polynucleotide library of corresponding substantially to any combination of at least one polynucleotide sequence selected among those included in each one of predefined polynucleotide sequences sets 1 to set 212 as defined in table 4

The invention relates obviously to polynucleotide libraries comprising at least one polynucleotide selected among those included in at least 50%, preferably 75% and more preferably 100% of said predefined sets, allowing to obtain a discriminating gene pattern, namely to distinguish between normal patients and patients suffering from tumor pathology, between patients having an hormone sensitive tumor and patients having an hormone resistant tumor, between patients having a tumor with lymph nodes from patients having a tumor without lymph nodes, between patients having an antracycline-sensitive tumor from patients having an antracycline-insensitive tumor and between patients having good prognosis primary breast tumors and patients having poor prognosis primary breast tumors.

Polynucleotide sequences library useful for the realization of the invention can comprise also any sequence comprised between 3'end and 5'end of each polynucleotide sequence set as defined in table 4, allowing the complete detection of the implicated genes.

The invention relates also to a polynucleotide library useful to differentiate a normal cell from a cancer cell wherein the pool of polynucleotide sequences or subsequences correspond substantially to any combination of at least one polynucleotide sequence selected among those included in each one of predefined polynucleotide sequences sets indicated on table 5, useful in differentiating a normal cell from a cancer cell.

Preferably the polynucleotide library useful to differentiate a normal cell from a cancer cell correspond

substantially to any combination of at least one polynucleotide sequence selected among those included in each one of predefined polynucleotide sequences sets indicated on table 5A, and of at least one polynucleotide sequence selected among those included in each one of predefined polynucleotide sequences sets indicated in table 5B.

The detection of an overexpression of genes identified with sets of polynucleotides sequences defined on table 5A, together with detection of an underexpression of genes identified with sets of polynucleotides sequences defined in table 5B allows to distinguish between normal patients, and patients suffering from tumor pathology.

The invention relates also to a polynucleotide library useful to detect a hormone sensitive tumor cell wherein the pool of polynucleotide sequences or subsequences correspond substantially to any combination of at least one polynucleotide sequence selected among those included in each one of predefined polynucleotide sequences sets defined in table 6

Preferably the polynucleotide library useful to detect a hormone sensitive tumor cell correspond substantially to any combination of at least one polynucleotide sequence selected among those included in each one of predefined polynucleotide sequences sets defined in table 6A together with at least one polynucleotide sequence selected among those included in each one of predefined polynucleotide sequences sets defined in table 6B.

The detection of an overexpression of genes identified with sets of polynucleotides sequences defined on table 6A, together with detection of an underexpression of

genes identified with sets of polynucleotides sequences defined in table 6B allows to distinguish between patients having an hormone sensitive tumor and patients having an hormone resistant tumor.

5

The invention concerns also a polynucleotide library useful to differentiate a tumor with lymph nodes from a tumor without lymph nodes wherein the pool of polynucleotide sequences or subsequences correspond substantially to any combination of at least one polynucleotide sequence selected among those included in each one of predefined polynucleotide sequences sets defined in table 7.

Preferably, the polynucleotide library useful to differentiate a tumor with lymph nodes from a tumor without lymph nodes correspond substantially to any combination of at least one polynucleotide sequence selected among those included in each one of predefined polynucleotide sequences sets defined in table 7A together with at least one polynucleotide sequence selected among those included in each one of predefined polynucleotide sequences sets defined in table 7B.

The detection of an overexpression of genes identified with sets of polynucleotides sequences defined on table 7A, together with detection of an underexpression of genes identified with sets of polynucleotides sequences defined in table 7B allows to distinguish between patients having a tumor with lymph nodes from patients having a tumor without lymph nodes.

The invention concerns also a polynucleotide library useful to differentiate anthracycline-sensitive tumors

from antracycline-insensitive tumors wherein the pool of polynucleotide sequences or subsequences correspond substantially to any combination of at least one polynucleotide sequence selected among those included in each one of predefined polynucleotide sequences sets defined in table 8.

Preferably, the polynucleotide library useful to differentiate antracycline-sensitive tumors from antracycline-insensitive tumors correspond substantially to any combination of at least one polynucleotide sequence selected among those included in each one of predefined polynucleotide sequences sets defined in table 8A together with at least one polynucleotide sequence selected among those included in each one of predefined polynucleotide sequences sets defined in table 8B.

The detection of an overexpression of genes identified with sets of polynucleotides sequences defined on table 8A, together with detection of an underexpression of genes identified with sets of polynucleotides sequences defined in table 8B allows to distinguish between patients having an antracycline-sensitive tumor from patients having an antracycline-insensitive tumor.

The invention concerns also a polynucleotide library useful to classify good and poor prognosis primary breast tumors wherein the pool of polynucleotide sequences or subsequences correspond substantially to any combination of at least one polynucleotide sequence selected among those included in each one of predefined polynucleotide sequences sets defined in table 9.

Preferably, the polynucleotide library useful to classify good and poor prognosis primary breast tumors correspond substantially to any combination of at least one

polynucleotide sequence selected among those included in each one of predefined polynucleotide sequences sets defined in table 9A together with at least one polynucleotide sequence selected among those included in each one of predefined polynucleotide sequences sets defined in table 9B.

The detection of an overexpression of genes identified with sets of polynucleotides sequences defined on table 9A, together with detection of an underexpression of genes identified with sets of polynucleotides sequences defined in table 9B allows to classify patients having good and poor prognosis primary breast tumors.

In a preferred embodiment, the tumor cell presenting underexpressed or overpressed sequences from the polynucleotide library of the invention are breast tumor cells.

In a particular embodiment the polynucleotides of the polynucleotide library of the present invention are immobilized on a solid support in order to form a polynucleotide array, and said solid support is selected from the group consisting of a nylon membrane, nitrocellulose membrane, glass slide, glass beads, membranes on glass support or a silicon chip.

Another object of the present invention concerns a polynucleotide array useful for prognosis or diagnostic of tumor comprising at least one immobilized polynucleotide library set as previously defined.

Then the invention concerns a polynucleotide array useful to differentiate a normal cell from a cancer cell comprising any combination of at least one polynucleotide sequence selected among those included in each

one of predefined polynucleotide sequences sets indicated on table 5, useful in differentiating a normal cell from a cancer cell.

5 Preferably the polynucleotide array useful to differentiate a normal cell from a cancer cell bears any combination of at least one polynucleotide sequence selected among those included in each one of predefined polynucleotide sequences sets indicated on table 5A, and of at least one polynucleotide sequence selected among those included in each
10 one of predefined polynucleotide sequences sets indicated in table 5B.

The invention relates also to a polynucleotide array useful to detect a hormone sensitive tumor cell
15 comprising any combination of at least one polynucleotide sequence selected among those included in each one of predefined polynucleotide sequences sets defined in table 6

20 Preferably the polynucleotide array useful to detect a hormone sensitive tumor cell bears any combination of at least one polynucleotide sequence selected among those included in each one of predefined polynucleotide sequences sets defined in table 6A together with at least one polynucleotide sequence selected among those included in each one of predefined polynucleotide sequences sets defined in
25 table 6B.

The invention concerns also a polynucleotide array useful to differentiate a tumor with lymph nodes from a tumor without lymph nodes comprising any combination of at
30 least one polynucleotide sequence selected among those included in each one of predefined polynucleotide sequences sets defined in table 7.

Preferably, the polynucleotide array useful to differentiate a tumor with lymph nodes from a tumor without lymph nodes bears any combination of at least one polynucleotide sequence selected among those included in each one of predefined polynucleotide sequences sets defined in table 7A together with at least one polynucleotide sequence selected among those included in each one of predefined polynucleotide sequences sets defined in table 7B.

The invention concerns also a polynucleotide array useful to differentiate anthracycline-sensitive tumors from anthracycline-insensitive tumors comprising any combination of at least one polynucleotide sequence selected among those included in each one of predefined polynucleotide sequences sets defined in table 8.

Preferably, the polynucleotide array useful to differentiate anthracycline-sensitive tumors from anthracycline-insensitive tumors bears any combination of at least one polynucleotide sequence selected among those included in each one of predefined polynucleotide sequences sets defined in table 8A together with at least one polynucleotide sequence selected among those included in each one of predefined polynucleotide sequences sets defined in table 8B.

The invention concerns also a polynucleotide array useful to classify good and poor prognosis primary breast tumors comprising any combination of at least one polynucleotide sequence selected among those included in each one of predefined polynucleotide sequences sets defined in table 9.

Preferably, the polynucleotide array useful to classify good and poor prognosis primary breast tumors bears any combination of at least one polynucleotide sequence selected among those included in each one of predefined polynucleotide sequences sets defined in table 9A together with at least one polynucleotide sequence selected among those included in each one of predefined polynucleotide sequences sets defined in table 9B.

The present invention concerns also a method for detecting differentially expressed polynucleotide sequences that are correlated with a cancer, said method comprising:

a) obtaining a polynucleotide sample from a patient; and

b) reacting the sample polynucleotide obtained in step (a) with a probe immobilized on a solid support wherein said probe comprises any of the polynucleotide sequences of the libraries previously defined or an expression product encoded by any of the polynucleotide sequences of the libraries previously defined

c) detecting the reaction product of step (b).

Preferably, the polynucleotide sample obtained at step (a) is labeled before its reaction at step (b) with the probe immobilized on a solid support.

The label of the polynucleotide sample is selected from the group consisting of radioactive, colorimetric, enzymatic, molecular amplification, bioluminescent or fluorescent.

In a particular embodiment the reaction product of step (c) is quantified by further comparison of said reaction product to a control sample.

5 In a first embodiment, the polynucleotide sample isolated from the patient and obtained at step (a) is either RNA or mRNA.

In another embodiment the polynucleotide sample isolated from the patient is cDNA is obtained by reverse transcription of the mRNA.

10 Preferably the reaction step (b) of the method for detecting differentially expressed polynucleotide sequences comprises a hybridization of the sample RNA issued from patient with the probe.

15 Preferably the sample RNA is labeled before hybridization with the probe and the label is selected from the group consisting of radioactive, colorimetric, enzymatic, molecular amplification, bioluminescent or fluorescent.

20 This method for detecting differentially expressed polynucleotide sequences is particularly useful for detecting, diagnosing, staging, monitoring, prognosticating, preventing or treating conditions associated with cancer, and particularly breast cancer.

25 The method for detecting differentially expressed polynucleotide sequences is also particularly useful when the product encoded by any of the polynucleotide sequences or subsequences set is involved in a receptor-ligand reaction on which detection is based.

30 The present invention is also related with a method for screening an anti-tumor agent comprising the method the above-depicted method for detecting differentially expressed polynucleotide sequences wherein the sample has been treated with the anti-tumor agent to be screened.

In a particular embodiment the method for screening an anti-tumor agent comprises detecting polynucleotide sequences reacting with at least one library of polynucleotides or polynucleotide sequences set as previously defined or of products encoded by said library in a sample obtained from a patient.

The invention is illustrated by examples detailed below related to particular experimental results obtained with selected libraries of polypeptides useful to identify and distinguish tumor samples from normal ones.

Tumor samples and RNA extraction

To avoid any bias of selection as to the type and size of the tumors, the RNAs to be tested were prepared from unselected samples. Samples of primary invasive breast carcinomas were collected from 34 patients undergoing surgery at the Institute Paoli-Calmette. After surgical resection, the tumors were macrodissected: a section was taken for the pathologist's diagnosis and an adjacent piece was quickly frozen in liquid nitrogen for molecular analyses. The median age of patients at the time of diagnosis was 55 years (range 39, 83) and most of them were post-menopausal. Tumors were classified according to the WHO histological typing of breast tumors in: 29 ductal carcinomas, 2 lobular carcinomas, 1 mixed ductal and lobular carcinoma, and 2 medullar carcinomas. They had various sizes, inferior or equal to 20 mm (n = 13), between 20 and 50 mm (n = 18) or superior to 50 mm (n = 3), axillary's lymph node status (negative: 19 tumors, positive: 15 tumors), SBR grading (I: 3 tumors, II: 20 tumors, III: 10 tumors, not evaluable: 1 tumor), and estrogen receptor status (ER) evaluated by

immunohistochemical assay (23 ER-positive, 11 ER-negative). ER positivity cutoff value was 10%. Adjuvant treatment with radiotherapy and when necessary multi-agent anthracyclin-based chemotherapy (n = 16) was given to patients according to local practice.

Total RNA was extracted from tumor samples by standard methods (43). Total RNA from normal breast tissue was obtained from Clontech (Palo Alto, CA): RNA was isolated from 8 tissue specimens from Caucasian females, age range 23 - 47. RNA integrity was controlled by denaturing formaldehyde agarose gel electrophoresis and Northern blots using a 28S-specific oligonucleotide.

cDNA arrays preparation

Gene expression was analyzed by hybridization of arrays with radioactive probes. The arrays contained PCR products of 5 control clones, and 180 IMAGE human cDNA clones selected with practical criteria (3' sequence of mRNA, same cloning vector, host bacteria and insert size). This represented 176 genes (4 genes were represented by 2 different clones): 121 with proven or putative implication in cancer and 55 implicated in immune reactions (the list is available on the web site: <http://tagc.univ-mrs.fr/pub/Cancer/>). Their identity was verified by 5' tag-sequencing of plasmid DNA and comparison with sequences in the EST (dbEST) and nucleotide (GenBank) databases at the NCBI. Identity was confirmed for all but 14 clones without significant gene similarity, which were referenced by their GenBank accession number. The control clones were: Arabidopsis thaliana cytochrome c554 gene (used for hybridization signal normalization), 3 poly(A) sequences of different sizes and the vector pT7T3D (negative controls).

PCR amplification, purification and robotical spotting of PCR products onto Hybond-N+ membranes (Amersham) were done according to described protocols (4). All PCR products were spotted in duplicate. For normalization purpose, the c554 gene was spotted 96-fold scattered over the whole membrane.

cDNA array hybridizations

Hybridizations were done successively with a vector oligonucleotide (to precisely determine the amount of target DNA accessible to hybridization in each spot), then after stripping of vector probe, with complex probes made from the RNAs (4). Each complex probe was hybridized to a distinct filter. Probes were prepared from total RNA with an excess of oligo(dT25) to saturate the poly(A) tails of the messengers, and to insure that the reverse transcribed product did not contain long poly(T) sequences. A precise amount of c554 mRNA was added to the total RNA before labeling to allow normalization of the data.

Five ng of total RNA (~100ng of mRNA) from tissue samples were used for each labeling. Probe preparation and hybridization of the membranes were done according to known procedures (<http://tagc.univ-mrs.fr/pub/Cancer/>).

Hybridization was done in excess of target (~15 ng of DNA in each spot) and binding of cDNAs to the targets was linear and proportional to the quantity of cDNA in the probe.

Detection and quantification of cDNA array hybridization signals

Quantitative data were obtained using an imaging plate device. Hybridization signal detection with a FUJI BAS 1500 machine and quantification with the HDG Analyzer

software (Genomic Solutions, Ann Arbor, MI) were done as previously described (<http://tagc.univ-mrs.fr/pub/Cancer/>): Quantification was done by integrating all spot pixel intensities and subtracting a spot background value determined in the neighboring area. Spots were located with a LaPlacian transformation. Spot background level was the median intensity of all the pixels present in a small window centered on the spot and which were not part of any spot (44). Quantified data were normalized in three steps and expressed as absolute gene expression levels (i.e. in percentage of abundance of individual mRNA with respect to mRNA within the sample), as described (4).

Array data analysis

Before analysis of the results, the reproducibility of the experiments was verified by comparing duplicate spots, or one hybridization with the same probe on two independent arrays, or two independent hybridizations with probes prepared from the same RNA. In every case, the results showed good reproducibility with respective correlation coefficients of 0.95, 0.98 and 0.98 (data not shown). Moreover, genes represented by two different clones on the array, such as CDK4 or ETV5, displayed similar expression profiles for the two clones in all samples. This reproducibility was sufficient enough to consider a 2-fold expression difference as significantly differential.

For graphical representation, data were displayed as absolute expression levels (Fig. 2a). For better visualization of clustering, results were log-transformed and displayed as relative values median-centered in each row and in each column (Fig. 2b). Hierarchical clustering was applied to the tissue samples and the genes using the Cluster program developed by Eisen (45) (average linkage clustering

using Pearson correlation as similarity metric). Results in Figs. 2 and 3 were displayed with the TreeView program (45).

Subsequent analysis was done using Excel software (Microsoft) and statistical analyses with the SPSS software. Metastasis-free survival and overall survival were measured from diagnosis until the first metastatic relapse or death respectively. They were estimated with the Kaplan-Meier method and compared between groups with the Log-Rank test. Correlations of gene pairs based on expression profiles were measured with the correlation coefficient r . The search for genes with expression levels correlated with tumor parameters was done in several successive steps.

First, genes were detected by comparing their median expression level in the two subgroups of tumors discordant according to the parameter of interest. The median values rather than the mean values were used because of the high variability of the expression levels for many genes, resulting in a standard deviation of expression level similar or superior to the mean value and making comparisons with means impossible. Second, these detected genes were inspected visually on graphics, and finally, an appropriate statistical analysis was applied to those that were convincing to validate the correlation. Comparison of GATA3 expression between ER-positive tumors and ER-negative tumors was validated using a Mann-Witney test. Correlation coefficients were used to compare the gene expression levels to the number of axillary nodes involved.

Northern blot analysis

Seventy-nine breast tumors, including 22 of the 34 tested on the arrays, were analyzed for GATA3 expression by Northern blot hybridization. RNA extraction from tumor samples and Northern blots were done as previously described

(43). The GATA3 probe was prepared from the IMAGE cDNA clone 129757, which corresponds to the 3' region (from +843 to +1689) of the GATA3 cDNA sequence (GenBank accession no. X55122). The insert (846 bp) was obtained by digestion of the clone with EcoRI and PacI enzymes. Northern blots were stripped and re-hybridized using a α -actin probe (46).

Fig. 1 shows an example of differential gene expression between normal breast tissue (NB) and breast tumor samples. Each cDNA array on Nylon filter was hybridized with a complex probe made from 5 μ g of total RNA. The top image corresponds to the whole membrane. For the two bottom images, only the right portion of the membranes is shown. Numbers below the spots indicate housekeeping genes (1, GAPDH and 2, actin), negative control clones (3, 4 and 5) and examples of genes differentially expressed between NB and breast tumor (6, stromelysin3; 7, ERBB2; 8, MYBL2; 9, FOS; 10, TGF β 3; 11, desmin), and between ER- breast tumor and ER+ breast tumor (12, GATA3).

Fig. 2 is a representation of expression levels of 176 genes in normal breast tissue (NB) and 34 samples of breast carcinoma. Each column corresponds to a single tissue, and each row to a single gene. (a) The results are expressed as percentage abundance of individual mRNA within the sample, and are represented using a blue color scale. The color scale (log scale with a 3-fold interval) indicated at the bottom left ranges from light blue (expression level 0.001%) to dark blue (expression level > 3%). White squares indicate clones with undetectable expression levels and gray squares indicate missing data. The tissue samples are arbitrarily ordered and the clones are ordered from top to bottom according to increasing median expression levels. Horizontal black arrows on the right of the figure mark three clones with highly variable expression levels between the

tumors (stromelysin3, IGF2, GATA3 from top to bottom). (b) The results are shown as relative expression levels (relative to the median value of each row and each column) and are represented with a color scale indicated at the bottom left ranging from 1/100 to 100 fold changes (gray squares: missing data). Eighteen clones with median expression level equal to zero in the 34 tumors are omitted. The clustering program arranges samples (n = 35) along the horizontal axis so that those with the most similar expression profiles are placed adjacent to each other. Similarly, clones (n = 162) are near each other along the vertical axis if they show a strong expression profile correlation across all tissues. The length of the branches of the dendrograms capturing respectively the samples (top) and the clones (left) reflects the similarity of the related elements. Two groups of tumors are separated and color coded: group A (blue) and group B (orange). Horizontal black and horizontal red arrows on the right of the figure respectively mark three genes with highly variable expression levels between the tumors (IGF2, GATA3, stromelysin3 from top to bottom) and four pairs of different clones representing four genes. (c) Zoom representation of group A from Figure 2b, excluding the two outlier tumors at the right. The clustering separates two subgroups of tumors, A1 and A2. The dotted branches correspond to tumors associated with metastatic relapse and death. Follow-up was longer in A2 than in A1 (median 81 months vs 47 for A1).

Fig. 3 is prognostic classification of breast cancer by gene expression profiling showing that gene expression-based tumour classification correlates with clinical outcome. The 12 samples of group A (see figure 2b and 2c) were reclustered using the top 32 differentially expressed genes between A1 and A2 subgroups. Data were displayed as in Fig. 2b and shown with the same color key.

The hierarchical clustering was applied to expression data from the 23 clones, out of 32, of which expression levels presented an at least two-fold change in at least two samples (out of 12). Two subgroups of tumors A1 and A2 are shown as well as two groups of differentially expressed clones. The dotted branches of tumor cluster A1 correspond to samples associated with metastatic relapse and death. Figure 3a shows Two-dimensional representation of hierarchical clustering results shown in figures 2a and 2b. The analysis delineates 4 groups of tumours A, B, C and D. Black squares indicate patients alive at last follow-up visit and red squares indicate patients who died. Three classes of patients with a statistically different clinical outcome were defined according to gene expression profiles: class A (n = 16), class B+C (n = 34), class D (n = 5). Figure 3b illustrates Kaplan-Meier plot of overall survival of the 3 classes of patients ($p < 0.005$, log-rank test). And figure 3c illustrates Kaplan-Meier plot of metastasis-free survival of the 3 classes of patients ($p < 0.05$, log-rank test).

Fig. 4 shows the correlation of GATA3 expression with ER phenotype. (a) The expression levels of GATA3 in 34 breast cancer samples (y axis) monitored by cDNA array analysis are reported in percentage of abundance of individual mRNA with respect to mRNA within the sample (log scale). GATA3 is significantly overexpressed in the ER-positive tumors (n = 23) versus the ER-negative tumors (n = 11) using the Mann-Witney test ($p = 0.0004$). The expression level of GATA3 in normal breast tissue is reported on the right (NB). (b) Northern blot analysis of GATA3 in normal breast sample (NB) and 9 breast cancer samples (AT: tumor analyzed with cDNA array and Northern blot; NT: tumor analyzed with Northern blot). Blots were probed successively

with cDNA from GATA3 (top) and α -actin (bottom). ER status is indicated for each tumor sample.

Data representation

5 Fig. 1 shows examples of hybridizations of cDNA arrays with probes made from RNA extracted from normal breast tissue and breast tumors.

10 The crude results of all hybridizations were processed to be presented either as absolute or relative values in schematic figures. The normalization procedure allowed display of absolute values expressed in percent of abundance of mRNA in the probe as shown in Fig. 2a. Each level of the blue color ladder represents a 3-fold interval of absolute abundance of mRNA. Each column corresponds to a tissue sample and each row to a gene. For graphic purposes, 15 genes were ordered from top to bottom according to increasing median expression levels. Tumor samples were not ordered. The values in each sample displayed a wide range of intensities (3 decades in log scale) corresponding to 20 expression levels ranging from approximately 0.002% to 5% of mRNA abundance. Many genes (see for example stromelysin 3, IGF2 and GATA3, arrows) displayed highly variable expression levels across all tumor samples, scattered over the whole dynamic range of values. A representation of relative values 25 is shown in Fig. 2b. Absolute values were log-transformed, omitting 18 clones whose median intensity was equal to zero across all tissues. Data for each of the 162 remaining clones were then median-centered, as well as data for each sample, so that the relative variation was shown, rather than 30 the absolute intensity. A color scale was used to display data: red for expression level higher than the median and green for expression level lower than the median. The magnitude of the deviation from the median was represented by

the color intensity. A hierarchical clustering program was then applied to group the 35 samples according to their overall gene expression profiles, and to group the 162 clones on the basis of similarity of their expression levels in all tissues. This resulted in a picture highlighting groups of correlated tissues and groups of correlated genes as depicted by dendrograms.

Breast tumor classification

As shown in Fig. 2b, the clustering algorithm identified two groups of samples, designated A ($n = 15$, including normal breast, NB) and B ($n = 20$). These groups were similar with respect to patient age, menopausal status at diagnosis, SBR grading and tumor pathological size. However, 72% of tumors in group A were node-positive and 75% in group B were node-negative. Moreover, 80% of the tumors in group B were estrogen receptor (ER) positive and 50% in group A were ER-negative. With a median follow-up of 44 months after diagnosis, overall survival was different between A and B groups: 5 women died in A (median follow-up 58 months) and 1 in B (median follow-up 40 months). But the frequency of metastatic relapse was relatively similar in the two groups, with 5 women who relapsed in A and 6 in B. Because the time between the diagnosis of metastasis and last follow-up is too short in B, a longer follow-up is needed to determine if these two different groups, defined with expression profiles, have really a different outcome with respect to overall survival.

In the group A of 15 samples, three samples (normal breast and two tumors) were different from each other and from the other 12 samples. The latter constituted two subgroups of tumors, A1 ($n = 6$) and A2 ($n = 6$), which could be further separated by clustering as shown in Fig. 2c. The

12 tumors had an uniformly high risk of metastatic relapse according to conventional prognostic features as shown in Table 1. Most of them had received comparable adjuvant anthracyclin-based chemotherapy after surgery, with more women treated in the A1 subgroup. Interestingly, these two subgroups, which could not be distinguished with commonly used histoclinical features, had a very different clinical outcome: there were 4 metastatic relapses and 4 deaths in A1 (median follow-up: 44 months). In contrast and despite a longer median follow-up (90 months), no metastasis or death occurred in A2. This resulted in a significant better metastasis-free survival ($p = 0.01$) and overall survival ($p = 0.005$) for group A2 than for group A1 tumors. No such subgrouping could be done in B.

TABLE 1

Subgroup	A1						A2					
Tumor position in the cluster	1	2	3	4	5	6	7	8	9	10	11	12
Age, years	46	58	60	63	51	58	46	47	50	47	46	66
Nodal status	1	0	0	16	13	37	10	4	1	2	0	0
Histological size, mm	60	20	26	35	20	30	27	25	30	25	20	22
SBR grade												
ER status	neg	neg	neg	neg	neg	neg	pos	neg	pos	pos	pos	pos
Adjuvant chemotherapy	yes	yes	no	yes	yes	yes	yes	yes	no	yes	no	no
Metastasis	yes	no	yes	yes	no	yes	no	no	no	no	no	no
Follow-up, months	58	106	35	47	41	31	85	98	95	49	19	141
Patient status	D	A	D	D	A	D	A	A	A	A	A	A

Patient characteristics in subgroups A1 and A2. The 12 tumors are numbered from 1 to 12 according to their position from left to right in the clustering graphic displayed in Fig. 3. Adjuvant chemotherapy was anthracyclin-based. In the line concerning the patient status, A means alive and D means death from cancer progression.

Genes responsible for group A substructure were searched. These are potentially relevant to the prognosis and the sensitivity to chemotherapy in these tumors. Thirty-two genes out of 188 were identified by comparing their median expression level in A1 vs A2. Then, the 12 tumors were reclustered using the expression profiles of these genes as shown in Fig. 3. The same subgroups A1 and A2 were evident and separated by 2 groups of genes: as expected, high expression of ERBB2, MYC and EGFR was associated with bad prognosis subgroup A1 (6-8), and that of E-cadherin and the proto-oncogene MYB with good prognosis subgroup A2 (9, 10). For most of the other genes, these results may stimulate new investigations. Differentiation state is a good prognostic factor in breast cancer and, accordingly, genes associated with cell differentiation, such as GATA3 (11) and CRABP2 (12), had a high level of expression in the better outcome group. The high expression of Ephrin-A1 mRNA in the bad prognosis subgroup suggests a role of this growth factor in breast cancer and can be paralleled with its up-regulation during melanoma progression (13).

Differential gene expression between normal breast and breast tumors

To identify genes differentially expressed between breast tumors (T) and normal breast (NB), the NB value for each gene was compared to its expression level in each tumor. When the expression level of a gene in NB was undetectable, only qualitative information could be deduced and the mRNA was considered as differentially expressed if the signal intensity in the tumor was superior to the reproducibility threshold (0.002% of mRNA abundance). In the other cases, differential expression was defined by an at least 2-fold expression difference. Also, the number of

tumors where it was over- or underexpressed was measured. Table 2 shows a list of the top 20 over- and underexpressed genes. For these genes, the T/NB ratio is reported, where T represented their median expression value in the 34 tumors. This ratio ranged from 2.70 (ABCC5) to 17.76 (GATA3) for the overexpressed genes, and from 0.00 (desmin) to 0.29 (APC) for the underexpressed genes.

TABLE 2

Clone ID	Gene/Protein identity	Gene symbol	Chrom. location	N	T/NB
	Overexpressed genes				
154343	Granzyme H	GZMH	14q11.2	32	9,51
235947	Stromelysin 3	STMY3	22q11.2	31	15,92
207378	MYB Related Protein B	MYBL2	20q13.1	31	(a)
153275	Cellular Retinoic Acid Binding Protein 2	CRABP2	1q21.3	29	7,16
129757	GATA-binding protein 3	GATA3	10p15	28	17,76
120649	T-Lymphocyte surface CD2 antigen	CD2	1p13.1	28	7,54
109677	CREB Binding Protein	CREBBP	16p13.3	28	5,08
172152	EGFR-binding protein GRB2	GRB2	17q24-q25	28	5,00
66969	Transcription factor RELB	RELB	19	28	3,61
182007	ETS-Related Transcription Factor ELF1	ELF1	13q13	27	3,58
153446	LIM domain protein RIL	RIL	5q31.1	26	4,03
203394	ETS Variant gene 5 (ETS-related molecule)	ETV5	3q28	25	3,67
160963	Thrombospondin 1	THBS1	15q15	25	3,39
188393	POU domain, class 2, transcription Factor 2	POU2F2	19	24	4,02

Clone ID	Gene/Protein identity	Gene symbol	Chrom. location	N	T/NB
187822	Integrin, beta 2	ITGB2	21q22.3	24	3,01
243907	Nuclear Factor of Activating T cell Subunit p45	NF45	1	24	2,84
158347	EST H27202	EST		23	2,91
230933	EST AW184517	EST		22	2,85
212366	ATP-Binding Cassette, sub-family C (CFTR/MRP), 5	ABCC5	3q27	22	2,70
149401	Cathepsin D	CTSD	11p15.5	21	2,97
	Underexpressed genes				
153854	Desmin	DES	2q35	34	0,00
208717	P55-C-FOS proto-oncogene protein	FOS	14q24.3	33	0,05
159093	Transcription Factor AP4	TFAP4	16p13	33	0,11
124340	Tenascin XA	TNXA	6p21.3	33	0,14
133738	Prolactin	PRL	6p22.2-p21.3	32	0,00
133891	Chorionic Somatomammotropin Hormone 1	CSH1	17q22-q24	32	0,00
151501	Tyrosine Kinase Receptor TEK	TEK	9p21	32	0,00
183030	Activating Transcription Factor 3	ATF3	1	32	0,07
120916	Phosphodiesterase I	PDNP2	8q24.1	32	0,14
155716	EST R72075	EST		31	0,00
208118	Transforming Growth Factor Beta Receptor Type III	TGFBR3	1p33-p32	31	0,14
187547	Diphtheria Toxin Receptor	DTR	5q23	31	0,17
108490	HIV-1 Rev Binding protein	HRB	2q36	31	0,20
147002	B-cell CLL/lymphoma 2	BCL2	18q21.3	31	0,26
182610	Microsomal Glutathione S Transferase 1	MGST1	12p12.3-p12.1	31	0,28
152802	Phospholipase A2 Membrane	PLA2G2A	1p35	30	0,03

Clone ID	Gene/Protein identity	Gene symbol	Chrom. location	N	T/NB
	Associated, group IIA				
183087	Interleukin 3 Receptor Alpha chain	IL3RA	Xp22.3;Yp13.3	30	0,24
108571	Retinoblastoma-Like 2 (p130)	RBL2	16q12.2	29	0,28
125294	Adenomatous Polyposis Coli Protein	APC	5q21-q22	29	0,29
151767	FASL Receptor	TNFRSF6	10q24.1	28	0,27

List of the genes that show the most frequent differential expression between normal breast tissue and 34 breast carcinomas as measured by cDNA array analysis. N indicates the number of tumor samples where the gene is dysregulated (fold change > 2) compared to normal breast tissue. T/NB represents the ratio: median expression level in 34 breast tumors / expression level in normal breast. (a) MYBL2 transcript displayed a median expression level of 0.025% in breast tumors and was undetectable in NB.

High expression of mucin 1, NM23, ERBB2, FGFR1 and FGFR2, MYC, stromelysin3, cathepsin D and downregulation of FOS, APC, RBL2, FAS, BCL2 were found, reflecting what is known about their biology in cancer. GATA3, which codes for a member of the GATA family of zinc finger transcription factors, and CRABP2, encoding one of the two cellular retinoic acid-binding proteins, showed high expression of mRNA, extending previous results on cDNA arrays (4).

Differential gene expression among various breast tumors and correlation with histoclinical prognostic parameters

To search for potential prognostic markers in breast cancer, genes with expression levels correlated with conventional histoclinical prognostic parameters were looked for: age of patients, axillary node status, tumor size, histological grade and ER status. No significant correlation was found with age, tumor size and histological grade. However, the expression profiles of some genes correlated with ER status and axillary node involvement.

To identify genes potentially relevant to the hormone-responsive phenotype, the gene expression profiles in ER-positive breast cancers (n = 23) vs ER-negative breast cancers (n = 11) were compared. Sixteen clones displayed a median intensity of 0 in both groups. Twenty-five presented a fold change superior to 2. Table 3a displays the top 10 over- and underexpressed genes. Among them, the most differentially expressed was GATA3 with a median intensity ratio ER+/ER- of 28.6 and a value for the first quartile of ER-positive tumors superior (5-fold) to the value of the third quartile of the ER-negative tumors as shown in Fig. 4a. The high expression of GATA3 in ER-positive tumors was statistically significant using a Mann-Witney test (p 0.001). All ER-positive tumors and only 18% of ER-negative tumors displayed a GATA3 expression level greatly superior (fold change > 3) to the normal breast value. Furthermore GATA3 expression was analyzed by Northern blot hybridization (Fig. 4b) in a panel of 79 breast cancers (21 ER-negative tumors and 58 ER-positive tumors), including 22 of the tumors analyzed with cDNA arrays. It confirmed the array results for those 22 tumors as well as the strong correlation between ER status and GATA3 RNA expression (Mann-Witney test, p ≤ 0.0001).

TABLE 3A

Clone ID	Gene/Protein identity	Gene symbol	ER+/ER-
129757	GATA-binding protein 3	GATA3	28,6
356763	Granzyme A	GZMA	5,7
248613	MYB proto-oncogene	MYB	3,4
211999	KIAA1075 protein	KIAA1075	3,3
235947	Stromelysin 3	STMY3	3,1
229839	Macrophage Stimulating 1	MST1	2,8
153275	Cellular Retinoic Acid Binding Protein 2	CRABP2	2,7
301950	X-box Binding Protein 1	XBP1	2,7
205314	Tumor Protein p53	TP53	2,5
126233	Insulin-like Growth Factor 2	IGF2	2,4
66322	CD3G antigen, Gamma	CD3G	0,0
195022	Interleukin 2 Receptor Gamma chain	IL2RG	0,0
111461	SOX4 Protein	SOX4	0,4
151475	Epidermal Growth Factor Receptor	EGFR	0,5
195022	Interleukin 2 Receptor Beta chain	IL2RB	0,5
130788	Topoisomerase (DNA) II beta (180kD)	TOP2B	0,6
323948	SOX9 Protein	SOX9	0,6
183641	S100 calcium-binding protein Beta	S100B	0,6
246620	EST N53133	EST	0,6
231424	Glutathione S Transferase Pi	GSTP1	0,6

To search for genes whose expression profile was correlated with axillary lymph node status, a strong prognostic factor in breast cancer, the group of node-negative tumors (n = 19) was compared with the group of tumors with massive axillary extension (10 or more positive nodes). Furthermore, because survival decreases with the increase of the number of tumor-involved lymph nodes and because the expression measurements were quantitative, it was looked for a correlation between the expression levels of

these genes and the number of tumor-involved nodes (quantitative variables). Table 3b shows a list of the top 10 over- and underexpressed genes between these 2 groups. Most of these genes have not been previously reported as associated with node status, but some of these results are in agreement with literature data. The gene encoding the tyrosine kinase receptor ERBB2 was the most significantly overexpressed gene in node-positive tumors and displayed the highest correlation coefficient ($r = 0.68$; $p \leq 0.0001$).

TABLE 3B

Clone ID	Gene/Protein identity	Gene symbol	N-/10N+
129757	GATA-binding protein 3	GATA3	11,0
160963	Thrombospondin 1	THBS1	6,6
151475	Epidermal Growth Factor Receptor	EGFR	5,4
120916	Phosphodiesterase I	PDNP2	4,9
183030	Activating Transcription Factor 3	ATF3	4,6
211999	KIAA1075 protein	KIAA1075	4,5
110480	Nuclear Factor 1 A-type	NF1A	4,5
182264	P-Selectin	SELP	4,4
356763	Granzyme A	GZMA	4,3
214008	E-cadherin	CDH1	4,0
147016	ERBB2 Receptor Protein-Tyrosine Kinase	ERBB2	0,2
179197	Protein Phosphatase PP2A, 55 kD Subunit	PP2A BR gamma	0,2
231424	Glutathione S Transferase Pi	GSTP1	0,4
111461	SOX4 Protein	SOX4	0,4
195022	Interleukin 2 Receptor Beta chain	IL2RB	0,4
220451	Zinc Finger protein 144	ZNF144	0,5
125413	Mucin 1	MUC1	0,6
290007	CD44 antigen, epithelial form	CD44	0,6
108571	Retinoblastoma-Like 2 (p130)	RBL2	0,7
130788	Topoisomerase (DNA) II Beta (180kD)	TOP2B	0,7

Gene clusters

Gene clustering from Fig. 2b showed groups of genes with correlated expression across samples. When different clones represented the same gene, they were

clustered next to each other (red arrows). Correlation coefficients between gene pairs in the 34 tumors were often high (1% of the 13,041 gene pairs showed a correlation coefficient superior to 0.95 - not shown). An example of highly correlated gene expression is that of BCL2 and RBL2. Such correlated expression, although it has not been described in the literature, probably reflects a common mechanism of regulation for these two genes. Furthermore, these genes also exhibited significant correlated expression with other genes such as PPP2CA, AKT2, PRKCSH or TNFRSF6/FAS. In particular, a striking correlated expression between BCL2 and FAS could be observed ($r = 0.91$; data not shown). The exact meaning of this correlation is unknown, although it may reflect the necessary balance between apoptosis and anti-apoptosis for cell survival.

Although in human cancer the proportion of changes that is reflected at the RNA level is not known, monitoring gene expression patterns appears as a very promising way of increasing the knowledge of the disease. Several different types of cancer have been investigated using cDNA arrays: cervical (14), hepatocellular (15), ovarian (16), colon (17) and renal carcinomas (18), glioblastomas (19), melanomas (20) (21), rhabdomyosarcomas (22), acute leukemias (23) and lymphomas (24). In breast cancer, pioneering studies have yielded the first expression patterns (4, 25-31). They have in particular addressed the important issue of molecular differences in hormone responsive and non-responsive breast tumors. Thus, Yang et al. (28) and Hoch et al. (25) compared expression profiles of breast carcinoma cell lines known to represent these two categories and identified a few genes with differential expression. One of these genes was GATA3. In these studies, cell lines were mostly used and tumor samples were rarely

tested and generally in small numbers. The first study analyzing the expression profiles of a large series of breast cancers was published recently (32), but no correlation with clinical outcome was mentioned.

5 Several interesting points can be made based on the present experimentation. First, the differences in expression patterns among the tumors provided molecular transcriptional evidence of the histoclinical heterogeneity of breast cancer. This diversity was multifactorial, linked
10 to many different genes, highlighting the interest of high throughput analysis in this context. It was possible, with a hierarchical clustering program integrating the expression profiles, to separate normal breast tissue from most tumors and, moreover, to identify two different groups of tumors.
15 Most importantly, two different subgroups of tumors with a very distinct clinical outcome that could not be predicted with classical prognostic factors have been identified by clustering. Indeed, all these tumors had a theoretically bad prognosis as evaluated by current histoclinical tools. All
20 these patients would be at the present time treated with adjuvant chemotherapy, but without the capacity for the physicians to identify patients who will benefit of this treatment and those who will not benefit.

 Gene expression profiles were able to make this
25 discrimination. Such predictive tools have important therapeutic implications. Patients with features of poor prognosis are candidates for other treatment than standard chemotherapy, avoiding loss of time and toxicities related to first-line chemotherapy. These results suggest that the
30 histoclinical category of poor prognosis breast cancer, currently treated with adjuvant anthracyclin-based chemotherapy, groups together at least two molecularly distinct subgroups of tumors with different outcome which

would require distinct chemotherapy regimens. Expression profiles could thus provide a new and more accurate way of classifying breast tumors of poor prognosis and managing patients.

5 Similarly, despite molecular heterogeneity, significant correlations between the expression level of genes (GATA3, ERBB2) and histological tumor parameters were identified. The ER-positivity in breast cancer has been correlated with tumor differentiation, low proliferating
10 rate, favorable prognosis and response to hormonal therapy. The relation between hormone sensitivity of breast cancer and ER status is not perfect, and it is possible that some genes related to ER expression are more important than ER to characterize the hormone sensitive phenotype. These genes
15 could serve as predictive factors to guide the therapy.

 GATA3 mRNA expression was highly correlated with ER status. GATA3, which is not estrogen-regulated (25), is a transcription factor that could regulate the expression of genes involved in the ER-positive phenotype. Among the other
20 genes that were found associated with ER status during the experimental work leading to the present invention, some, such as MYB (10), stromelysin 3 (33), and CRABP2 (34), have been previously reported expressed at high levels in ER-positive breast tumors. The higher levels of TP53 mRNA in
25 ER-positive tumors studied were surprising, although in agreement with a recent study (27). Most studies concerning TP53 expression analyzed the protein level rather than the mRNA level, and TP53 protein levels are classically negatively correlated with the ER status (35). The high
30 expression of CRABP2 could be related to the better differentiated status of the ER-positive tumors. The low expression of the three immunity-related genes IL2RB, IL2RG and CD3G may be related to the low lymphoid infiltration in

these well differentiated tumors. ERBB2 high expression in breast cancer has been associated with a poor prognosis and some resistance to hormonal therapy and chemotherapy (36). It is involved in the regulation of cellular differentiation, adhesion, and motility. The motility-enhancing activity of ERBB2 (37) could be responsible for the increased metastatic potential and the unfavorable prognosis of the breast tumors that overexpress ERBB2. The low expression of E-cadherin and thrombospondin 1 in node-positive tumors are consistent with their putative role in different steps of metastatic spread: E-cadherin is an epithelial cell adhesion molecule whose disturbance is a prerequisite for the release of invasive cells in carcinomas (38) and thrombospondin 1 inhibits angiogenesis (39). Similarly, the high expression of the molecule surface antigen Mucin 1 in node-positive tumors (40) can reduce cell-cell interactions facilitating cell detachment and metastasis. CD44, encoding a transmembrane glycoprotein involved in cell adhesion and lymph node homing (41) was expressed at high levels in node-positive tumors as well as GSTP1 (Glutathione-S-Transferase Pi), recently reported associated with increased tumor size (27).

Second, there were a number of genes with highly correlated expression patterns. Gene correlations have already been reported with larger series of genes, essentially under dynamic experimental conditions (42) and recently in steady states (17). Here, correlations were based on expression profiles of a relatively small but selected series of genes and in steady states represented by different breast tumors. Gene correlations are potentially useful tools for cancer research in two ways: i)- they can provide information about the general regulation circuitry of a cancerous cell, allowing the identification of regulatory elements controlling expression networks; ii)- they offer the

possibility of reducing the complexity of the system analyzed by replacing, for example, the intensities of a large number of genes present in a gene cluster by their respective mean intensities.

5 Finally, these results highlight the great potential of cDNA array in cancer research. The gene expression profiles confirmed the heterogeneity of breast cancer, and most importantly allowed us to identify, among a series of poor prognosis breast tumors, two subtypes of the
10 disease not yet recognized with usual histoclinical parameters but with a different clinical outcome after adjuvant chemotherapy. Furthermore, the present invention allows detecting genes of which expression was correlated with classical prognostic factors.

15 Table 4 displays a library of polynucleotides SEQ ID NO :1 to SEQ ID NO : 468 corresponding to a population of polynucleotide sequences underexpressed or overexpressed in cells derived from tumors, more particularly breast tumors,
20 and their respective complements.

TABLE 4

Gene symbol	SET No	Name	Seq3'	Seq5'	Ref
HRB	1	hiv-1 rev binding protein	SEQ ID No:1		SEQ ID No:2
GATA1	2	gata-binding protein 1 (globin transcription factor 1)		SEQ ID No:3	SEQ ID No:4
TLK2	3	tousled-like kinase 2		SEQ ID No:5	SEQ ID No:6
EST T81919	4	ests, weakly similar to alu7_human alu subfamily sq sequence contamination warning entry [h.sapiens]	SEQ ID No:7	SEQ ID No:8	
CCND1	5	cyclin d1 (prad1: parathyroid adenomatosis 1)	SEQ ID No:9		SEQ ID No:10
STAT1	6	signal transducer and activator of transcription 1, 91kd		SEQ ID No:11	SEQ ID No:12
FGFR2	7	fibroblast growth factor receptor 2 (bacteria-expressed kinase, keratinocyte growth factor receptor, craniofacial dysostosis 1, crouzon syndrome, pfeiffer syndrome, jackson-weiss syndrome)	SEQ ID No:13	SEQ ID No:14	SEQ ID No:15
EST T89980	8	ests	SEQ ID No:16		
PPP3CC	9	protein phosphatase 3 (formerly 2b), catalytic subunit, gamma isoform (calcineurin a gamma)	SEQ ID No:17	SEQ ID No:18	SEQ ID No:19
EST T90726	10	ests	SEQ ID No:20	SEQ ID No:21	
SOX4	11	sry (sex determining region y)-box 4	SEQ ID No:22	SEQ ID No:23	SEQ ID No:24
RNF5	12	ring finger protein 5		SEQ ID No:25	SEQ ID No:26
AXL	13	axl receptor tyrosine kinase	SEQ ID No:27	SEQ ID No:28	SEQ ID No:29
CTSB	14	cathepsin b		SEQ ID No:30	SEQ ID No:31
PPP4C	15	protein phosphatase 4 (formerly x), catalytic subunit	SEQ ID No:32	SEQ ID No:33	SEQ ID No:34
EST T79867	16	ests	SEQ ID No:35		
FGFR4	17	fibroblast growth factor receptor 4	SEQ ID No:36	SEQ ID No:37	SEQ ID No:38
ENPP2	18	ectonucleotide pyrophosphatase/phosphodiesterase 2	SEQ ID No:39	SEQ ID No:40	SEQ ID No:41

Gene symbol	SET No	Name	Seq3'	Seq5'	Ref
		(autotaxin)			
RELA	19	v-rel avian reticuloendotheliosis viral oncogene homolog a (nuclear factor of kappa light polypeptide gene enhancer in b-cells 3 (p65))	SEQ ID No:42		SEQ ID No:43
ITK	20	il2-inducible t-cell kinase		SEQ ID No:44	SEQ ID No:45
TNXB	21	tenascin xb		SEQ ID No:46	SEQ ID No:47
CSF1	22	colony stimulating factor 1 (macrophage)	SEQ ID No:48	SEQ ID No:49	SEQ ID No:50
VIL2	23	villin 2 (ezrin)	SEQ ID No:51	SEQ ID No:52	SEQ ID No:53
APC	24	adenomatosis polyposis coli	SEQ ID No:54	SEQ ID No:55	SEQ ID No:56
MUC1	25	mucin 1, transmembrane		SEQ ID No:57	SEQ ID No:58
IGF2	26	insulin-like growth factor 2 (somatomedin a)	SEQ ID No:59	SEQ ID No:60	SEQ ID No:61
EMR1	27	egf-like module containing, mucin-like, hormone receptor-like sequence 1	SEQ ID No:62	SEQ ID No:63	SEQ ID No:64
KIAA0427	28	kiaa0427 gene product	SEQ ID No:65	SEQ ID No:66	SEQ ID No:67
SYK	29	spleen tyrosine kinase	SEQ ID No:68	SEQ ID No:69	SEQ ID No:70
IL7R	30	interleukin 7 receptor		SEQ ID No:71	SEQ ID No:72
MYC	31	v-myc avian myelocytomatosis viral oncogene homolog	SEQ ID No:73	SEQ ID No:74	SEQ ID No:75
GATA3	32	gata-binding protein 3	SEQ ID No:76	SEQ ID No:77	SEQ ID No:78
GRB7	33	growth factor receptor-bound protein 7	SEQ ID No:79	SEQ ID No:80	SEQ ID No:81
TOP2B	34	topoisomerase (dna) ii beta (180kd)		SEQ ID No:82	SEQ ID No:83
CASP4	35	caspase 4, apoptosis-related cysteine protease	SEQ ID No:84		SEQ ID No:85
TIMP2	36	tissue inhibitor of metalloproteinase 2		SEQ ID No:86	SEQ ID No:87
DDT	37	d-dopachrome tautomerase	SEQ ID No:88	SEQ ID No:89	SEQ ID No:90
PRL	38	prolactin	SEQ ID	SEQ ID	SEQ ID

Gene symbol	SET No	Name	Seq3'	Seq5'	Ref
			No:91	No:92	No:93
PRLR	39	prolactin receptor	SEQ ID No:94	SEQ ID No:95	SEQ ID No:96
IL2RB	40	interleukin 2 receptor, beta	SEQ ID No:97	SEQ ID No:98	SEQ ID No:99
GATA3	41	gata-binding protein 3	SEQ ID No:100	SEQ ID No:101	SEQ ID No:78
PGF	42	placental growth factor, vascular endothelial growth factor-related protein		SEQ ID No:102	SEQ ID No:103
UBE3A	43	ubiquitin protein ligase e3a (human papilloma virus e6-associated protein, angelman syndrome)		SEQ ID No:104	SEQ ID No:105
TC21	44	oncogene tc21	SEQ ID No:106	SEQ ID No:107	SEQ ID No:108
TIE	45	tyrosine kinase with immunoglobulin and epidermal growth factor homology domains		SEQ ID No:109	SEQ ID No:110
AMFR	46	autocrine motility factor receptor	SEQ ID No:111	SEQ ID No:112	SEQ ID No:113
EST R81127	47	homo sapiens mrna; cdna dkfzp434c136 (from clone dkfzp434c136)	SEQ ID No:114		
BCL2	48	b-cell cll/lymphoma 2	SEQ ID No:115	SEQ ID No:116	SEQ ID No:117
ERBB2	49	v-erb-b2 avian erythroblastic leukemia viral oncogene homolog 2 (neuro/glioblastoma derived oncogene homolog)		SEQ ID No:118	SEQ ID No:119
MDM2	50	mouse double minute 2, human homolog of; p53-binding protein		SEQ ID No:120	SEQ ID No:121
GATA3	51	gata-binding protein 3	SEQ ID No:122		SEQ ID No:78
HIP-55	52	src homology 3 domain-containing protein hip-55	SEQ ID No:123	SEQ ID No:124	SEQ ID No:125
CTSD	53	cathepsin d (lysosomal aspartyl protease)	SEQ ID No:126	SEQ ID No:127	SEQ ID No:128
IGF1R	54	insulin-like growth factor 1 receptor		SEQ ID No:129	SEQ ID No:130
INSR	55	insulin receptor		SEQ ID No:131	SEQ ID No:132
FOXO1A	56	forkhead box o1a (rhabdomyosarcoma)		SEQ ID No:133	SEQ ID No:134
EGFR	57	epidermal growth factor receptor	SEQ ID	SEQ ID	SEQ ID

Gene symbol	SET No	Name	Seq3'	Seq5'	Ref
		(avian erythroblastic leukemia viral (v-erb-b) oncogene homolog)	No:135	No:136	No:137
TEK	58	tek tyrosine kinase, endothelial (venous malformations, multiple cutaneous and mucosal)	SEQ ID No:138	SEQ ID No:139	SEQ ID No:140
TNFRSF6	59	tumor necrosis factor receptor superfamily, member 6	SEQ ID No:141	SEQ ID No:142	SEQ ID No:143
CDKN1A	60	cyclin-dependent kinase inhibitor 1a (p21, cip1)	SEQ ID No:144	SEQ ID No:145	SEQ ID No:146
PLA2G2A	61	phospholipase a2, group iia (platelets, synovial fluid)	SEQ ID No:147	SEQ ID No:148	SEQ ID No:149
GAPD	62	glyceraldehyde-3-phosphate dehydrogenase	SEQ ID No:150	SEQ ID No:151	SEQ ID No:152
JUNB	63	jun b proto-oncogene	SEQ ID No:153	SEQ ID No:154	SEQ ID No:155
CRABP2	64	cellular retinoic acid-binding protein 2	SEQ ID No:156	SEQ ID No:157	SEQ ID No:158
ACVRL1	65	activin a receptor type ii-like 1	SEQ ID No:159	SEQ ID No:160	SEQ ID No:161
RIL	66	lim domain protein		SEQ ID No:162	SEQ ID No:163
SHC1	67	shc (src homology 2 domain-containing) transforming protein 1		SEQ ID No:164	SEQ ID No:165
GAPD	68	glyceraldehyde-3-phosphate dehydrogenase	SEQ ID No:166	SEQ ID No:167	SEQ ID No:152
DES	69	desmin	SEQ ID No:168	SEQ ID No:169	SEQ ID No:170
CSNK2B	70	casein kinase 2, beta polypeptide		SEQ ID No:171	SEQ ID No:172
GLG1	71	golgi apparatus protein 1	SEQ ID No:173	SEQ ID No:174	SEQ ID No:175
EDNRB	72	endothelin receptor type b		SEQ ID No:176	SEQ ID No:177
GZMB	73	granzyme b (granzyme 2, cytotoxic t-lymphocyte-associated serine esterase 1)	SEQ ID No:178		SEQ ID No:179
FGFR1	74	fibroblast growth factor receptor 1 (fms-related tyrosine kinase 2, pfeiffer syndrome)	SEQ ID No:180	SEQ ID No:181	SEQ ID No:182
PPP2CA	75	protein phosphatase 2 (formerly 2a), catalytic subunit, alpha isoform		SEQ ID No:183	SEQ ID No:184
EST R55460	76	homo sapiens, clone image:4054156, mRNA, partial cds		SEQ ID No:185	

Gene symbol	SET No	Name	Seq3'	Seq5'	Ref
IGKC	77	immunoglobulin kappa constant	SEQ ID No:186		
MC1R	78	melanocortin 1 receptor (alpha melanocyte stimulating hormone receptor)		SEQ ID No:187	SEQ ID No:188
NRG1	79	neuregulin 1	SEQ ID No:189	SEQ ID No:190	SEQ ID No:191
CNTFR	80	ciliary neurotrophic factor receptor		SEQ ID No:192	SEQ ID No:193
ANG	81	angiogenin, ribonuclease, rnase a family, 5		SEQ ID No:194	SEQ ID No:195
ENG	82	endoglin (osler-rendu-weber syndrome 1)	SEQ ID No:196	SEQ ID No:197	SEQ ID No:198
EGF	83	epidermal growth factor (beta-urogastrone)	SEQ ID No:199		SEQ ID No:200
HRMT1L1	84	hmt1 (hmrnp methyltransferase, s. cerevisiae)-like 1	SEQ ID No:201	SEQ ID No:202	SEQ ID No:203
ETV4	85	ets variant gene 4 (ela enhancer-binding protein, elaf)	SEQ ID No:204	SEQ ID No:205	
ANXA11	86	annexin a11		SEQ ID No:206	SEQ ID No:207
PDGFRB	87	platelet-derived growth factor receptor, beta polypeptide		SEQ ID No:208	SEQ ID No:209
WBSCR14	88	williams-beuren syndrome chromosome region 14		SEQ ID No:210	SEQ ID No:211
CD74	89	cd74 antigen (invariant polypeptide of major histocompatibility complex, class ii antigen-associated)		SEQ ID No:212	SEQ ID No:213
ANXA7	90	annexin a7		SEQ ID No:214	SEQ ID No:215
THBS1	91	thrombospondin 1	SEQ ID No:216		SEQ ID No:217
PTPN2	92	protein tyrosine phosphatase, non-receptor type 2	SEQ ID No:218	SEQ ID No:219	SEQ ID No:220
EPHA2	93	epha2	SEQ ID No:221		SEQ ID No:222
TIMP1	94	tissue inhibitor of metalloproteinase 1 (erythroid potentiating activity, collagenase inhibitor)	SEQ ID No:223	SEQ ID No:224	SEQ ID No:225
EFNA1	95	ephrin-a1		SEQ ID No:226	SEQ ID No:227

Gene symbol	SET No	Name	Seq3'	Seq5'	Ref
EDNRA	96	endothelin receptor type a	SEQ ID No:228		SEQ ID No:229
GRB2	97	growth factor receptor-bound protein 2	SEQ ID No:230	SEQ ID No:231	SEQ ID No:232
JUND	98	jun d proto-oncogene	SEQ ID No:233		SEQ ID No:234
SMARCA2	99	swi/snf related, matrix associated, actin dependent regulator of chromatin, subfamily a, member 2	SEQ ID No:235	SEQ ID No:236	SEQ ID No:237
PPP2R2C	100	protein phosphatase 2 (formerly 2a), regulatory subunit b (pr 52), gamma isoform	SEQ ID No:238	SEQ ID No:239	
THBS3	101	thrombospondin 3	SEQ ID No:240		SEQ ID No:241
ACTG1	102	actin, gamma 1	SEQ ID No:242	SEQ ID No:243	SEQ ID No:244
ITGA6	103	integrin, alpha 6	SEQ ID No:245	SEQ ID No:246	SEQ ID No:247
RAD9	104	rad9 (s. pombe) homolog	SEQ ID No:248		SEQ ID No:249
ATF3	105	activating transcription factor 3	SEQ ID No:250	SEQ ID No:251	SEQ ID No:252
AKT2	106	v-akt murine thymoma viral oncogene homolog 2	SEQ ID No:253		SEQ ID No:254
S100B	107	s100 calcium-binding protein, beta (neural)		SEQ ID No:255	SEQ ID No:256
ABCB1	108	atp-binding cassette, sub-family b (mdr/tap), member 1	SEQ ID No:257		SEQ ID No:258
SELE	109	selectin e (endothelial adhesion molecule 1)	SEQ ID No:259	SEQ ID No:260	SEQ ID No:261
EGF	110	epidermal growth factor (beta-urogastrone)	SEQ ID No:262		SEQ ID No:200
PRKCSH	111	protein kinase c substrate 80k-h		SEQ ID No:263	SEQ ID No:264
DTR	112	diphtheria toxin receptor (heparin-binding epidermal growth factor-like growth factor)		SEQ ID No:265	SEQ ID No:266
ITGB2	113	integrin, beta 2 (antigen cd18 (p95), lymphocyte function-associated antigen 1; macrophage antigen 1 (mac-1) beta subunit)		SEQ ID No:267	SEQ ID No:268
NEO1	114	neogenin (chicken) homolog 1		SEQ ID No:269	SEQ ID No:270
POU2F2	115	pou domain, class 2, transcription	SEQ ID		SEQ ID

Gene symbol	SET No	Name	Seq3'	Seq5'	Ref
		factor 2	No:271		No:272
BIRC4	116	baculoviral iap repeat-containing 4	SEQ ID No:273		SEQ ID No:274
DAP3	117	death associated protein 3	SEQ ID No:275		SEQ ID No:276
GNRH1	118	gonadotropin-releasing hormone 1 (leutinizing-releasing hormone)		SEQ ID No:277	SEQ ID No:278
IL2RG	119	interleukin 2 receptor, gamma (severe combined immunodeficiency)	SEQ ID No:279	SEQ ID No:280	SEQ ID No:281
DAP3	120	death associated protein 3	SEQ ID No:282	SEQ ID No:283	SEQ ID No:276
PTK2	121	ptk2 protein tyrosine kinase 2		SEQ ID No:284	SEQ ID No:285
CDK4	122	cyclin-dependent kinase 4	SEQ ID No:286	SEQ ID No:287	SEQ ID No:288
BTF3	123	basic transcription factor 3	SEQ ID No:289		SEQ ID No:290
CSF1R	124	colony stimulating factor 1 receptor, formerly mcdonough feline sarcoma viral (v-fms) oncogene homolog	SEQ ID No:291		SEQ ID No:292
FLI1	125	friend leukemia virus integration 1	SEQ ID No:293	SEQ ID No:294	SEQ ID No:295
EST R97218	126	ests, highly similar to tvhume hepatocyte growth factor receptor precursor [h.sapiens]	SEQ ID No:296	SEQ ID No:297	
ETV5	127	ets variant gene 5 (ets-related molecule)	SEQ ID No:298	SEQ ID No:299	SEQ ID No:300
CDK4	128	cyclin-dependent kinase 4	SEQ ID No:301	SEQ ID No:302	SEQ ID No:288
YES1	129	v-yes-1 yamaguchi sarcoma viral oncogene homolog 1	SEQ ID No:303		SEQ ID No:304
IFI75	130	interferon-induced protein 75, 52kd	SEQ ID No:305	SEQ ID No:306	SEQ ID No:307
MYBL2	131	v-myb avian myeloblastosis viral oncogene homolog-like 2	SEQ ID No:308	SEQ ID No:309	SEQ ID No:310
TGFBR3	132	transforming growth factor, beta receptor iii (betaglycan, 300kd)	SEQ ID No:311	SEQ ID No:312	SEQ ID No:313
PRDX2	133	peroxiredoxin 2	SEQ ID No:314	SEQ ID No:315	SEQ ID No:316
FOS	134	v-fos fbj murine osteosarcoma viral oncogene homolog		SEQ ID No:317	SEQ ID No:318

Gene symbol	SET No	Name	Seq3'	Seq5'	Ref
RBBP7	135	retinoblastoma-binding protein 7	SEQ ID No:319	SEQ ID No:320	SEQ ID No:321
KIAA1075	136	kiaa1075 protein	SEQ ID No:322	SEQ ID No:323	
ABCC5	137	atp-binding cassette, sub-family c (cftr/mrp), member 5		SEQ ID No:324	SEQ ID No:325
CDH1	138	cadherin 1, type 1, e-cadherin (epithelial)	SEQ ID No:326	SEQ ID No:327	SEQ ID No:328
ZNF144	139	zinc finger protein 144 (mel-18)		SEQ ID No:329	SEQ ID No:330
MST1	140	macrophage stimulating 1 (hepatocyte growth factor-like)	SEQ ID No:331	SEQ ID No:332	SEQ ID No:333
GSTP1	141	glutathione s-transferase pi	SEQ ID No:334	SEQ ID No:335	SEQ ID No:336
BCL2	142	b-cell cll/lymphoma 2	SEQ ID No:337	SEQ ID No:338	SEQ ID No:117
PCNA	143	proliferating cell nuclear antigen	SEQ ID No:339	SEQ ID No:340	SEQ ID No:341
BS69	144	adenovirus 5 ela binding protein	SEQ ID No:342	SEQ ID No:343	SEQ ID No:344
MMP11	145	matrix metalloproteinase 11 (stromelysin 3)	SEQ ID No:345		SEQ ID No:346
MGC13071	146	hypothetical protein mgc13071	SEQ ID No:347	SEQ ID No:348	SEQ ID No:349
ILF2	147	interleukin enhancer binding factor 2, 45kd		SEQ ID No:350	SEQ ID No:351
FLJ11307	148	hypothetical protein flj11307	SEQ ID No:352		SEQ ID No:353
MYB	149	v-myb avian myeloblastosis viral oncogene homolog		SEQ ID No:354	SEQ ID No:355
ZNF9	150	zinc finger protein 9 (a cellular retroviral nucleic acid binding protein)	SEQ ID No:356		SEQ ID No:357
CREM	151	camp responsive element modulator	SEQ ID No:358	SEQ ID No:359	SEQ ID No:360
CTSB	152	cathepsin b	SEQ ID No:361		SEQ ID No:31
MLANA	153	melan-a	SEQ ID No:362	SEQ ID No:363	SEQ ID No:364
APR-1	154	apr-1 protein	SEQ ID No:365	SEQ ID No:366	SEQ ID No:367
ETV5	155	ets variant gene 5 (ets-related	SEQ ID	SEQ ID	SEQ ID

Gene symbol	SET No	Name	Seq3'	Seq5'	Ref
		molecule)	No:368	No:369	No:300
CD69	156	cd69 antigen (p60, early t-cell activation antigen)		SEQ ID No:370	SEQ ID No:371
TC21	157	oncogene tc21	SEQ ID No:372	SEQ ID No:373	SEQ ID No:108
CD44	158	cd44 antigen (homing function and indian blood group system)	SEQ ID No:374	SEQ ID No:375	SEQ ID No:376
CDKN3	159	cyclin-dependent kinase inhibitor 3 (cdk2-associated dual specificity phosphatase)	SEQ ID No:377	SEQ ID No:378	SEQ ID No:379
MXI1	160	max-interacting protein 1		SEQ ID No:380	SEQ ID No:381
HOXA5	161	homeo box a5	SEQ ID No:382	SEQ ID No:383	SEQ ID No:384
XBP1	162	x-box binding protein 1	SEQ ID No:385	SEQ ID No:386	SEQ ID No:387
TNFAIP3	163	tumor necrosis factor, alpha-induced protein 3	SEQ ID No:388	SEQ ID No:389	SEQ ID No:390
SRF	164	serum response factor (c-fos serum response element-binding transcription factor)	SEQ ID No:391	SEQ ID No:392	SEQ ID No:393
SOX9	165	sry (sex determining region y)-box 9 (campomelic dysplasia, autosomal sex-reversal)	SEQ ID No:394		SEQ ID No:395
CDH15	166	cadherin 15, m-cadherin (myotubule)	SEQ ID No:396	SEQ ID No:397	SEQ ID No:398
BCL2	167	b-cell cl1/lymphoma 2	SEQ ID No:399	SEQ ID No:400	SEQ ID No:117
EST W73386	168	ests	SEQ ID No:401		
GZMA	169	granzyme a (granzyme 1, cytotoxic t-lymphocyte-associated serine esterase 3)	SEQ ID No:402		SEQ ID No:403
FOS	170	v-fos fbj murine osteosarcoma viral oncogene homolog	SEQ ID No:404	SEQ ID No:405	SEQ ID No:318
ILF1	171	interleukin enhancer binding factor 1	SEQ ID No:406	SEQ ID No:407	SEQ ID No:408
ARHGDIA	172	rho gdp dissociation inhibitor (gdi) alpha	SEQ ID No:409	SEQ ID No:410	SEQ ID No:411
C4A	173	complement component 4a	SEQ ID No:412		SEQ ID No:413
CD3G	174	cd3g antigen, gamma polypeptide (tit3 complex)	SEQ ID No:414	SEQ ID No:415	SEQ ID No:416

Gene symbol	SET No	Name	Seq3'	Seq5'	Ref
RELB	175	v-rel avian reticuloendotheliosis viral oncogene homolog b (nuclear factor of kappa light polypeptide gene enhancer in b-cells 3)	SEQ ID No:417	SEQ ID No:418	SEQ ID No:419
ESR1	176	estrogen receptor 1	SEQ ID No:420	SEQ ID No:421	SEQ ID No:422
PBX1	177	pre-b-cell leukemia transcription factor 1	SEQ ID No:423	SEQ ID No:424	SEQ ID No:425
GLI3	178	gli-kruppel family member gli3 (greig cephalopolysyndactyly syndrome)	SEQ ID No:426	SEQ ID No:427	SEQ ID No:428
ILF1	179	interleukin enhancer binding factor 1	SEQ ID No:429		SEQ ID No:408
EST T80406	180	similar to SP:S36648 S36648 RB2/P130 PROTEIN	SEQ ID No:430		
EST T95640	181	similar to gb:M16336 T-CELL SURFACE ANTIGEN CD2	SEQ ID No:431		
EST R28523	182	similar to placental lactogen (CSH1)	SEQ ID No:432		
ESTs H21879 & H21880	183	Homo sapiens plasminogen activator (PLAT)	SEQ ID No:433	SEQ ID No:434	
ESTs H24628 & H24592	184	Homo sapiens aminoacylase 1 (ACY1)	SEQ ID No:435	SEQ ID No:436	
EST H28056	185	Homo sapiens E74-like factor 1 (ets domain transcription factor) (ELF1)	SEQ ID No:437		
ESTs H30141 & H27466	186	Homo sapiens selectin P	SEQ ID No:438	SEQ ID No:439	
ESTs H42957 & H42888	187	Human interleukin 3 receptor (hIL-3Ra)	SEQ ID No:440	SEQ ID No:441	
EST H57912	188	Human tumor protein p53 (Li-Fraumeni syndrome) (TP53)	SEQ ID No:442	SEQ ID No:443	
ERBB2	189	v-erb-b2 avian erythroblastic leukemia viral oncogene homolog 2 (neuro/glioblastoma derived oncogene homolog) (ERBB2)	SEQ ID No:444		
ZNF144	190	zinc finger protein 144 (Mel-18) (ZNF144)	SEQ ID No:445		

Gene symbol	SET No	Name	Seq3'	Seq5'	Ref
MARK3	191	MAP/microtubule affinity-regulating kinase 3 (MARK3)	SEQ ID No:446	SEQ ID No:447	
EST N68536	192	EST N68536 MAX-interacting protein 1 (MXI1)	SEQ ID No:448		
EST R81126	193	EST R81126 lymphotoxin beta receptor (LTBR)		SEQ ID No:449	
POU2F2	194	(POU2F2)		SEQ ID No:450	
CASP1	195	caspase 4, apoptosis-related cysteine protease (CASP4) (ex CASP1)		SEQ ID No:451	
HRB	196	syndecan 1 (SDC1) (ex HRB)		SEQ ID No:452	
ITGB2	197	integrin, beta 2 (antigen CD18 (p95), lymphocyte function-associated antigen 1; macrophage antigen 1 (mac-1) beta subunit) (ITGB2)	SEQ ID No:453		
MGST1	198	protein phosphatase 1, catalytic subunit, alpha isoform (PPP1CA) (ex MGST1)		SEQ ID No:454	
PPP2CA	199	protein phosphatase 2 (formerly 2A), catalytic subunit, alpha isoform (PPP2CA)	SEQ ID No:455		
SUI1	200	S100 calcium-binding protein A11 (calgizzarin) (S100A11)		SEQ ID No:456	
GZMA	201	granzyme A (granzyme 1, cytotoxic T-lymphocyte-associated serine esterase 3) (GZMA)		SEQ ID No:457	
EDN1	202	endothelin 1 (EDN1)	SEQ ID No:458		
PTPN6	203	protein tyrosine phosphatase, non-receptor type 6 (PTPN6)	SEQ ID No:459		
TFAP4	204	transcription factor AP-4 (activating enhancer binding protein 4) (TFAP4)	SEQ ID No:460		
CCND2	205	cyclin D2 (CCND2)	SEQ ID No:461		
JUP	206	junction plakoglobin (JUP)	SEQ ID No:462		
GADD45A	207	growth arrest and DNA-damage-inducible, alpha (GADD45A)	SEQ ID No:463		
nm23	208	non-metastatic cells 1, protein (NM23A) expressed in (NME1)	SEQ ID No:464		
BBC1	209	ribosomal protein L13 (RPL13) (ex	SEQ ID		

Gene symbol	SET No	Name	Seq3'	Seq5'	Ref
		BBC1)	No:465		
VEGFB	210	vascular endothelial growth factor B (VEGFB)	SEQ ID No:466		
LAMR1	211	laminin receptor 1 (67kD, ribosomal protein SA) (LAMR1)	SEQ ID No:467		
CSH1	212	Chorionic somatomammotropin hormone 1 (placental lactogen) = LACTOGEN Precursor		SEQ ID No:468	

Tables 5A and 5B hereunder displays two subpopulations corresponding to the 5 top overexpressed and to the 5 top underexpressed polynucleotide sequences particularly interesting to distinguish healthy person from cancer patient.

TABLE 5A

overexpressed genes : top 5

Gene symbol	SET No	Name	Seq3'	Seq5'	Ref
GATA3	32	gata-binding protein 3	SEQ ID No:76	SEQ ID No:77	SEQ ID No:78
GZMB	73	granzyme b (granzyme 2, cytotoxic t-lymphocyte-associated serine esterase 1)	SEQ ID No:178		SEQ ID No:179
MYBL2	131	v-myb avian myeloblastosis viral oncogene homolog-like 2	SEQ ID No:308	SEQ ID No:309	SEQ ID No:310
MMP11	145	matrix metalloproteinase 11 (stromelysin 3)	SEQ ID No:345		SEQ ID No:346
EST T95640	181	similar to gb:M16336 T-CELL SURFACE ANTIGEN CD2	SEQ ID No:431		

TABLE 5B
underexpressed genes : top 5

Gene symbol	SET No	Name	Seq3'	Seq5'	Ref
PRL	38	prolactin	SEQ ID No:91	SEQ ID No:92	SEQ ID No:93
TEK	58	tek tyrosine kinase, endothelial (venous malformations, multiple cutaneous and mucosal)	SEQ ID No:138	SEQ ID No:139	SEQ ID No:140
PLA2G2A	61	phospholipase a2, group iia (platelets, synovial fluid)	SEQ ID No:147	SEQ ID No:148	SEQ ID No:149
DES	69	desmin	SEQ ID No:168	SEQ ID No:169	SEQ ID No:170
EST R28523	182	similar to placental lactogen (CSH1)	SEQ ID No:432		

5

Table 6 hereunder relate to sub populations of polynucleotide sequences interesting to detect hormone sensitive tumors allowing to distinguish between ER+ and ER- samples.

10

TABLE 6

Gene symbol	SET No	Name	Seq3'	Seq5'	Ref
SOX4	11	sry (sex determining region y)-box 4	SEQ ID No:22	SEQ ID No:23	SEQ ID No:24
IGF2	26	insulin-like growth factor 2 (somatomedin a)	SEQ ID No:59	SEQ ID No:60	SEQ ID No:61
GATA3	32	gata-binding protein 3	SEQ ID No:76	SEQ ID No:77	SEQ ID No:78
TOP2B	34	topoisomerase (dna) ii beta (180kd)		SEQ ID No:82	SEQ ID No:83
IL2RB	40	interleukin 2 receptor, beta	SEQ ID No:97	SEQ ID No:98	SEQ ID No:99
EGFR	57	epidermal growth factor receptor (avian erythroblastic leukemia viral (v-erb-b) oncogene homolog)	SEQ ID No:135	SEQ ID No:136	SEQ ID No:137
CRABP2	64	cellular retinoic acid-binding protein 2	SEQ ID No:156	SEQ ID No:157	SEQ ID No:158

Gene symbol	SET No	Name	Seq3'	Seq5'	Ref
S100B	107	s100 calcium-binding protein, beta (neural)		SEQ ID No:255	SEQ ID No:256
IL2RG	119	interleukin 2 receptor, gamma (severe combined immunodeficiency)	SEQ ID No:279	SEQ ID No:280	SEQ ID No:281
KIAA1075	136	kiaa1075 protein	SEQ ID No:322	SEQ ID No:323	
MST1	140	macrophage stimulating 1 (hepatocyte growth factor-like)	SEQ ID No:331	SEQ ID No:332	SEQ ID No:333
GSTP1	141	glutathione s-transferase pi	SEQ ID No:334	SEQ ID No:335	SEQ ID No:336
MMP11	145	matrix metalloproteinase (stromelysin 3)	SEQ ID No:345		SEQ ID No:346
FLJ11307	148	hypothetical protein flj11307	SEQ ID No:352		SEQ ID No:353
MYB	149	v-myb avian myeloblastosis viral oncogene homolog		SEQ ID No:354	SEQ ID No:355
XBP1	162	x-box binding protein 1	SEQ ID No:385	SEQ ID No:386	SEQ ID No:387
SOX9	165	sry (sex determining region y)-box 9 (campomelic dysplasia, autosomal sex-reversal)	SEQ ID No:394		SEQ ID No:395
GZMA	169	granzyme a (granzyme 1, cytotoxic t-lymphocyte-associated serine esterase 3)	SEQ ID No:402		SEQ ID No:403
CD3G	174	cd3g antigen, gamma polypeptide (tit3 complex)	SEQ ID No:414	SEQ ID No:415	SEQ ID No:416
EST H57912	188	Human tumor protein p53 (Li-Fraumeni syndrome) (TP53)	SEQ ID No:442		

Tables 6A et 6B hereunder relate to two sub populations of polynucleotide sequences particularly interesting to detect hormone sensitive tumors allowing to distinguish between ER+ and ER- samples

Table 6A

overexpressed genes : top 5

ER + / ER -

Gene symbol	SET No	Name	Seq3'	Seq5'	Ref
GATA3	32	gata-binding protein 3	SEQ ID No:76	SEQ ID No:77	SEQ ID No:78
KIAA1075	136	kiaa1075 protein	SEQ ID No:322	SEQ ID No:323	
MMP11	145	matrix metalloproteinase 11 (stromelysin 3)	SEQ ID No:345		SEQ ID No:346
MYB	149	v-myb avian myeloblastosis viral oncogene homolog		SEQ ID No:354	SEQ ID No:355
GZMA	169	granzyme a (granzyme 1, cytotoxic t-lymphocyte-associated serine esterase 3)	SEQ ID No:402		SEQ ID No:403

5

Table 6B

underexpressed genes : top 5

Gene symbol	SET No	Name	Seq3'	Seq5'	Ref
SOX4	11	sry (sex determining region y)-box 4	SEQ ID No:22	SEQ ID No:23	SEQ ID No:24
IL2RB	40	interleukin 2 receptor, beta	SEQ ID No:97	SEQ ID No:98	SEQ ID No:99
EGFR	57	epidermal growth factor receptor (avian erythroblastic leukemia viral (v-erb-b) oncogene homolog)	SEQ ID No:135	SEQ ID No:136	SEQ ID No:137
IL2RG	119	interleukin 2 receptor, gamma (severe combined immunodeficiency)	SEQ ID No:279	SEQ ID No:280	SEQ ID No:281
CD3G	174	cd3g antigen, gamma polypeptide (tit3 complex)	SEQ ID No:414	SEQ ID No:415	SEQ ID No:416

10

Tables 7 hereunder relates to subpopulations of polynucleotide sequences interesting to distinguish tumors with lymph node from tumors with no lymph node.

TABLE 7

Gene symbol	SET No	Name	Seq3'	Seq5'	Ref
EST T89980	8	ests	SEQ ID No:16		
SOX4	11	sry (sex determining region y)-box 4	SEQ ID No:22	SEQ ID No:23	SEQ ID No:24
ENPP2	18	ectonucleotide pyrophosphatase/phosphodiesterase 2 (autotaxin)	SEQ ID No:39	SEQ ID No:40	SEQ ID No:41
MUC1	25	mucin 1, transmembrane		SEQ ID No:57	SEQ ID No:58
GATA3	32	gata-binding protein 3	SEQ ID No:76	SEQ ID No:77	SEQ ID No:78
TOP2B	34	topoisomerase (dna) ii beta (180kd)		SEQ ID No:82	SEQ ID No:83
IL2RB	40	interleukin 2 receptor, beta	SEQ ID No:97	SEQ ID No:98	SEQ ID No:99
ERBB2	49	v-erb-b2 avian erythroblastic leukemia viral oncogene homolog 2 (neuro/glioblastoma derived oncogene homolog)		SEQ ID No:118	SEQ ID No:119
EGFR	57	epidermal growth factor receptor (avian erythroblastic leukemia viral (v-erb-b) oncogene homolog)	SEQ ID No:135	SEQ ID No:136	SEQ ID No:137
THBS1	91	thrombospondin 1	SEQ ID No:216		SEQ ID No:217
PPP2R2C	100	protein phosphatase 2 (formerly 2a), regulatory subunit b (pr 52), gamma isoform	SEQ ID No:238	SEQ ID No:239	
ATF3	105	activating transcription factor 3	SEQ ID No:250	SEQ ID No:251	SEQ ID No:252
KIAA1075	136	kiaa1075 protein	SEQ ID No:322	SEQ ID No:323	
CDH1	138	cadherin 1, type 1, e-cadherin (epithelial)	SEQ ID No:326	SEQ ID No:327	SEQ ID No:328
ZNF144	139	zinc finger protein 144 (mel-18)		SEQ ID No:329	SEQ ID No:330
GSTP1	141	glutathione s-transferase pi	SEQ ID No:334	SEQ ID No:335	SEQ ID No:336
CD44	158	cd44 antigen (homing function and indian blood group system)	SEQ ID No:374	SEQ ID No:375	SEQ ID No:376
GZMA	169	granzyme a (granzyme 1, cytotoxic t-lymphocyte-associated serine esterase 3)	SEQ ID No:402		SEQ ID No:403

Gene symbol	SET No	Name	Seq3'	Seq5'	Ref
EST T80406	180	similar to SP:S36648 S36648 RB2/P130 PROTEIN	SEQ ID No:430		
ESTs H30141 & H27466	186	Homo sapiens selectin P	SEQ ID No:438	SEQ ID No:439	

Tables 7A and 7B hereunder relate to two sub populations of polynucleotide sequences particularly interesting to distinguish tumors with lymph node from tumors with no lymph node.

TABLE 7A

Overexpressed genes : top 5

Gene symbol	SET No	Name	Seq3'	Seq5'	Ref
ENPP2	18	ectonucleotide pyrophosphatase/phosphodiesterase 2 (autotaxin)	SEQ ID No:39	SEQ ID No:40	SEQ ID No:41
GATA3	32	gata-binding protein 3	SEQ ID No:76	SEQ ID No:77	SEQ ID No:78
EGFR	57	epidermal growth factor receptor (avian erythroblastic leukemia viral (v-erb-b) oncogene homolog)	SEQ ID No:135	SEQ ID No:136	SEQ ID No:137
THBS1	91	thrombospondin 1	SEQ ID No:216		SEQ ID No:217
ATF3	105	activating transcription factor 3	SEQ ID No:250	SEQ ID No:251	SEQ ID No:252

TABLE 7B

Underexpressed genes : top 5

Gene symbol	SET No	Name	Seq3'	Seq5'	Ref
SOX4	11	sry (sex determining region Y)-box 4	SEQ ID No:22	SEQ ID No:23	SEQ ID No:24
IL2RB	40	interleukin 2 receptor, beta	SEQ ID No:97	SEQ ID No:98	SEQ ID No:99

Gene symbol	SET No	Name	Seq3'	Seq5'	Ref
ERBB2	49	v-erb-b2 avian erythroblastic leukemia viral oncogene homolog 2 (neuro/glioblastoma derived oncogene homolog)		SEQ ID No:118	SEQ ID No:119
PPP2R2C	100	protein phosphatase 2 (formerly 2a), regulatory subunit b (pr 52), gamma isoform	SEQ ID No:238	SEQ ID No:239	
GSTP1	141	glutathione s-transferase pi	SEQ ID No:334	SEQ ID No:335	SEQ ID No:336

Tables 8, 8A and 8B hereunder relates to sub populations of polynucleotide sequences particularly interesting to distinguish tumors sensitive to antracycline from tumors unsensitive to antracycline.

TABLE 8

A1 /A2

Gene symbol	SET No	Name	Seq3'	Seq5'	Ref
SOX4	11	sry (sex determining region y)-box 4	SEQ ID No:22	SEQ ID No:23	SEQ ID No:24
CSF1	22	colony stimulating factor 1 (macrophage)	SEQ ID No:48	SEQ ID No:49	SEQ ID No:50
VIL2	23	villin 2 (ezrin)	SEQ ID No:51	SEQ ID No:52	SEQ ID No:53
IGF2	26	insulin-like growth factor 2 (somatomedin a)	SEQ ID No:59	SEQ ID No:60	SEQ ID No:61
KIAA0427	28	kiaa0427 gene product	SEQ ID No:65	SEQ ID No:66	SEQ ID No:67
MYC	31	v-myc avian myelocytomatosis viral oncogene homolog	SEQ ID No:73	SEQ ID No:74	SEQ ID No:75
GATA3	32	gata-binding protein 3	SEQ ID No:76	SEQ ID No:77	SEQ ID No:78
TOP2B	34	topoisomerase (dna) ii beta (180kd)		SEQ ID No:82	SEQ ID No:83
ERBB2	49	v-erb-b2 avian erythroblastic leukemia viral oncogene homolog 2 (neuro/glioblastoma derived oncogene homolog)		SEQ ID No:118	SEQ ID No:119
EGFR	57	epidermal growth factor receptor (avian erythroblastic leukemia viral (v-erb-b) oncogene homolog)	SEQ ID No:135	SEQ ID No:136	SEQ ID No:137

Gene symbol	SET No	Name	Seq3'	Seq5'	Ref
CRABP2	64	cellular retinoic acid-binding protein 2	SEQ ID No:156	SEQ ID No:157	SEQ ID No:158
GZMB	73	granzyme b (granzyme 2, cytotoxic t-lymphocyte-associated serine esterase 1)	SEQ ID No:178		SEQ ID No:179
IGKC	77	immunoglobulin kappa constant	SEQ ID No:186		
ANG	81	angiogenin, ribonuclease, rnase a family, 5		SEQ ID No:194	SEQ ID No:195
EFNA1	95	ephrin-a1		SEQ ID No:226	SEQ ID No:227
MYBL2	131	v-myb avian myeloblastosis viral oncogene homolog-like 2	SEQ ID No:308	SEQ ID No:309	SEQ ID No:310
CDH1	138	cadherin 1, type 1, e-cadherin (epithelial)	SEQ ID No:326	SEQ ID No:327	SEQ ID No:328
MST1	140	macrophage stimulating 1 (hepatocyte growth factor-like)	SEQ ID No:331	SEQ ID No:332	SEQ ID No:333
MYB	149	v-myb avian myeloblastosis viral oncogene homolog		SEQ ID No:354	SEQ ID No:355
XBP1	162	x-box binding protein 1	SEQ ID No:385	SEQ ID No:386	SEQ ID No:387
SRF	164	serum response factor (c-fos serum response element-binding transcription factor)	SEQ ID No:391	SEQ ID No:392	SEQ ID No:393
SOX9	165	sry (sex determining region y)-box 9 (campomelic dysplasia, autosomal sex-reversal)	SEQ ID No:394		SEQ ID No:395
ESTs H21879 & H21880	183	Homo sapiens plasminogen activator (PLAT)	SEQ ID No:433	SEQ ID No:434	

Tables 8A and 8B hereunder relate to two sub populations of polynucleotide sequences particularly interesting to distinguish tumors sensitive to antracycline from tumors unsensitive to antracycline.

TABLEAU 8A

overexpressed genes : top 5

Gene symbol	SET No	Name	Seq3'	Seq5'	Ref
GATA3	32	gata-binding protein 3	SEQ ID No:76	SEQ ID No:77	SEQ ID No:78
KIAA1075	136	kiaa1075 protein	SEQ ID No:322	SEQ ID No:323	
MMP11	145	matrix metalloproteinase 11 (stromelysin 3)	SEQ ID No:345		SEQ ID No:346
MYB	149	v-myb avian myeloblastosis viral oncogene homolog		SEQ ID No:354	SEQ ID No:355
GZMA	169	granzyme a (granzyme 1, cytotoxic t-lymphocyte-associated serine esterase 3)	SEQ ID No:402		SEQ ID No:403

5

TABLEAU 8B

underexpressed genes : top 5

Gene symbol	SET No	Name	Seq3'	Seq5'	Ref
SOX4	11	sry (sex determining region y)-box 4	SEQ ID No:22	SEQ ID No:23	SEQ ID No:24
IL2RB	40	interleukin 2 receptor, beta	SEQ ID No:97	SEQ ID No:98	SEQ ID No:99
EGFR	57	epidermal growth factor receptor (avian erythroblastic leukemia viral (v-erb-b) oncogene homolog)	SEQ ID No:135	SEQ ID No:136	SEQ ID No:137
IL2RG	119	interleukin 2 receptor, gamma (severe combined immunodeficiency)	SEQ ID No:279	SEQ ID No:280	SEQ ID No:281
CD3G	174	cd3g antigen, gamma polypeptide (tit3 complex)	SEQ ID No:414	SEQ ID No:415	SEQ ID No:416

10

Tables 9, 9A and 9B hereunder relates to sub populations of polynucleotide sequences particularly interesting in classifying good and poor prognosis primary breast tumors.

TABLE 9

Gene symbol	SET No	Name	Seq3'	Seq5'	Ref
CTSB	14	cathepsin b		SEQ ID No:30	SEQ ID No:31
VIL2	23	villin 2 (ezrin)	SEQ ID No:51	SEQ ID No:52	SEQ ID No:53
MUC1	25	mucin 1, transmembrane		SEQ ID No:57	SEQ ID No:58
EMR1	27	egf-like module containing, mucin-like, hormone receptor-like sequence 1	SEQ ID No:62	SEQ ID No:63	SEQ ID No:64
KIAA0427	28	kiaa0427 gene product	SEQ ID No:65	SEQ ID No:66	SEQ ID No:67
GATA3	32	gata-binding protein 3	SEQ ID No:76	SEQ ID No:77	SEQ ID No:78
PRLR	39	prolactin receptor	SEQ ID No:94	SEQ ID No:95	SEQ ID No:96
GATA3	41	gata-binding protein 3	SEQ ID No:100	SEQ ID No:101	SEQ ID No:78
TC21	44	oncogene tc21	SEQ ID No:106	SEQ ID No:107	SEQ ID No:108
BCL2	48	b-cell cll/lymphoma 2	SEQ ID No:115	SEQ ID No:116	SEQ ID No:117
GATA3	51	gata-binding protein 3	SEQ ID No:122		SEQ ID No:78
CRABP2	64	cellular retinoic acid-binding protein 2	SEQ ID No:156	SEQ ID No:157	SEQ ID No:158
ANG	81	angiogenin, ribonuclease, rnase a family, 5		SEQ ID No:194	SEQ ID No:195
EGF	83	epidermal growth factor (beta-urogastrone)	SEQ ID No:199		SEQ ID No:200
THBS1	91	thrombospondin 1	SEQ ID No:216		SEQ ID No:217
EDNRA	96	endothelin receptor type a	SEQ ID No:228		SEQ ID No:229
SMARCA2	99	swi/snf related, matrix associated, actin dependent regulator of chromatin, subfamily a, member 2	SEQ ID No:235	SEQ ID No:236	SEQ ID No:237
ABCB1	108	atp-binding cassette, subfamily b (mdr/tap), member 1	SEQ ID No:257		SEQ ID No:258
EGF	110	epidermal growth factor (beta-urogastrone)	SEQ ID No:262		SEQ ID No:200
BIRC4	116	baculoviral iap repeat-containing 4	SEQ ID No:273		SEQ ID No:274
DAP3	117	death associated protein 3	SEQ ID		SEQ ID

Gene symbol	SET No	Name	Seq3'	Seq5'	Ref
			No:275		No:276
GNRH1	118	gonadotropin-releasing hormone 1 (leutinizing-releasing hormone)		SEQ ID No:277	SEQ ID No:278
DAP3	120	death associated protein 3	SEQ ID No:282	SEQ ID No:283	SEQ ID No:276
EST R97218	126	ests, highly similar to tvhume hepatocyte growth factor receptor precursor [h.sapiens]	SEQ ID No:296	SEQ ID No:297	
BCL2	142	b-cell cll/lymphoma 2	SEQ ID No:337	SEQ ID No:338	SEQ ID No:117
BS69	144	adenovirus 5 e1a binding protein	SEQ ID No:342	SEQ ID No:343	SEQ ID No:344
MYB	149	v-myb avian myeloblastosis viral oncogene homolog		SEQ ID No:354	SEQ ID No:355
CTSB	152	cathepsin b	SEQ ID No:361		SEQ ID No:31
MLANA	153	melan-a	SEQ ID No:362	SEQ ID No:363	SEQ ID No:364
APR-1	154	apr-1 protein	SEQ ID No:365	SEQ ID No:366	SEQ ID No:367
TC21	157	oncogene tc21	SEQ ID No:372	SEQ ID No:373	SEQ ID No:108
CDKN3	159	cyclin-dependent kinase inhibitor 3 (cdk2-associated dual specificity phosphatase)	SEQ ID No:377	SEQ ID No:378	SEQ ID No:379
XBP1	162	x-box binding protein 1	SEQ ID No:385	SEQ ID No:386	SEQ ID No:387
CDH15	166	cadherin 15, m-cadherin (myotubule)	SEQ ID No:396	SEQ ID No:397	SEQ ID No:398
BCL2	167	b-cell cll/lymphoma 2	SEQ ID No:399	SEQ ID No:400	SEQ ID No:117
EST W73386	168	ests	SEQ ID No:401		
ILF1	171	interleukin enhancer binding factor 1	SEQ ID No:406	SEQ ID No:407	SEQ ID No:408
ARHGDIA	172	rho gdp dissociation inhibitor (gdi) alpha	SEQ ID No:409	SEQ ID No:410	SEQ ID No:411
C4A	173	complement component 4a	SEQ ID No:412		SEQ ID No:413
ESR1	176	estrogen receptor 1	SEQ ID No:420	SEQ ID No:421	SEQ ID No:422
PBX1	177	pre-b-cell leukemia transcription factor 1	SEQ ID No:423	SEQ ID No:424	SEQ ID No:425
GLI3	178	gli-kruppel family member gli3 (greig)	SEQ ID No:426	SEQ ID No:427	SEQ ID No:428

Gene symbol	SET No	Name	Seq3'	Seq5'	Ref
		cephalopolysyndactyly syndrome)			
ILF1	179	interleukin enhancer binding factor 1	SEQ ID No:429		SEQ ID No:408
ESTs H24628 & H24592	184	Homo sapiens aminoacylase 1 (ACY1).	SEQ ID No:435	SEQ ID No:436	
EST H28056	185	Homo sapiens E74-like factor 1 (ets domain transcription factor) (ELF1)	SEQ ID No:437		

TABLE 9A

Gene symbol	SET N°	Name	Seq3'	Seq5'	Ref
VIL2	23	villin 2 (ezrin)	SEQ ID No:51	SEQ ID No:52	SEQ ID No:53
MUC1	25	mucin 1, transmembrane		SEQ ID No:57	SEQ ID No:58
GATA3	32	gata-binding protein 3	SEQ ID No:76	SEQ ID No:77	SEQ ID No:78
GATA3	41	gata-binding protein 3	SEQ ID No:100	SEQ ID No:101	SEQ ID No:78
BCL2	48	b-cell cll/lymphoma 2	SEQ ID No:115	SEQ ID No:116	SEQ ID No:117
GATA3	51	gata-binding protein 3	SEQ ID No:122		SEQ ID No:78
CRABP2	64	cellular retinoic acid-binding protein 2	SEQ ID No:156	SEQ ID No:157	SEQ ID No:158
ANG	81	angiogenin, ribonuclease, rnase a family, 5		SEQ ID No:194	SEQ ID No:195
EGF	83	epidermal growth factor (beta-urogastrone)	SEQ ID No:199		SEQ ID No:200
THBS1	91	thrombospondin 1	SEQ ID No:216		SEQ ID No:217
SMARCA2	99	swi/snf related, matrix associated, actin dependent regulator of chromatin, subfamily a, member 2	SEQ ID No:235	SEQ ID No:236	SEQ ID No:237
EGF	110	epidermal growth factor (beta-urogastrone)	SEQ ID No:262		SEQ ID No:200
BIRC4	116	baculoviral iap repeat-containing 4	SEQ ID No:273		SEQ ID No:274
BCL2	142	b-cell cll/lymphoma 2	SEQ ID No:337	SEQ ID No:338	SEQ ID No:117

Gene symbol	SET N°	Name	Seq3'	Seq5'	Ref
BS69	144	adenovirus 5 ela binding protein	SEQ ID No:342	SEQ ID No:343	SEQ ID No:344
MYB	149	v-myb avian myeloblastosis viral oncogene homolog		SEQ ID No:354	SEQ ID No:355
XBP1	162	x-box binding protein 1	SEQ ID No:385	SEQ ID No:386	SEQ ID No:387
BCL2	167	b-cell cll/lymphoma 2	SEQ ID No:399	SEQ ID No:400	SEQ ID No:117
ILF1	171	interleukin enhancer binding factor 1	SEQ ID No:406	SEQ ID No:407	SEQ ID No:408
ARHGDI A	172	rho gdp dissociation inhibitor (gdi) alpha	SEQ ID No:409	SEQ ID No:410	SEQ ID No:411
C4A	173	complement component 4a	SEQ ID No:412		SEQ ID No:413
ESR1	176	estrogen receptor 1	SEQ ID No:420	SEQ ID No:421	SEQ ID No:422
PBX1	177	pre-b-cell leukemia transcription factor 1	SEQ ID No:423	SEQ ID No:424	SEQ ID No:425
GLI3	178	gli-kruppel family member gli3 (greig cephalopolysyndactyly syndrome)	SEQ ID No:426	SEQ ID No:427	SEQ ID No:428
ILF1	179	interleukin enhancer binding factor 1	SEQ ID No:429		SEQ ID No:408
ESTs H24628 & H24592	184	Homo sapiens aminoacylase 1 (ACY1).	SEQ ID No:435	SEQ ID No:436	
EST H28056	185	Homo sapiens E74-like factor 1 (ets domain transcription factor) (ELF1)	SEQ ID No:437		

TABLE 9B

Gene symbol	SET No	Name	Seq3'	Seq5'	Ref
CTSB	14	cathepsin b		SEQ ID No:30	SEQ ID No:31
EMR1	27	egf-like module containing, mucin-like, hormone receptor-like sequence 1	SEQ ID No:62	SEQ ID No:63	SEQ ID No:64
KIAA0427	28	kiaa0427 gene product	SEQ ID No:65	SEQ ID No:66	SEQ ID No:67
PRLR	39	prolactin receptor	SEQ ID No:94	SEQ ID No:95	SEQ ID No:96
TC21	44	oncogene tc21	SEQ ID No:106	SEQ ID No:107	SEQ ID No:108

Gene symbol	SET No	Name	Seq3'	Seq5'	Ref
EDNRA	96	endothelin receptor type a	SEQ ID No:228		SEQ ID No:229
ABCB1	108	atp-binding cassette, sub-family b (mdr/tap), member 1	SEQ ID No:257		SEQ ID No:258
DAP3	117	death associated protein 3	SEQ ID No:275		SEQ ID No:276
GNRH1	118	gonadotropin-releasing hormone 1 (leutinizing-releasing hormone)		SEQ ID No:277	SEQ ID No:278
DAP3	120	death associated protein 3	SEQ ID No:282	SEQ ID No:283	SEQ ID No:276
EST R97218	126	ests, highly similar to tvhume hepatocyte growth factor receptor precursor [h.sapiens]	SEQ ID No:296	SEQ ID No:297	
CTSB	152	cathepsin b	SEQ ID No:361		SEQ ID No:31
MLANA	153	melan-a	SEQ ID No:362	SEQ ID No:363	SEQ ID No:364
APR-1	154	apr-1 protein	SEQ ID No:365	SEQ ID No:366	SEQ ID No:367
TC21	157	oncogene tc21	SEQ ID No:372	SEQ ID No:373	SEQ ID No:108
CDKN3	159	cyclin-dependent kinase inhibitor 3 (cdk2-associated dual specificity phosphatase)	SEQ ID No:377	SEQ ID No:378	SEQ ID No:379
CDH15	166	cadherin 15, m-cadherin (myotubule)	SEQ ID No:396	SEQ ID No:397	SEQ ID No:398
EST W73386	168	ests	SEQ ID No:401		

Overexpression of genes detected by using at least one polynucleotide sequence selected among those included in each one of predefined polynucleotide sequences indicated in table 9A combined with underexpression of genes detected with at least one polynucleotide sequence selected among those included in each one of predefined polynucleotide sequence indicated on table 9B present a Good outcome.

So, a preferred DNA array according to the invention comprises at least one polynucleotide sequence selected among those included in each one of predefined polynucleotide sequences indicated in table 9A and at least

one polynucleotide sequence selected among those included in each one of predefined polynucleotide sequence indicated on table 9B.

5 Such DNA arrays are particularly useful to distinguish patients having a high risk (Bad Outcome) from those having a good pronostic (Good Outcome).

TABLE 10

CORRELATION BETWEEN SEQ ID NO AS FILED WITH US PROVISIONAL APPLICATION N° 60/254,090
and SEQ ID NO FILED WITH PCT APPLICATION

Symbole gène	N°	Nom	Image	Seq3' US PROV LISTING	Seq5' US PROV LISTING	Seq3' PCT Listing	Seq5' PCT Listing	(mRNA) PCT Listing
GATA3	1	GATA-binding protein 3 (GATA3)	129757	SEQ ID No : 1		SEQ ID No:76	SEQ ID No:77	SEQ ID No:78
MYB	2	v-myb avian myeloblastosis viral oncogene homolog (MYB)	248613		SEQ ID No : 2	0	SEQ ID No:354	SEQ ID No:355
KIAA1075	3	KIAA1075 protein	211999	SEQ ID No : 3	SEQ ID No : 4	SEQ ID No:322	SEQ ID No:323	0
STMY3	4	matrix metalloproteinase 11 (stromelysin 3) (MMP11) (ex STMY3)	235947	SEQ ID No : 5		SEQ ID No:345	0	SEQ ID No:346
HGFL	5	macrophage-stimulating protein (MST1) (ex HGFL)	229839	SEQ ID No : 6	SEQ ID No : 7	SEQ ID No:331	SEQ ID No:332	SEQ ID No:333
CRABP	6	cellular retinoic acid-binding protein 2 (CRABP2)	153275	SEQ ID No : 8	SEQ ID No : 9	SEQ ID No:156	SEQ ID No:157	SEQ ID No:158
XBP1	7	X-box binding protein 1 (XBP1)	301950	SEQ ID No : 10	SEQ ID No : 11	SEQ ID No:385	SEQ ID No:386	SEQ ID No:387
TP53	8	tumor protein p53 (Li-Fraumeni syndrome) (TP53)	205314		SEQ ID No : 12	SEQ ID No:442	0	0
IGF2	9	insulin-like growth factor 2 (somatomedin A) (IGF2)	126233	SEQ ID No : 13	SEQ ID No : 14	SEQ ID No:59	SEQ ID No:60	SEQ ID No:61
CD3G	10	CD3G antigen, gamma polypeptide (TIT3 complex) (CD3G)	66322	SEQ ID No : 15	SEQ ID No : 16	SEQ ID No:414	SEQ ID No:415	SEQ ID No:416
IL2RG	11	interleukin 2 receptor, gamma (severe combined immunodeficiency) (IL2RG)	195022	SEQ ID No : 17	SEQ ID No : 18	SEQ ID No:279	SEQ ID No:280	SEQ ID No:281
SOX4	12	SRV (sex determining region Y)-box 4 (SOX4)	111461	SEQ ID No : 19	SEQ ID No : 20	SEQ ID No:22	SEQ ID No:23	SEQ ID No:24
EGFR	13	epidermal growth factor receptor (avian erythroblastic)	151475	SEQ ID No : 21	SEQ ID No : 22	SEQ ID No:135	SEQ ID No:136	SEQ ID No:137
TOP2B	14	topoIIb mRNA for topoisomerase IIb.	130788		SEQ ID No : 23	0	SEQ ID No:82	SEQ ID No:83
S100B	15	S100 calcium-binding protein, beta (neural) (S100B)	183641		SEQ ID No : 24	0	SEQ ID No:255	SEQ ID No:256
EST N53133	16	EST N53133	246620	SEQ ID No : 25		SEQ ID No:352	0	SEQ ID No:353
GSTP1	17	glutathione S-transferase pi (GSTP1)	231424	SEQ ID No : 26	SEQ ID No : 27	SEQ ID No:334	SEQ ID No:335	SEQ ID No:336
THBS1	18	thrombospondin 1 (THBS1)	160963	SEQ ID No : 28		SEQ ID No:216	0	SEQ ID No:217

Symbole gène	N°	Nom	Image	Seq3' US PROV LISTING	Seq5' US PROV LISTING	Seq3' PCT Listing	Seq5' PCT Listing	(mRNA) PCT Listing
PDNP2	19	actonucleotide pyrophosphatase/phosphodiesterase 2 (autotaxin) (ENPP2) (ex PDNP2)	120916	SEQ ID No : 29	SEQ ID No : 30	SEQ ID No:39	SEQ ID No:40	SEQ ID No:41
ATF3	20	activating transcription factor 3 (ATF3)	183030	SEQ ID No : 31	SEQ ID No : 32	SEQ ID No:250	SEQ ID No:251	SEQ ID No:252
NF1A	21	(ex NF1A)	110480	SEQ ID No : 33		SEQ ID No:16	0	0
SELP	22	selectin P (granule membrane protein 140kD, antigen CD62) (SELP)	182264		SEQ ID No : 34	SEQ ID No:438	SEQ ID No:439	0
CDH1	23	cadherin 1, E-cadherin (epithelial) (CDH1)	214008	SEQ ID No : 35	SEQ ID No : 36	SEQ ID No:326	SEQ ID No:327	SEQ ID No:328
ERBB2	24	v-erb-b2 avian erythroblastic leukemia viral oncogene homolog 2 (neuro/glioblastoma derived oncogene homolog) (ERBB2)	147016	SEQ ID No : 37		0	SEQ ID No:118	SEQ ID No:119
PP2A BR gamma	25	(PP2A BR gamma)	179197	SEQ ID No : 38	SEQ ID No : 39	SEQ ID No:238	SEQ ID No:239	0
ZNF144	26	zinc finger protein 144 (Mel-18) (ZNF144)	220451	SEQ ID No : 40	SEQ ID No : 41	0	SEQ ID No:329	SEQ ID No:330
MUC1	27	mucin 1, transmembrane (MUC1)	125413		SEQ ID No : 42	0	SEQ ID No:57	SEQ ID No:58
CD44	28	CD44E (epithelial form)	290007	SEQ ID No : 43	SEQ ID No : 44	SEQ ID No:374	SEQ ID No:375	SEQ ID No:376
PLA2G2A	29	phospholipase A2, group IIA (platelets, synovial fluid) (PLA2G2A), nuclear gene encoding mitochondrial protein	152802	SEQ ID No : 45	SEQ ID No : 46	SEQ ID No:147	SEQ ID No:148	SEQ ID No:149
ACVRL1	30	activin A receptor type II-like 1 (ACVRL1)	153350	SEQ ID No : 47	SEQ ID No : 48	SEQ ID No:159	SEQ ID No:160	SEQ ID No:161
AXL	31	AXL receptor tyrosine kinase (AXL)	112500	SEQ ID No : 49	SEQ ID No : 50	SEQ ID No:27	SEQ ID No:28	SEQ ID No:29
PKU-ALPHA	32	KU-alpha, partial cds (new gene symbol Tik2)	109569		SEQ ID No : 51	0	SEQ ID No:5	SEQ ID No:6
ABCC5	33	ATP-binding cassette, sub-family C (CFTR/MRP), member 5 (ABCC5)	212366		SEQ ID No : 52	0	SEQ ID No:324	SEQ ID No:325
EDNRB	34	endothelin receptor type B (EDNRB), transcript variant1	154244		SEQ ID No : 53	0	SEQ ID No:176	SEQ ID No:177
DTR	35	diphtheria toxin receptor (heparin-binding epidermal)	187547		SEQ ID No : 54	0	SEQ ID No:265	SEQ ID No:266
IGF1R	36	insulin-like growth factor 1 receptor (IGF1R)	150361		SEQ ID No : 55	0	SEQ ID No:129	SEQ ID No:130
KIAA0427	37	KIAA0427	127507	SEQ ID No : 56	SEQ ID No : 57	SEQ ID No:65	SEQ ID No:66	SEQ ID No:67
CD69	38	CD69 antigen (p60, early T-cell activation antigen)	276727		SEQ ID No : 58	0	SEQ ID No:370	SEQ ID No:371
FGFR4	39	fibroblast growth factor receptor 4 (FGFR4)	116781	SEQ ID No : 59	SEQ ID No : 60	SEQ ID No:36	SEQ ID No:37	SEQ ID No:38
EST T85683	40	EST T85683 cathepsin B (CTSB)	112622		SEQ ID No : 61	0	SEQ ID No:30	SEQ ID No:31
EST R00569	41	EST R00569 IL2-inducible T-cell kinase (ITK)	123871		SEQ ID No : 62	0	SEQ ID No:44	SEQ ID No:45

Symbole gène	N°	Nom	Image	Seq3' US PROV LISTING	Seq5' US PROV LISTING	Seq3' PCT Listing	Seq5' PCT Listing	(mRNA) PCT Listing
TGFR3	42	transforming growth factor, beta receptor III (TGFR3)	208118	SEQ ID No : 63	SEQ ID No : 64	SEQ ID No:311	SEQ ID No:312	SEQ ID No:313
INSR	43	insulin receptor (INSR)	151149		SEQ ID No : 65	0	SEQ ID No:131	SEQ ID No:132
MARK3	44	MAP/microtubule affinity-regulating kinase 3 (MARK3)	110599	SEQ ID No : 66	SEQ ID No : 67	#N/A	#N/A	#N/A
TIMP2	45	tissue inhibitor of metalloproteinase 2 (TIMP2)	131504		SEQ ID No : 68	0	SEQ ID No:86	SEQ ID No:87
EST R85557	46	EST R85557 thrombospondin 3 (THBS3)	180219	SEQ ID No : 69		SEQ ID No:240	0	SEQ ID No:241
GNRH1	47	gonadotropin-releasing hormone 1 (GNRH1)	192688		SEQ ID No : 70	0	SEQ ID No:277	SEQ ID No:278
FGFR2	48	fibroblast growth factor receptor 2 (FGFR2)	110387	SEQ ID No : 71	SEQ ID No : 72	SEQ ID No:13	SEQ ID No:14	SEQ ID No:15
NFKB2	49	NFKB2	114879	SEQ ID No : 73		SEQ ID No:35	0	0
VIL2	50	villin 2 (ezrin) (VIL2)	124701	SEQ ID No : 74	SEQ ID No : 75	SEQ ID No:51	SEQ ID No:52	SEQ ID No:53
ENG	51	endoglin (ENG)	156979	SEQ ID No : 76	SEQ ID No : 77	SEQ ID No:196	SEQ ID No:197	SEQ ID No:198
EPHA2	52	EphA2 (EPHA2)	162004	SEQ ID No : 78		SEQ ID No:221	0	SEQ ID No:222
CREM	53	cAMP responsive element modulator (CREM)	258584	SEQ ID No : 79	SEQ ID No : 80	SEQ ID No:358	SEQ ID No:359	SEQ ID No:360
ETV5-a	54	ets variant gene 5 (ETV5)	270549	SEQ ID No : 81	SEQ ID No : 82	SEQ ID No:368	SEQ ID No:369	SEQ ID No:300
EST N68536	55	EST N68536 MAX-interacting protein 1 (MXI1)	298242	SEQ ID No : 83	SEQ ID No : 84	0	SEQ ID No:380	SEQ ID No:381
EST R81126	56	EST R81126 lymphotoxin beta receptor (LTBR)	146635	SEQ ID No : 85	SEQ ID No : 86	SEQ ID No:114	0	0
POU2F2	57	(POU2F2)	188393	SEQ ID No : 87	SEQ ID No : 88	SEQ ID No:271	0	SEQ ID No:272
FLI1	58	Friend leukemia virus integration 1 (FLI1)	198144	SEQ ID No : 89	SEQ ID No : 90	SEQ ID No:293	SEQ ID No:294	SEQ ID No:295
TIE	59	tyrosine kinase with immunoglobulin and epidermal growth factor homology domains (TIE)	144081		SEQ ID No : 91	0	SEQ ID No:109	SEQ ID No:110
PRLR	60	prolactin receptor (PRLR)	138788	SEQ ID No : 92	SEQ ID No : 93	SEQ ID No:94	SEQ ID No:95	SEQ ID No:96
PPP3CA	61	protein phosphatase 3 (formerly 2B), catalytic subunit, gamma isoform (calcineurin A gamma) (PPP3CC) (ex PPP3CA)	110481	SEQ ID No : 94	SEQ ID No : 95	SEQ ID No:17	SEQ ID No:18	SEQ ID No:19
PTPN2	62	protein tyrosine phosphatase, non-receptor type 2 (PTPN2)	161451	SEQ ID No : 96	SEQ ID No : 97	SEQ ID No:218	SEQ ID No:219	SEQ ID No:220
PGF	63	placental growth factor, vascular endothelial growth factor-related protein (PGF)	139326		SEQ ID No : 98	0	SEQ ID No:102	SEQ ID No:103
TNFAIP3	64	tumor necrosis factor, alpha-induced	309943	SEQ ID No : 99		SEQ ID No:388	SEQ ID No:389	SEQ ID No:390

Symbole gène	N°	Nom	Image	Seq3' US PROV LISTING	Seq5' US PROV LISTING	Seq3' PCT Listing	Seq5' PCT Listing	(mRNA) PCT Listing
		protein 3 (TNFAIP3)						
PHB	65	PHB (prohibitin)	236008	SEQ ID No : 100		SEQ ID No:347	SEQ ID No:348	SEQ ID No:349
RIL	66	LIM domain protein (RIL)	153446		SEQ ID No : 101	0	SEQ ID No:162	SEQ ID No:163
MYBL2	67	v-myb avian myeloblastosis viral oncogene homolog-like 2 (MYBL2)	207378	SEQ ID No : 102	SEQ ID No : 103	SEQ ID No:308	SEQ ID No:309	SEQ ID No:310
RELB	68	v-rel avian reticuloendotheliosis virus oncogene homolog B (nuclear factor of kappa light polypeptide gene enhancer in B-cells 3) (RELB)	66969	SEQ ID No : 104	SEQ ID No : 105	SEQ ID No:417	SEQ ID No:418	SEQ ID No:419
EST R97218	69	Est R97218	200394	SEQ ID No : 106		SEQ ID No:296	SEQ ID No:297	0
GZMH	70	granzyme B (granzyme 2, cytotoxic T-lymphocyte-associated serine esterase 1) (GZMB) (ex GZMH)	154343	SEQ ID No : 107		SEQ ID No:178	0	SEQ ID No:179
MYC	71	c-myc proto-oncogene	129438	SEQ ID No : 108	SEQ ID No : 109	SEQ ID No:73	SEQ ID No:74	SEQ ID No:75
CASP1	72	caspase 4, apoptosis-related cysteine protease (CASP4) (ex CASP1)	131502		SEQ ID No : 110	SEQ ID No:84	0	SEQ ID No:85
SYK	73	spleen tyrosine kinase (SYK)	128142	SEQ ID No : 111	SEQ ID No : 112	SEQ ID No:68	SEQ ID No:69	SEQ ID No:70
EST H27202	74	EST H27202 transcription factor E1AF gene	158347	SEQ ID No : 113	SEQ ID No : 114	SEQ ID No:204	SEQ ID No:205	0
HRB	75	syndecan 1 (SDC1) (ex HRB)	108490	SEQ ID No : 115	SEQ ID No : 116	SEQ ID No:1	0	SEQ ID No:2
SHC1	76	p85shc (SHC)	153548		SEQ ID No : 117	0	SEQ ID No:164	SEQ ID No:165
CSF1	77	colony stimulating factor 1 (CSF1)	124554	SEQ ID No : 118	SEQ ID No : 119	SEQ ID No:48	SEQ ID No:49	SEQ ID No:50
UBE3A	78	ubiquitin protein ligase E3A (UBE3A)	141924		SEQ ID No : 120	0	SEQ ID No:104	SEQ ID No:105
FKHR	79	forkhead box O1A (rhabdomyosarcoma) (FOXO1A) (ex FKHR)	151247		SEQ ID No : 121	0	SEQ ID No:133	SEQ ID No:134
CSF1R	80	colony stimulating factor 1 receptor (CSF1R)	196282	SEQ ID No : 122		SEQ ID No:291	0	SEQ ID No:292
IFI75	81	interferon-induced protein 75 (IFI75)	205612	SEQ ID No : 123	SEQ ID No : 124	SEQ ID No:305	SEQ ID No:306	SEQ ID No:307
GATA1	82	GATA-binding protein 1 (globin transcription factor 1) (GATA1)	109093		SEQ ID No : 125	0	SEQ ID No:3	SEQ ID No:4
STAT1	83	signal transducer and activator of transcription 1 (STAT1)	110101		SEQ ID No : 126	0	SEQ ID No:11	SEQ ID No:12
CREBBP	84	CREB binding protein (Rubinstein-Taybi syndrome) (CREBBP)	109677	SEQ ID No : 127	SEQ ID No : 128	SEQ ID No:7	SEQ ID No:8	0
IL7R	85	interleukin 7 receptor (IL7R)	129059		SEQ ID No : 129	0	SEQ ID No:71	SEQ ID No:72
ANXA7	86	annexin A7 (ANXA7)	160580		SEQ ID No : 130	0	SEQ ID No:214	SEQ ID No:215

Symbole gène	N°	Nom	Image	Seq3' US PROV LISTING	Seq5' US PROV LISTING	Seq3' PCT Listing	Seq5' PCT Listing	(mRNA) PCT Listing
TNXA	87	tenascin XA (TNXA)	124340		SEQ ID No : 131	0	SEQ ID No:46	SEQ ID No:47
CNBP1	88	zinc finger protein 9 (a cellular retroviral nucleic acid binding protein) (ZNF9) (ex CNBP1)	251963	SEQ ID No : 132		SEQ ID No:356	0	SEQ ID No:357
CDK4-a	89	cyclin-dependent kinase 4 (CDK4)	204586	SEQ ID No : 133	SEQ ID No : 134	SEQ ID No:301	SEQ ID No:302	SEQ ID No:288
CSNK2B	90	gene for casein kinase II subunit beta (EC 2.7.1.37)	153879		SEQ ID No : 135	0	SEQ ID No:171	SEQ ID No:172
EFNA1	91	ephrin-A1 (EFNA1)	162997		SEQ ID No : 136	0	SEQ ID No:226	SEQ ID No:227
SELE	92	selectin E (endothelial adhesion molecule 1) (SELE)	186132	SEQ ID No : 137	SEQ ID No : 138	SEQ ID No:259	SEQ ID No:260	SEQ ID No:261
APC	93	adenomatosis polyposis coli (APC)	125294	SEQ ID No : 139	SEQ ID No : 140	SEQ ID No:54	SEQ ID No:55	SEQ ID No:56
FAK	94	PTK2 protein tyrosine kinase 2 (PTK2) (ex FAK)	195731		SEQ ID No : 141	0	SEQ ID No:284	SEQ ID No:285
FOS-a	95	v-fos FBJ murine osteosarcoma viral oncogene homolog (FOS)	208717		SEQ ID No : 142	0	SEQ ID No:317	SEQ ID No:318
FGFR1	96	fibroblast growth factor receptor (FGFR)	154472	SEQ ID No : 143	SEQ ID No : 144	SEQ ID No:180	SEQ ID No:181	SEQ ID No:182
MC1R	97	melanocortin 1 receptor (alpha melanocyte stimulating hormone receptor) (MC1R)	155691		SEQ ID No : 145	0	SEQ ID No:187	SEQ ID No:188
PCNA	98	proliferating cell nuclear antigen (PCNA)	232941	SEQ ID No : 146	SEQ ID No : 147	SEQ ID No:339	SEQ ID No:340	SEQ ID No:341
DDT	99	D-dopachrome tautomerase (DDT)	132109	SEQ ID No : 148	SEQ ID No : 149	SEQ ID No:88	SEQ ID No:89	SEQ ID No:90
GRB2	100	growth factor receptor-bound protein 2 (GRB2)	172152	SEQ ID No : 150	SEQ ID No : 151	SEQ ID No:230	SEQ ID No:231	SEQ ID No:232
AMFR	101	autocrine motility factor receptor (AMFR)	146280	SEQ ID No : 152	SEQ ID No : 153	SEQ ID No:111	SEQ ID No:112	SEQ ID No:113
ITGB2	102	integrin, beta 2 (antigen CD18 (p95), lymphocyte function-associated antigen 1; macrophage antigen 1 (mac-1) beta subunit) (ITGB2)	187822	SEQ ID No : 154		0	SEQ ID No:267	SEQ ID No:268
JUND	103	Jun D proto-oncogene (JUND)	175421	SEQ ID No : 155		SEQ ID No:233	0	SEQ ID No:234
NF45	104	interleukin enhancer binding factor 2 (ILF2) (ex NF45)	243907		SEQ ID No : 156	0	SEQ ID No:350	SEQ ID No:351
PPP4C	105	protein phosphatase 4 (formerly X) (PPP4C)	114097	SEQ ID No : 157	SEQ ID No : 158	SEQ ID No:32	SEQ ID No:33	SEQ ID No:34
EMS1	106	ATX1 (antioxidant protein 1, yeast) homolog 1 (ATOX1) (ex EMS1)	149172	SEQ ID No : 159		SEQ ID No:123	SEQ ID No:124	SEQ ID No:125
BCL2	107	B-cell CLL/lymphoma 2 (BCL2), nuclear gene encoding mitochondrial protein, transcript variant alpha	147002	SEQ ID No : 160	SEQ ID No : 161	SEQ ID No:115	SEQ ID No:116	SEQ ID No:117
MGST1	108	protein phosphatase 1, catalytic subunit,	182610	SEQ ID No : 162	SEQ ID No : 163	SEQ ID No:248	0	SEQ ID No:249

Symbole gène	N°	Nom	Image	Seq3' US PROV LISTING	Seq5' US PROV LISTING	Seq3' PCT Listing	Seq5' PCT Listing	(mRNA) PCT Listing
		alpha isoform (PPP1CA) (ex MGST1)						
PDGFRB	109	platelet-derived growth factor receptor, beta polypeptide (PDGFRB)	158976		SEQ ID No : 164	0	SEQ ID No:208	SEQ ID No:209
ANXA11	110	annexin A11 (ANXA11)	158992		SEQ ID No : 165	0	SEQ ID No:206	SEQ ID No:207
GPX1	111	histocompatibility class II antigen gamma chain (CD74) (ex GPX1 Glutathion S transférase)	159809		SEQ ID No : 166	0	SEQ ID No:212	SEQ ID No:213
CFR-1	112	Golgi apparatus protein 1 (GLG1) (ex CFR-1)	153974	SEQ ID No : 167	SEQ ID No : 168	SEQ ID No:173	SEQ ID No:174	SEQ ID No:175
BTF3L3	113	basic transcription factor 3 (BTF3)	195889	SEQ ID No : 169		SEQ ID No:289	0	SEQ ID No:290
EST R55460	114	EST R55460	154997		SEQ ID No : 170	0	SEQ ID No:185	0
AKT2	115	v-akt murine thymoma viral oncogene homolog 2 (AKT2)	183552	SEQ ID No : 171		SEQ ID No:253	0	SEQ ID No:254
CDKN1A	116	cyclin-dependent kinase inhibitor (CDKN1A)	152524	SEQ ID No : 172	SEQ ID No : 173	SEQ ID No:144	SEQ ID No:145	SEQ ID No:146
PPP2CA	117	protein phosphatase 2 (formerly 2A), catalytic subunit, alpha isoform (PPP2CA)	154685	SEQ ID No : 174	SEQ ID No : 175	0	SEQ ID No:183	SEQ ID No:184
MDM2	118	mouse double minute 2, human homolog of p53-binding protein (MDM2), transcript variant MDM2	148052	SEQ ID No : 176		0	SEQ ID No:120	SEQ ID No:121
TNFRSF6	119	tumor necrosis factor receptor superfamily, member 6 (TNFRSF6)	151767	SEQ ID No : 177	SEQ ID No : 178	SEQ ID No:141	SEQ ID No:142	SEQ ID No:143
CNTRF	120	ciliary neurotrophic factor receptor (CNTRF)	156431		SEQ ID No : 179	0	SEQ ID No:192	SEQ ID No:193
JUNB	121	Jun B proto-oncogene (JUNB)	153213	SEQ ID No : 180	SEQ ID No : 181	SEQ ID No:153	SEQ ID No:154	SEQ ID No:155
CCND1	122	cyclin D1 (PRAD1; parathyroid adenomatosis 1) (CCND1)	110022	SEQ ID No : 182		SEQ ID No:9	0	SEQ ID No:10
TDPX1	123	peroxiredoxin 2 (PRDX2) (ex TDPX1)	208439	SEQ ID No : 183	SEQ ID No : 184	SEQ ID No:314	SEQ ID No:315	SEQ ID No:316
GRB7	124	growth factor receptor-bound protein 7 (GRB7)	130323	SEQ ID No : 185	SEQ ID No : 186	SEQ ID No:79	SEQ ID No:80	SEQ ID No:81
RBBP7	125	retinoblastoma-binding protein 7 (RBBP7)	210874	SEQ ID No : 187	SEQ ID No : 188	SEQ ID No:319	SEQ ID No:320	SEQ ID No:321
TIMP1	126	tissue inhibitor of metalloproteinase 1 (matrilysin 1) (TIMP1)	162246	SEQ ID No : 189	SEQ ID No : 190	SEQ ID No:223	SEQ ID No:224	SEQ ID No:225
YES1	127	v-yes-1 Yamaguchi sarcoma viral oncogene homolog 1 (YES1)	204634	SEQ ID No : 191		SEQ ID No:303	0	SEQ ID No:304
RNF5	128	ring finger protein 5 (RNF5)	112098		SEQ ID No : 192	0	SEQ ID No:25	SEQ ID No:26
PRKCSH	129	protein kinase C substrate 80K-H (PRKCSH)	187232		SEQ ID No : 193	0	SEQ ID No:263	SEQ ID No:264

Symbole gène	N°	Nom	Image	Seq3' US PROV LISTING	Seq5' US PROV LISTING	Seq3' PCT Listing	Seq5' PCT Listing	(mRNA) PCT Listing
CTSD	130	cathepsin D (lysosomal aspartyl protease) (CTSD)	149401	SEQ ID No : 194	SEQ ID No : 195	SEQ ID No:126	SEQ ID No:127	SEQ ID No:128
NEO1	131	neogenin (chicken) homolog 1 (NEO1)	188380		SEQ ID No : 196	0	SEQ ID No:269	SEQ ID No:270
GAPD-a	132	glyceraldehyde-3-phosphate dehydrogenase (GAPD)	152847	SEQ ID No : 197		SEQ ID No:150	SEQ ID No:151	SEQ ID No:152
ACTG1	133	actin, gamma 1 (ACTG1)	182291	SEQ ID No : 198	SEQ ID No : 199	SEQ ID No:242	SEQ ID No:243	SEQ ID No:244
ITGA6	134	integrin, alpha 6 (ITGA6)	182431	SEQ ID No : 200	SEQ ID No : 201	SEQ ID No:245	SEQ ID No:246	SEQ ID No:247
GAPD-b	135	glyceraldehyde-3-phosphate dehydrogenase (GAPD)	153607	SEQ ID No : 202	SEQ ID No : 203	SEQ ID No:166	SEQ ID No:167	SEQ ID No:152
ETV5-b	136	ets variant gene 5 (ets-related molecule) (ETV5)	203394	SEQ ID No : 204	SEQ ID No : 205	SEQ ID No:298	SEQ ID No:299	SEQ ID No:300
CDK4-b	137	cyclin-dependent kinase 4 (CDK4)	195800	SEQ ID No : 206	SEQ ID No : 207	SEQ ID No:286	SEQ ID No:287	SEQ ID No:288
FOS-b	138	v-fos FBJ murine osteosarcoma viral oncogene homolog (FOS)	363796	SEQ ID No : 208	SEQ ID No : 209	SEQ ID No:404	SEQ ID No:405	SEQ ID No:318
HOXA5	139	homeobox protein (HOX-1.3) (ex Hox A5)	300564	SEQ ID No : 210	SEQ ID No : 211	SEQ ID No:382	SEQ ID No:383	SEQ ID No:384
RELA	140	NF-kappa-B transcription factor p65 DNA binding subunit (ex RELa)	122056	SEQ ID No : 212		SEQ ID No:42	0	SEQ ID No:43
SUI1	141	S100 calcium-binding protein A11 (calgizarin) (S100A11)	155345	SEQ ID No : 213	SEQ ID No : 214	SEQ ID No:186	0	0
ANG	142	angiotensin, ribonuclease, RNase A family, 5 (ANG)	156720		SEQ ID No : 215	0	SEQ ID No:194	SEQ ID No:195
ITGA6	143	integrin, alpha 6 (ITGA6)	182431	SEQ ID No : 216	SEQ ID No : 217	SEQ ID No:245	SEQ ID No:246	SEQ ID No:247
PRMT2	144	HMT1 (hnRNP methyltransferase, S. cerevisiae)-like 1 (HRMT1L1) (ex PRMT2)	158038	SEQ ID No : 218	SEQ ID No : 219	SEQ ID No:201	SEQ ID No:202	SEQ ID No:203
EST R55460	145	EST R55460	154997		SEQ ID No : 220	0	SEQ ID No:185	0
GZMA	146	granzyme A (granzyme 1, cytotoxic T- lymphocyte-associated serine esterase 3) (GZMA)	356763	SEQ ID No : 221	SEQ ID No : 222	SEQ ID No:402	0	SEQ ID No:403
SOX9	147	SRX (sex-determining region Y)-box 9 (campomelic dysplasia, autosomal sex- reversal) (SOX9)	323948	SEQ ID No : 223		SEQ ID No:394	0	SEQ ID No:395
SRF	148	serum response factor (c-fos serum response element-binding transcription factor) (SRF)	321329		SEQ ID No : 224	SEQ ID No:391	SEQ ID No:392	SEQ ID No:393
EDN1	149	endothelin 1 (EDN1)	153424	SEQ ID No : 225		#N/A	#N/A	#N/A
PTPN6	150	protein tyrosine phosphatase, non-receptor type 6 (PTPN6)	66778	SEQ ID No : 226		#N/A	#N/A	#N/A
TFAP4	151	transcription factor AP-4 (activating	159093	SEQ ID No : 227		0	SEQ ID No:210	SEQ ID No:211

Symbole gène	N°	Nom	Image	Seq3' US PROV LISTING	Seq5' US PROV LISTING	Seq3' PCT Listing	Seq5' PCT Listing	(mRNA) PCT Listing
		enhancer binding protein 4) (TFAP4)						
ELF1	152	Human cis-acting sequence.Elf-1	182007	SEQ ID No : 228		SEQ ID No:437	0	0
CD2	153	CD2 antigen (p50), sheep red blood cell receptor (CD2)	120649	SEQ ID No : 229		SEQ ID No:431	0	0
CCND2	154	cyclin D2 (CCND2)	175256	SEQ ID No : 230		#N/A	#N/A	#N/A
IL3RA	155	interleukin 3 receptor (hIL-3Ra)	183087	SEQ ID No : 231		SEQ ID No:440	SEQ ID No:441	0
JUP	156	junction plakoglobin (JUP)	157958	SEQ ID No : 232		#N/A	#N/A	#N/A
RBL2	157	retinoblastoma-like 2 (p130) (RBL2)	108571	SEQ ID No : 233		SEQ ID No:430	0	0
HOXA4	158	homeo box A4 (HOXA4)	110731	SEQ ID No : 234		SEQ ID No:20	SEQ ID No:21	0
ACY1	159	aminoacylase 1 (ACY1)	160764	SEQ ID No : 235		SEQ ID No:435	SEQ ID No:436	0
GADD45A	160	growth arrest and DNA-damage-inducible, alpha (GADD45A)	115176	SEQ ID No : 236		#N/A	#N/A	#N/A
nm23	161	non-metastatic cells 1, protein (NM23A) expressed in (NME1)	174388	SEQ ID No : 237		#N/A	#N/A	#N/A
BBC1	162	ribosomal protein L13 (RPL13) (ex BBC1)	178317	SEQ ID No : 238		#N/A	#N/A	#N/A
VEGFB	163	vascular endothelial growth factor B (VEGFB)	162499	SEQ ID No : 239		#N/A	#N/A	#N/A
LAMR1	164	laminin receptor 1 (67kD, ribosomal protein SA) (LAMR1)	199837	SEQ ID No : 240		#N/A	#N/A	#N/A
IL2RB	165	interleukin 2 receptor, beta (IL2RB)	139073	SEQ ID No : 241	SEQ ID No : 242	SEQ ID No:97	SEQ ID No:98	SEQ ID No:99
DES	166	desmin	153854	SEQ ID No : 243		SEQ ID No:168	SEQ ID No:169	SEQ ID No:170
PRL	167	prolactin	133738	SEQ ID No : 244		SEQ ID No:91	SEQ ID No:92	SEQ ID No:93
CSH1	168	Chorionic somatomammotropin hormone 1 (placental lactogen) = LACTOGEN Precursor	133891		SEQ ID No : 245	SEQ ID No:432	0	0
TEK	169	tyrosine protein kinase receptor	151501	SEQ ID No : 246	SEQ ID No : 247	SEQ ID No:138	SEQ ID No:139	SEQ ID No:140
Nrg1	170	neuregulin 1 (EST R72075)	155716	SEQ ID No : 248	SEQ ID No : 249	SEQ ID No:189	SEQ ID No:190	SEQ ID No:191
PLAT	rien	pas d'EST ni mRNA	160149			SEQ ID No:433	SEQ ID No:434	0
EST	rien		Image ?					
AW184517								

References

1. DeRisi, J., Penland, L., Brown, P. O., Bittner, M. L., Meltzer, P. S., Ray, M., Chen, Y., Su, Y. A., and Trent, J. M. (1996) Use of a cDNA microarray to analyze gene expression patterns in human cancer. *Nat Genet* ,14, 457-460.

2. Jordan, B. R. (1998) Large-scale expression measurement by hybridization methods: from high- density membranes to "DNA chips". *J Biochem (Tokyo)* ,124, 251-258.

3. Nguyen, C., Rocha, D., Granjeaud, S., Baldit, M., Bernard, K., Naquet, P., and Jordan, B. R. (1995) Differential gene expression in the murine thymus assayed by quantitative hybridization of arrayed cDNA clones. *Genomics* ,29, 207-216.

4. Bertucci, F., Van Hulst, S., Bernard, K., Lloriod, B., Granjeaud, S., Tagett, R., Starkey, M., Nguyen, C., Jordan, B., and Birnbaum, D. (1999) Expression scanning of an array of growth control genes in human tumor cell lines. *Oncogene* ,18, 3905-3912.

5. Bertucci, F., Bernard, K., Lloriod, B., Chang, Y. C., Granjeaud, S., Birnbaum, D., Nguyen, C., Peck, K., and Jordan, B. R. (1999) Sensitivity issues in DNA array-based expression measurements and performance of nylon microarrays for small samples [In Process Citation]. *Hum Mol Genet* ,8, 1715-1722.

6. Ross, J. S. and Fletcher, J. A. (1999) The HER-2/neu oncogene: prognostic factor, predictive factor and target for therapy. *Semin Cancer Biol* ,9, 125-138.

7. Scorilas, A., Trangas, T., Yotis, J., Pateras, C., and Talieri, M. (1999) Determination of c-myc amplification and overexpression in breast cancer patients: evaluation of its prognostic value against c-erbB-2, cathepsin-D and clinicopathological characteristics using

univariate and multivariate analysis. Br J Cancer ,81, 1385-1391.

8. Fox, S. B., Smith, K., Hollyer, J., Greenall, M., Hastrich, D., and Harris, A. L. (1994) The epidermal growth factor receptor as a prognostic marker: results of 370 patients and review of 3009 patients. Breast Cancer Res Treat ,29, 41-49.

9. Heimann, R., Lan, F., McBride, R., and Hellman, S. (2000) Separating favorable from unfavorable prognostic markers in breast cancer: the role of E-cadherin. Cancer Res, 60, 298-304.

10. Guerin, M., Sheng, Z. M., Andrieu, N., and Riou, G. (1990) Strong association between c-myb and oestrogen-receptor expression in human breast cancer. Oncogene ,5, 131-135.

11. Lim, K. C., Lakshmanan, G., Crawford, S. E., Gu, Y., Grosveld, F., and Douglas Engel, J. (2000) Gata3 loss leads to embryonic lethality due to noradrenaline deficiency of the sympathetic nervous system. Nat Genet ,25, 209-212.

12. Mills, K. J., Vollberg, T. M., Nervi, C., Grippo, J. F., Dawson, M. I., and Jetten, A. M. (1996) Regulation of retinoid-induced differentiation in embryonal carcinoma PCC4.azalR cells: effects of retinoid-receptor selective ligands. Cell Growth Differ ,7, 327-337.

13. Easty, D. J., Hill, S. P., Hsu, M. Y., Fallowfield, M. E., Florenes, V. A., Herlyn, M., and Bennett, D. C. (1999) Up-regulation of ephrin-A1 during melanoma progression. Int J Cancer ,84, 494-501.

14. Shim, C., Zhang, W., Rhee, C. H., and Lee, J. H. (1998) Profiling of differentially expressed genes in human primary cervical cancer by complementary DNA expression array. Clin Cancer Res ,4, 3045-3050.

15. Tsou, A. P., Wu, K. M., Tsen, T. Y., Chi, C. W., Chiu, J. H., Lui, W. Y., Hu, C. P., Chang, C., Chou, C. K., and Tsai, S. F. (1998) Parallel hybridization analysis of multiple protein kinase genes: identification of gene expression patterns characteristic of human hepatocellular carcinoma. *Genomics* ,50, 331-340.

16. Schummer, M., Ng, W. V., Bumgarner, R. E., Nelson, P. S., Schummer, B., Bednarski, D. W., Hassell, L., Baldwin, R. L., Karlan, B. Y., and Hood, L. (1999) Comparative hybridization of an array of 21,500 ovarian cDNAs for the discovery of genes overexpressed in ovarian carcinomas. *Gene* ,238, 375-385.

17. Alon, U., Barkai, N., Notterman, D. A., Gish, K., Ybarra, S., Mack, D., and Levine, A. J. (1999) Broad patterns of gene expression revealed by clustering analysis of tumor and normal colon tissues probed by oligonucleotide arrays. *Proc Natl Acad Sci U S A* ,96, 6745-6750.

18. Moch, H., Schraml, P., Bubendorf, L., Mirlacher, M., Kononen, J., Gasser, T., Mihatsch, M. J., Kallioniemi, O. P., and Sauter, G. (1999) High-throughput tissue microarray analysis to evaluate genes uncovered by cDNA microarray screening in renal cell carcinoma. *Am J Pathol* ,154, 981-986.

19. Rhee, C. H., Hess, K., Jabbur, J., Ruiz, M., Yang, Y., Chen, S., Chenchik, A., Fuller, G. N., and Zhang, W. (1999) cDNA expression array reveals heterogeneous gene expression profiles in three glioblastoma cell lines. *Oncogene* ,18, 2711-2717.

20. Huang, F., Adelman, J., Jiang, H., Goldstein, N. I., and Fisher, P. B. (1999) Identification and temporal expression pattern of genes modulated during irreversible growth arrest and terminal differentiation in human melanoma cells. *Oncogene* ,18, 3546-3552.

21. Bittner, M., Meltzer, P., Chen, Y., Jiang, Y., Seftor, E., Hendrix, M., Radmacher, M., Simon, R., Yakhini, Z., Ben-Dor, A., Sampa, N., Dougherty, E., Wang, E., Marincola, F., Gooden, C., Lueders, J., Glatfelter, A., Pollock, P., Carpten, J., Gillanders, E., Leja, D., Dietrich, K., Beaudry, C., Berens, M., Alberts, D., and Sondak, V. (2000) Molecular classification of cutaneous malignant melanoma by gene expression profiling. *Nature* ,406, 536-540.
22. Khan, J., Simon, R., Bittner, M., Chen, Y., Leighton, S. B., Pohida, T., Smith, P. D., Jiang, Y., Gooden, G. C., Trent, J. M., and Meltzer, P. S. (1998) Gene expression profiling of alveolar rhabdomyosarcoma with cDNA microarrays. *Cancer Res* ,58, 5009-5013.
23. Golub, T. R., Slonim, D. K., Tamayo, P., Huard, C., Gaasenbeek, M., Mesirov, J. P., Coller, H., Loh, M. L., Downing, J. R., Caligiuri, M. A., Bloomfield, C. D., and Lander, E. S. (1999) Molecular classification of cancer: class discovery and class prediction by gene expression monitoring. *Science* ,286, 531-537.
24. Alizadeh, A. A., Eisen, M. B., Davis, R. E., Ma, C., Lossos, I. S., Rosenwald, A., Boldrick, J. C., Sabet, H., Tran, T., Yu, X., Powell, J. I., Yang, L., Marti, G. E., Moore, T., Hudson, J., Jr., Lu, L., Lewis, D. B., Tibshirani, R., Sherlock, G., Chan, W. C., Greiner, T. C., Weisenburger, D. D., Armitage, J. O., Warnke, R., and Staudt, L. M. (2000) Distinct types of diffuse large B-cell lymphoma identified by gene expression profiling [In Process Citation]. *Nature* ,403, 503-511.
25. Hoch, R. V., Thompson, D. A., Baker, R. J., and Weigel, R. J. (1999) GATA-3 is expressed in association with estrogen receptor in breast cancer. *Int J Cancer* ,84, 122-128.

26. Hilsenbeck, S. G., Friedrichs, W. E., Schiff, R., O'Connell, P., Hansen, R. K., Osborne, C. K., and Fuqua, S. A. (1999) Statistical analysis of array expression data as applied to the problem of tamoxifen resistance. J Natl Cancer Inst ,91, 453-459.

27. Martin, K. J., Kritzman, B. M., Price, L. M., Koh, B., Kwan, C. P., Zhang, X., Mackay, A., O'Hare, M. J., Kaelin, C. M., Mutter, G. L., Pardee, A. B., and Sager, R. (2000) Linking gene expression patterns to therapeutic groups in breast cancer. Cancer Res ,60, 2232-2238.

28. Yang, G. P., Ross, D. T., Kuang, W. W., Brown, P. O., and Weigel, R. J. (1999) Combining SSH and cDNA microarrays for rapid identification of differentially expressed genes. Nucleic Acids Res ,27, 1517-1523.

29. Perou, C. M., Jeffrey, S. S., van de Rijn, M., Rees, C. A., Eisen, M. B., Ross, D. T., Pergamenschikov, A., Williams, C. F., Zhu, S. X., Lee, J. C., Lashkari, D., Shalon, D., Brown, P. O., and Botstein, D. (1999) Distinctive gene expression patterns in human mammary epithelial cells and breast cancers. Proc Natl Acad Sci U S A ,96, 9212-9217.

30. Nacht, M., Ferguson, A. T., Zhang, W., Petroziello, J. M., Cook, B. P., Gao, Y. H., Maguire, S., Riley, D., Coppola, G., Landes, G. M., Madden, S. L., and Sukumar, S. (1999) Combining serial analysis of gene expression and array technologies to identify genes differentially expressed in breast cancer. Cancer Res ,59, 5464-5470.

31. Sgroi, D. C., Teng, S., Robinson, G., LeVangie, R., Hudson, J. R., Jr., and Elkahloun, A. G. (1999) In vivo gene expression profile analysis of human breast cancer progression. Cancer Res ,59, 5656-5661.

32. Perou, C. M., Sorlie, T., Eisen, M. B., van de Rijn, M., Jeffrey, S. S., Rees, C. A., Pollack, J. R.,

Ross, D. T., Johnsen, H., Akslen, L. A., Fluge, O., Pergamenschikov, A., Williams, C., Zhu, S. X., Lonning, P. E., Borresen-Dale, A. L., Brown, P. O., and Botstein, D. (2000) Molecular portraits of human breast tumours. *Nature* ,406, 747-752.

33. Hahnel, E., Harvey, J. M., Joyce, R., Robbins, P. D., Sterrett, G. F., and Hahnel, R. (1993) Stromelysin-3 expression in breast cancer biopsies: clinico-pathological correlations. *Int J Cancer* ,55, 771-774.

34. Skoog, L., Humla, S., Klintenberg, C., Pasqual, M., and Wallgren, A. (1985) Receptors for retinoic acid and retinol in human mammary carcinomas. *Eur J Cancer Clin Oncol* ,21, 901-906.

35. Thor, A. D., Moore, D. H., II, Edgerton, S. M., Kawasaki, E. S., Reihnsaus, E., Lynch, H. T., Marcus, J. N., Schwartz, L., Chen, L. C., Mayall, B. H., and et al. (1992) Accumulation of p53 tumor suppressor gene protein: an independent marker of prognosis in breast cancers. *J Natl Cancer Inst* ,84, 845-855.

36. Allred, D. C., Harvey, J. M., Berardo, M., and Clark, G. M. (1998) Prognostic and predictive factors in breast cancer by immunohistochemical analysis. *Mod Pathol* ,11, 155-168.

37. Spencer, K. S., Graus-Porta, D., Leng, J., Hynes, N. E., and Klemke, R. L. (2000) ErbB2 is necessary for induction of carcinoma cell invasion by ErbB family receptor tyrosine kinases. *J Cell Biol* ,148, 385-397.

38. Behrens, J. (1993) The role of cell adhesion molecules in cancer invasion and metastasis. *Breast Cancer Res Treat* ,24, 175-184.

39. Roberts, D. D. (1996) Regulation of tumor growth and metastasis by thrombospondin-1. *Faseb J* ,10, 1183-1191.

40. Taylor-Papadimitriou, J., Burchell, J., Miles, D. W., and Dalziel, M. (1999) MUC1 and cancer. *Biochim Biophys Acta* ,1455, 301-313.

5 41. Sneath, R. J. and Mangham, D. C. (1998) The normal structure and function of CD44 and its role in neoplasia. *Mol Pathol* ,51, 191-200.

10 42. Iyer, V. R., Eisen, M. B., Ross, D. T., Schuler, G., Moore, T., Lee, J. C. F., Trent, J. M., Staudt, L. M., Hudson, J., Jr., Boguski, M. S., Lashkari, D., Shalon, D., Botstein, D., and Brown, P. O. (1999) The transcriptional program in the response of human fibroblasts to serum. *Science* ,283, 83-87.

15 43. Theillet, C., Adelaide, J., Louason, G., Bonnet-Dorion, F., Jacquemier, J., Adnane, J., Longy, M., Katsaros, D., Sismondi, P., Gaudray, P., and et al. (1993) FGFR1 and PLAT genes and DNA amplification at 8p12 in breast and ovarian cancers. *Genes Chromosomes Cancer* ,7, 219-226.

20 44. Granjeaud, S., Nguyen, C., Rocha, D., Luton, R., and Jordan, B. R. (1996) From hybridization image to numerical values: a practical, high throughput quantification system for high density filter hybridizations. *Genet Anal* ,12, 151-162.

25 45. Eisen, M. B., Spellman, P. T., Brown, P. O., and Botstein, D. (1998) Cluster analysis and display of genome-wide expression patterns. *Proc Natl Acad Sci U S A* ,95, 14863-14868.

30 46. Ferrari, S., Battini, R., and Cossu, G. (1990) Differentiation-dependent expression of apolipoprotein A-I in chicken myogenic cells in culture. *Dev Biol* ,140, 430-436.

CLAIMS

1. A polynucleotide library useful in the molecular characterization of a carcinoma, said library comprising a pool of polynucleotide sequences or subsequences thereof wherein said sequences or subsequences are either underexpressed or overexpressed in tumor cells, further wherein said sequences or subsequences correspond substantially to any of the polynucleotide sequences set forth in any of SEQ ID Nos: 1 - 468 or the complement thereof.

2. A polynucleotide library according to Claim 1 wherein said polynucleotide sequences or subsequences thereof of said pool correspond to any combination of at least one polynucleotide selected among those included in anyone of the following predefined sets :

SET 1: (SEQ ID No:1; SEQ ID No:2); SET 2: (SEQ ID No:3; SEQ ID No:4); SET 3: (SEQ ID No:5; SEQ ID No:6); SET 4: (SEQ ID No:7; SEQ ID No:8); SET 5: (SEQ ID No:9; SEQ ID No:10); SET 6: (SEQ ID No:11; SEQ ID No:12); SET 7: (SEQ ID No:13; SEQ ID No:14; SEQ ID No:15); SET 8: (SEQ ID No:16); SET 9: (SEQ ID No:17; SEQ ID No:18; SEQ ID No:19); SET 10: (SEQ ID No:20; SEQ ID No:21); SET 11: (SEQ ID No:22; SEQ ID No:23; SEQ ID No:24); SET 12: (SEQ ID No:25; SEQ ID No:26); SET 13: (SEQ ID No:27; SEQ ID No:28; SEQ ID No:29); SET 14: (SEQ ID No:30; SEQ ID No:31); SET 15: (SEQ ID No:32; SEQ ID No:33; SEQ ID No:34) ; SET 16 : (SEQ ID No:35) ; SET 17 : (SEQ ID No:36; SEQ ID No:37; SEQ ID No:38) ; SET 18 : (SEQ ID No:39; SEQ ID No:40; SEQ ID No:41) ; SET 19 : (SEQ ID No:42; SEQ ID No:43) ; SET 20 : (SEQ ID No:44; SEQ ID No:45) ; SET 21 : (SEQ ID No:46; SEQ ID No:47) ; SET 22 : (SEQ ID No:48; SEQ ID No:49; SEQ ID No:50) ; SET 23 : (SEQ ID No:51; SEQ ID No:52; SEQ ID No:53) ; SET 24: (SEQ ID No:54; SEQ ID No:55; SEQ ID No:56) ; SET 25: (SEQ ID No:57; SEQ ID No:58) ; SET 26: (SEQ ID No:59; SEQ ID No:60; SEQ ID No:61) ; SET 27: (SEQ ID No:62; SEQ ID No:63; SEQ ID No:64) ; SET 28: (SEQ ID No:65; SEQ ID No:66; SEQ ID No:67) ;

5 SET 29: (SEQ ID No:68; SEQ ID No:69; SEQ ID No:70) ; SET 30: (SEQ
ID No:71; SEQ ID No:72) ; SET 31 : (SEQ ID No:73; SEQ ID No:74;
SEQ ID No:75) ; SET 32 : (SEQ ID No:76; SEQ ID No:77; SEQ ID
No:78) ; SET 33 : (SEQ ID No:79; SEQ ID No:80; SEQ ID No:81) ; SET
34: (SEQ ID No:82; SEQ ID No:83) ; SET 35: (SEQ ID No:84; SEQ ID
No:85) ; SET 36: (SEQ ID No:86; SEQ ID No:87) ; SET 37: (SEQ ID
No:88; SEQ ID No:89; SEQ ID No:90) ; SET 38: (SEQ ID No:91; SEQ ID
No:92; SEQ ID No:93) ; SET 39: (SEQ ID No:94; SEQ ID No:95; SEQ ID
No:96) ; SET 40: (SEQ ID No:97; SEQ ID No:98; SEQ ID No:99) ; SET
10 41: (SEQ ID No:100; SEQ ID No:101; SEQ ID No:102) ; SET 42: (SEQ ID
No:103; SEQ ID No:104) ; SET 43: (SEQ ID No:105; SEQ ID No:106) ;
SET 44: (SEQ ID No:107; SEQ ID No:108; SEQ ID No:109) ; SET 45:
(SEQ ID No:110; SEQ ID No:111) ; SET 46: (SEQ ID No:112; SEQ ID
No:113; SEQ ID No:114) ; SET 47: (SEQ ID No:115; SEQ ID No:116;
15 SEQ ID No:117) ; SET 48: (SEQ ID No:118; SEQ ID No:119) ; SET 49:
(SEQ ID No:120; SEQ ID No:121) ; SET 50: (SEQ ID No:122; SEQ ID
No:123; SEQ ID No:124) ; SET 51: (SEQ ID No:125; SEQ ID No:126;
SEQ ID No:127) ; SET 52: (SEQ ID No:128; SEQ ID No:129; SEQ ID
No:130) ; SET 53: (SEQ ID No:131; SEQ ID No:132) ; SET 54: (SEQ ID
No:133; SEQ ID No:134) ; SET 55: (SEQ ID No:135; SEQ ID No:136;
20 SEQ ID No:137) ; SET 56: (SEQ ID No:138; SEQ ID No:139; SEQ ID
No:140) ; SET 57: (SEQ ID No:141; SEQ ID No:142; SEQ ID No:143) ;
SET 58: (SEQ ID No:144; SEQ ID No:145; SEQ ID No:146) ; SET 59:
(SEQ ID No:147; SEQ ID No:148; SEQ ID No:149) ; SET 60: (SEQ ID
No:150; SEQ ID No:151; SEQ ID No:152) ; SET 61: (SEQ ID No:153;
25 SEQ ID No:154; SEQ ID No:155) ; SET 62: (SEQ ID No:156; SEQ ID
No:157; SEQ ID No:158) ; SET 63: (SEQ ID No:159; SEQ ID No:160;
SEQ ID No:161) ; SET 64: (SEQ ID No:162; SEQ ID No:163) ; SET 65:
(SEQ ID No:164; SEQ ID No:165) ; SET 66: (SEQ ID No:166; SEQ ID
No:167; SEQ ID No:168) ; SET 67: (SEQ ID No:169; SEQ ID No:170) ;
30 SET 68: (SEQ ID No:171; SEQ ID No:172) ; SET 69: (SEQ ID No:173;
SEQ ID No:174; SEQ ID No:175) ; SET 70: (SEQ ID No:176; SEQ ID
No:177) ; SET 71: (SEQ ID No:178; SEQ ID No:179) ; SET 72: (SEQ ID
No:180; SEQ ID No:181; SEQ ID No:182) ; SET 73: (SEQ ID No:183;
35 SEQ ID No:184) ; SET 74: (SEQ ID No:185) ; SET 75: (SEQ ID No:186)
; SET 76: (SEQ ID No:187; SEQ ID No:188) ; SET 77: (SEQ ID No:189;
SET 78: (SEQ ID No:190; SEQ ID No:191) ; SET 79: (SEQ ID No:192;
SEQ ID No:193) ; SET 80: (SEQ ID No:194; SEQ ID No:195) ; SET 81:
(SEQ ID No:196; SEQ ID No:197; SEQ ID No:198) ; SET 82: (SEQ ID
No:199; SEQ ID No:200) ; SET 83: (SEQ ID No:201; SEQ ID No:202)
; SET 84: (SEQ ID No:203; SEQ ID No:204; SEQ ID No:205) ; SET 85:
(SEQ ID No:206; SEQ ID No:207; SEQ ID No:208) ; SET 86: (SEQ ID
No:209; SEQ ID No:210; SEQ ID No:211) ; SET 87: (SEQ ID No:212;
SEQ ID No:213; SEQ ID No:214) ; SET 88: (SEQ ID No:215; SEQ ID
No:216; SEQ ID No:217) ; SET 89: (SEQ ID No:218; SEQ ID No:219;
SEQ ID No:220) ; SET 90: (SEQ ID No:221; SEQ ID No:222; SEQ ID
No:223) ; SET 91: (SEQ ID No:224; SEQ ID No:225; SEQ ID No:226)
; SET 92: (SEQ ID No:227; SEQ ID No:228; SEQ ID No:229) ; SET 93:
(SEQ ID No:230; SEQ ID No:231; SEQ ID No:232) ; SET 94: (SEQ ID
No:233; SEQ ID No:234; SEQ ID No:235) ; SET 95: (SEQ ID No:236;
SEQ ID No:237; SEQ ID No:238) ; SET 96: (SEQ ID No:239; SEQ ID
No:240; SEQ ID No:241) ; SET 97: (SEQ ID No:242; SEQ ID No:243;
SEQ ID No:244) ; SET 98: (SEQ ID No:245; SEQ ID No:246; SEQ ID
No:247) ; SET 99: (SEQ ID No:248; SEQ ID No:249; SEQ ID No:250)

SEQ ID No:190; SEQ ID No:191) ; SET 80: (SEQ ID No:192; SEQ ID No:193) ; SET 81: (SEQ ID No:194; SEQ ID No:195) ; SET 82: (SEQ ID No:196; SEQ ID No:197; SEQ ID No:198) ; SET 83: (SEQ ID No:199; SEQ ID No:200) ; SET 84: (SEQ ID No:201; SEQ ID No:202; SEQ ID No:203) ; SET 85: (SEQ ID No:204; SEQ ID No:205) ; SET 86: (SEQ ID No:206; SEQ ID No:207) ; SET 87: (SEQ ID No:208; SEQ ID No:209) ; SET 88: (SEQ ID No:210; SEQ ID No:211) ; SET 89: (SEQ ID No:212; SEQ ID No:213) ; SET 90: (SEQ ID No:214; SEQ ID No:215) ; SET 91: (SEQ ID No:216; SEQ ID No:217) ; SET 92: (SEQ ID No:218; SEQ ID No:219; SEQ ID No:220) ; SET 93: (SEQ ID No:221; SEQ ID No:222) ; SET 94: (SEQ ID No:223; SEQ ID No:224; SEQ ID No:225) ; SET 95: (SEQ ID No:226; SEQ ID No:227) ; SET 96: (SEQ ID No:228; SEQ ID No:229) ; SET 97: (SEQ ID No:230; SEQ ID No:231; SEQ ID No:232) ; SET 98: (SEQ ID No:233; SEQ ID No:234) ; SET 99: (SEQ ID No:235; SEQ ID No:236; SEQ ID No:237) ; SET 100: (SEQ ID No:238; SEQ ID No:239) ; SET 101: (SEQ ID No:240; SEQ ID No:241) ; SET 102: (SEQ ID No:242; SEQ ID No:243; SEQ ID No:244) ; SET 103: (SEQ ID No:245; SEQ ID No:246; SEQ ID No:247) ; SET 104: (SEQ ID No:248; SEQ ID No:249) ; SET 105: (SEQ ID No:250; SEQ ID No:251; SEQ ID No:252) ; SET 106: (SEQ ID No:253; SEQ ID No:254) ; SET 107: (SEQ ID No:255; SEQ ID No:256) ; SET 108: (SEQ ID No:257; SEQ ID No:258) ; SET 109: (SEQ ID No:259; SEQ ID No:260; SEQ ID No:261) ; SET 110: (SEQ ID No:262; SEQ ID No:200) ; SET 111: (SEQ ID No:263; SEQ ID No:264) ; SET 112: (SEQ ID No:265; SEQ ID No:266) ; SET 113: (SEQ ID No:267; SEQ ID No:268) ; SET 114: (SEQ ID No:269; SEQ ID No:270) ; SET 115: (SEQ ID No:271; SEQ ID No:272) ; SET 116: (SEQ ID No:273; SEQ ID No:274) ; SET 117: (SEQ ID No:275; SEQ ID No:276) ; SET 118: (SEQ ID No:277; SEQ ID No:278) ; SET 119: (SEQ ID No:279; SEQ ID No:280; SEQ ID No:281) ; SET 120: (SEQ ID No:282; SEQ ID No:283; SEQ ID No:276) ; SET 121: (SEQ ID No:284; SEQ ID No:285) ; SET 122: (SEQ ID No:286; SEQ ID No:287; SEQ ID No:288) ; SET 123: (SEQ ID No:289; SEQ ID No:290) ; SET 124: (SEQ ID No:291; SEQ ID No:292) ; SET 125: (SEQ ID No:293; SEQ ID No:294; SEQ ID No:295) ; SET 126: (SEQ ID No:296; SEQ ID No:297) ; SET 127: (SEQ ID No:298; SEQ ID No:299; SEQ ID No:300) ; SET 128: (SEQ ID No:301; SEQ ID No:302; SEQ ID No:288) ; SET 129: (SEQ ID No:303; SEQ ID No:304) ; SET 130: (SEQ ID No:305; SEQ ID No:306;

SEQ ID No:307) ; SET 131: (SEQ ID No:308; SEQ ID No:309; SEQ ID
No:310) ; SET 132: (SEQ ID No:311; SEQ ID No:312; SEQ ID No:313) ;
SET 133: (SEQ ID No:314; SEQ ID No:315; SEQ ID No:316) ; SET 134:
5 (SEQ ID No:317; SEQ ID No:318) ; SET 135: (SEQ ID No:319; SEQ ID
No:320; SEQ ID No:321) ; SET 136: (SEQ ID No:322; SEQ ID No:323) ;
SET 137: (SEQ ID No:324; SEQ ID No:325) ; SET 138: (SEQ ID No:326;
SEQ ID No:327; SEQ ID No:328) ; SET 139: (SEQ ID No:329; SEQ ID
No:330) ; SET 140: (SEQ ID No:331; SEQ ID No:332; SEQ ID No:333) ;
SET 141: (SEQ ID No:334; SEQ ID No:335; SEQ ID No:336) ; SET 142:
10 (SEQ ID No:337; SEQ ID No:338; SEQ ID No:117) ; SET 143: (SEQ ID
No:339; SEQ ID No:340; SEQ ID No:341) ; SET 144: (SEQ ID No:342;
SEQ ID No:343; SEQ ID No:344) ; SET 145: (SEQ ID No:345; SEQ ID
No:346) ; SET 146: (SEQ ID No:347; SEQ ID No:348; SEQ ID No:349) ;
SET 147: (SEQ ID No:350; SEQ ID No:351) ; SET 148: (SEQ ID No:352;
15 SEQ ID No:353) ; SET 149: (SEQ ID No:354; SEQ ID No:355) ; SET
150: (SEQ ID No:356; SEQ ID No:357) ; SET 151: (SEQ ID No:358; SEQ
ID No:359; SEQ ID No:360) ; SET 152: (SEQ ID No:361; SEQ ID No:31)
; SET 153: (SEQ ID No:362; SEQ ID No:363; SEQ ID No:364) ; SET
154: (SEQ ID No:365; SEQ ID No:366; SEQ ID No:367) ; SET 155: (SEQ
20 ID No:368; SEQ ID No:369; SEQ ID No:300) ; SET 156: (SEQ ID
No:370; SEQ ID No:371) ; SET 157: (SEQ ID No:372; SEQ ID No:373;
SEQ ID No:108) ; SET 158: (SEQ ID No:374; SEQ ID No:375; SEQ ID
No:376) ; SET 159: (SEQ ID No:377; SEQ ID No:378; SEQ ID No:379) ;
SET 160: (SEQ ID No:380; SEQ ID No:381) ; SET 161: (SEQ ID No:382;
25 SEQ ID No:383; SEQ ID No:384) ; SET 162: (SEQ ID No:385; SEQ ID
No:386; SEQ ID No:387) ; SET 163: (SEQ ID No:388; SEQ ID No:389;
SEQ ID No:390) ; SET 164: (SEQ ID No:391; SEQ ID No:392; SEQ ID
No:393) ; SET 165: (SEQ ID No:394; SEQ ID No:395) ; SET 166: (SEQ
ID No:396; SEQ ID No:397; SEQ ID No:398) ; SET 167: (SEQ ID
30 No:399; SEQ ID No:400; SEQ ID No:117) ; SET 168: (SEQ ID No:401) ;
SET 169: (SEQ ID No:402; SEQ ID No:403) ; SET 170: (SEQ ID No:404;
SEQ ID No:405; SEQ ID No:318) ; SET 171: (SEQ ID No:406; SEQ ID
No:407; SEQ ID No:408) ; SET 172: (SEQ ID No:409; SEQ ID No:410;
SEQ ID No:411) ; SET 173: (SEQ ID No:412; SEQ ID No:413) ; SET
35 174: (SEQ ID No:414; SEQ ID No:415; SEQ ID No:416) ; SET 175: (SEQ
ID No:417; SEQ ID No:418; SEQ ID No:419) ; SET 176: (SEQ ID
No:420; SEQ ID No:421; SEQ ID No:422) ; SET 177: (SEQ ID No:423;

SEQ ID No:424; SEQ ID No:425) ; SET 178: (SEQ ID No:426; SEQ ID No:427; SEQ ID No:428) ; SET 179: (SEQ ID No:429; SEQ ID No:408) ; SET 180: (SEQ ID No:430) ; SET 181: (SEQ ID No:431) ; SET 182: (SEQ ID No:432) ; SET 183: (SEQ ID No:433; SEQ ID No:434) ; SET 184: (SEQ ID No:435; SEQ ID No:436) ; SET 185: (SEQ ID No:437) ; SET 186: (SEQ ID No:438; SEQ ID No:439) ; SET 187: (SEQ ID No:440; SEQ ID No:441) ; SET 188: (SEQ ID No:442) ; SET 189: (SEQ ID No:444) ; SET 190: (SEQ ID No:445) ; SET 191 (SEQ ID No:446 ; SEQ ID No:447) ; SET 192: (SEQ ID No:448) ; SET 193: (SEQ ID No:449) ; SET 194: (SEQ ID No:450) ; SET 195: (SEQ ID No:451) ; SET 196: (SEQ ID No:452) ; SET 197: (SEQ ID No:453) ; SET 198: (SEQ ID No:454) ; SET 199: (SEQ ID No:455) ; SET 200: (SEQ ID No:456) ; SET 201: (SEQ ID No:457) ; SET 202: (SEQ ID No:458) ; SET 203: (SEQ ID No:459) ; SET 204: (SEQ ID No:460) ; SET 205: (SEQ ID No:461) ; SET 206: (SEQ ID No:462) ; SET 207: (SEQ ID No:463) ; SET 208: (SEQ ID No:464) ; SET 209: (SEQ ID No:465) ; SET 210: (SEQ ID No:466) ; SET 211: (SEQ ID No:467) ; SET 212: (SEQ ID No:468)

3. A polynucleotide library according to Claim 2 wherein said polynucleotide sequences or subsequences thereof of said pool correspond to any combination of at least one polynucleotide selected among those included in at least 50%, preferably 75% and more preferably 100% of the predefined sets.

4. A library according to anyone Claim 1 or 2 wherein the pool of polynucleotide sequences or subsequences correspond substantially to any combination of at least one polynucleotide sequence selected among those included in each one of predefined polynucleotide sequences sets comprising:

SET 1: (SEQ ID No:1 ; SEQ ID No:2) ; SET 4: (SEQ ID No:7 ; SEQ ID No:8) ; SET 18: (SEQ ID No:39 ; SEQ ID No:40 ; SEQ ID No:41) ; SET 21: (SEQ ID No:46 ; SEQ ID No:47) ; SET 24: (SEQ ID No:54 ; SEQ ID No:55 ; SEQ ID No:56) ; SET 32: (SEQ ID No:76 ; SEQ ID No:77 ; SEQ ID No:78) ; SET 38: (SEQ ID No:91 ; SEQ ID

No:92 ; SEQ ID No:93) ; SET 48: (SEQ ID No:115 ; SEQ ID No:116 ;
SEQ ID No:117) ; SET 53: (SEQ ID No:126 ; SEQ ID No:127 ; SEQ ID
No:128) ; SET 58: (SEQ ID No:138 ; SEQ ID No:139 ; SEQ ID No:140)
; SET 59: (SEQ ID No:141 ; SEQ ID No:142 ; SEQ ID No:143) ; SET
5 61: (SEQ ID No:147 ; SEQ ID No:148 ; SEQ ID No:149) ; SET 64: (SEQ
ID No:156 ; SEQ ID No:157 ; SEQ ID No:158) ; SET 66: (SEQ ID
No:162 ; SEQ ID No:163) ; SET 69: (SEQ ID No:168 ; SEQ ID No:169;
SEQ ID No:170) ; SET 73: (SEQ ID No:178; SEQ ID No:179) ; SET 85:
10 (SEQ ID No:204; SEQ ID No:205) ; SET 88: (SEQ ID No:210; SEQ ID
No:211) ; SET 91: (SEQ ID No:216; SEQ ID No:217) ; SET 97: (SEQ ID
No:230; SEQ ID No:231; SEQ ID No:232) ; SET 104: (SEQ ID No:248;
SEQ ID No:249) ; SET 105: (SEQ ID No:250 ; SEQ ID No:251 ; SEQ ID
No:252) ; SET 112: (SEQ ID No:265 ; SEQ ID No:266) ; SET 113: (SEQ
15 ID No:267 ; SEQ ID No:268) ; SET 115 ; (SEQ ID No:271 ; SEQ ID
No:272) ; SET 131: (SEQ ID No:308 ; SEQ ID No:309 ; SEQ ID No:310)
; SET 132: (SEQ ID No:311 ; SEQ ID No:312 ; SEQ ID No:313) ; SET
134: (SEQ ID No:317 ; SEQ ID No:318) ; SET 137: (SEQ ID No:324 ;
SEQ ID No:325) ; SET 145: (SEQ ID No:345 ; SEQ ID No:346) ; SET
147: (SEQ ID No:350 ; SEQ ID No:351) ; SET 155: (SEQ ID No:368 ;
20 SEQ ID No:369 ; SEQ ID No:300) ; SET 175: (SEQ ID No:417 ; SEQ ID
No:418 ; SEQ ID No:419) ; SET 180: (SEQ ID No:430) ; SET 181: (SEQ
ID No:431) ; SET 182: (SEQ ID No:432) ; SET 185: (SEQ ID No:437) ;
SET 187: (SEQ ID No:440 ; SEQ ID No:441,

wherein said sequences are useful in
25 differentiating a normal cell from a cancer cell.

5. A polynucleotide library according to Claim
4 wherein said polynucleotide sequences or subsequences
thereof of said pool correspond to any combination of at
30 least one polynucleotide selected among those included in at
least 50%, preferably 75% and more preferably 100% of the
predefined sets.

6. A polynucleotide library according to Claim 4
35 wherein the pool of polynucleotide sequences or subsequences

correspond substantially to any combination of at least one polynucleotide sequence selected among those included in each one of predefined polynucleotide sequences sets comprising:

5 SET 32: (SEQ ID No:76 ; SEQ ID No:77 ; SEQ ID No:78)
; SET 73: (SEQ ID No:178 ; SEQ ID No:179) ; SET 131: (SEQ ID
No:308 ; SEQ ID No:309 ; SEQ ID No:310) ; SET 145: (SEQ ID No:345
; SEQ ID No:346) and SET 181: (SEQ ID No:431)

10 and of at least one polynucleotide sequence
selected among those included in each one of predefined
polynucleotide sequences sets comprising:

15 SET 38: (SEQ ID No:91 ; SEQ ID No:92 ; SEQ ID No:93)
; SET 58: (SEQ ID No:138 ; SEQ ID No:139 ; SEQ ID No:140); SET 61:
(SEQ ID No:147 ; SEQ ID No:148 ; SEQ ID No:149); SET 69: (SEQ ID
No:168 ; SEQ ID No:169 ; SEQ ID No:170) and SET 182: (SEQ ID
No:432).

20 7 A polynucleotide library according to Claim
6 wherein said polynucleotide sequences or subsequences
thereof of said pool correspond to any combination of at
least one polynucleotide selected among those included in at
least 50%, preferably 75% and more preferably 100% of the
predefined sets.

25 8. A library according to anyone Claim 1 or 2
wherein the pool of polynucleotide sequences or subsequences
correspond substantially to any combination of at least one
polynucleotide sequence selected among those included in each
one of predefined polynucleotide sequences sets comprising:

30 SET 11: (SEQ ID No:22 ; SEQ ID No:23 ; SEQ ID No:24)
; SET 26: (SEQ ID No:59; SEQ ID No:60 ; SEQ ID No:61) ; SET 32:
(SEQ ID No:76; SEQ ID No:77 ; SEQ ID No:78) ; SET 34: (SEQ ID
No:82 ; SEQ ID No:83) ; SET 40: (SEQ ID No:97 ; SEQ ID No:98 ; SEQ
ID No:99) ; SET 57: (SEQ ID No:135 ; SEQ ID No:136 ;SEQ ID No:137)
; SET 64: (SEQ ID No:156 ; SEQ ID No:157; SEQ ID No:158) ; SET
35 107: (SEQ ID No:255 ; SEQ ID No:256) ; SET 119: (SEQ ID No:279 ;

SEQ ID No:280 ; SEQ ID No:281) ; SET 136: (SEQ ID No:322 ; SEQ ID No:323) ; SET 140: (SEQ ID No:331 ; SEQ ID No:332 ; SEQ ID No:333) ; SET 141: (SEQ ID No:334; SEQ ID No:335 ; SEQ ID No:336) ; SET 145: (SEQ ID No:345; SEQ ID No:346) ; SET 148: (SEQ ID No:352; SEQ ID No:353) ; SET 149: (SEQ ID No:354 ; SEQ ID No:355) ; SET 162: (SEQ ID No:385; SEQ ID No:386; SEQ ID No:387) ; SET 165: (SEQ ID No:394 ; SEQ ID No:395) ; SET 169: (SEQ ID No:402 ; SEQ ID No:403) ; SET 174: (SEQ ID No:414 ; SEQ ID No:415 ; SEQ ID No:416) and SET 188: (SEQ ID No:442),

wherein said sequences are useful in detecting a hormone sensitive tumor cell

9. A polynucleotide library according to Claim 8 wherein said polynucleotide sequences or subsequences thereof of said pool correspond to any combination of at least one polynucleotide selected among those included in at least 50%, preferably 75% and more preferably 100% of the predefined sets.

10. A library according to Claim 8 wherein the pool of polynucleotide sequences or subsequences correspond substantially to any combination of at least one polynucleotide sequence selected among those included in each one of predefined polynucleotide sequences sets comprising:

SET 32: (SEQ ID No:76 ; SEQ ID No:77 ; SEQ ID No:78) ; SET 136: (SEQ ID No:322 ; SEQ ID No:323) ; SET 145: (SEQ ID No:345 ; SEQ ID No:346); SET 149: (SEQ ID No:354 ; SEQ ID No:355) and SET 169: (SEQ ID No:402 ; SEQ ID No:403)

and of at least one polynucleotide sequence selected among those included in each one of predefined polynucleotide sequences sets comprising:

SET 11: (SEQ ID No:22 ; SEQ ID No:23 ; SEQ ID No:24) ; SET 40: (SEQ ID No:97 ; SEQ ID No:98 ; SEQ ID No:99); SET 57: (SEQ ID No:135 ; SEQ ID No:136 ; SEQ ID No:137); SET 119: (SEQ ID

No:279; SEQ ID No:280 ; SEQ ID No:281) and SET 174: (SEQ ID No:414 ; SEQ ID No:415 ; SEQ ID No:416)

11. A polynucleotide library according to Claim
5 10 wherein said polynucleotide sequences or subsequences thereof of said pool correspond to any combination of at least one polynucleotide selected among those included in at least 50%, preferably 75% and more preferably 100% of the predefined sets.

10 12. A library according to anyone Claim 1 or 2 wherein the pool of polynucleotide sequences or subsequences correspond substantially to any combination of at least one polynucleotide sequence selected among those included in each
15 one of predefined polynucleotide sequences sets comprising:

20 SET 8: (SEQ ID No:16) ; SET 11: (SEQ ID No:22 ; SEQ ID No:23 ; SEQ ID No:24) ; SET 18: (SEQ ID No:39 ; SEQ ID No:40 ; SEQ ID No:41) ; SET 25: (SEQ ID No:57 ; SEQ ID No:58) ; SET 32: (SEQ ID No:76 ; SEQ ID No:77 ; SEQ ID No:78) ; SET 34: (SEQ ID No:82 ; SEQ ID No:83) ; SET 40: (SEQ ID No:97 ; SEQ ID No:98 ; SEQ ID No:99) ; SET 49: (SEQ ID No:118 ; SEQ ID No:119) ; SET 57: (SEQ ID No:135 ; SEQ ID No:136 ; SEQ ID No:137) ; SET 91: (SEQ ID No:216 ; SEQ ID No:217) ; SET 100: (SEQ ID No:238 ; SEQ ID No:239) ; SET 105: (SEQ ID No:250 ; SEQ ID No:251 ; SEQ ID No:252) ; SET
25 136: (SEQ ID No:322 ; SEQ ID No:323) ; SET 138: (SEQ ID No:326 ; SEQ ID No:327 ; SEQ ID No:328) ; SET 139: (SEQ ID No:329 ; SEQ ID No:330) ; SET 141: (SEQ ID No:334 ; SEQ ID No:335 ; SEQ ID No:336) ; SET 158: (SEQ ID No:374 ; SEQ ID No:375 ; SEQ ID No:376) ; SET 169: (SEQ ID No:402 ; SEQ ID No:403) ; SET 180: (SEQ ID No:430) and SET 186: (SEQ ID No:438 ; SEQ ID No:439),

30 wherein said sequences are useful in differentiating a tumor with lymph nodes from a tumor without lymph nodes.

13. A polynucleotide library according to Claim 12 wherein said polynucleotide sequences or subsequences thereof of said pool correspond to any combination of at least one polynucleotide selected among those included in at least 50%, preferably 75% and more preferably 100% of the predefined sets.

14. A library according to Claim 12 wherein the pool of polynucleotide sequences or subsequences correspond substantially to any combination of at least one polynucleotide sequence selected among those included in each one of predefined polynucleotide sequences sets comprising

SET 18: (SEQ ID No:39 ; SEQ ID No:40 ; SEQ ID No:41) ; SET 32: (SEQ ID No:76 ; SEQ ID No:77 ; SEQ ID No:78) ; SET 57: (SEQ ID No:135 ; SEQ ID No:136; SEQ ID No:137); SET 91: (SEQ ID No:216 ; SEQ ID No:217) and SET 105: (SEQ ID No:250 ; SEQ ID No:251 ; SEQ ID No:252)

and of at least one polynucleotide sequence selected among those included in each one of predefined polynucleotide sequences sets comprising:

SET 11: (SEQ ID No:22 ; SEQ ID No:23; SEQ ID No:24) ; SET 40: (SEQ ID No:97; SEQ ID No:98 SEQ ID No:99) ; SET 49: (SEQ ID No:118 ; SEQ ID No:119) ; SET 100: (SEQ ID No:238 ; SEQ ID No:239) and SET 141: (SEQ ID No:334; SEQ ID No:335 ; SEQ ID No:336).

15. A polynucleotide library according to Claim 14 wherein said polynucleotide sequences or subsequences thereof of said pool correspond to any combination of at least one polynucleotide selected among those included in at least 50%, preferably 75% and more preferably 100% of the predefined sets.

16. A library according to anyone of Claims 1 or 2 wherein the pool of polynucleotide sequences or

subsequences correspond substantially to any combination of at least one polynucleotide sequence selected among those included in each one of predefined polynucleotide sequences sets comprising:

5 SET 11: (SEQ ID No:22 ; SEQ ID No:23 ; SEQ ID No:24)
; SET 22: (SEQ ID No:48 ; SEQ ID No:49 ; SEQ ID No:50) ; SET 23:
(SEQ ID No:51 ; SEQ ID No:52 ; SEQ ID No:53) ; SET 26: (SEQ ID
No:59 ; SEQ ID No:60 ; SEQ ID No:61) ; SET 28: (SEQ ID No:65 ; SEQ
10 ID No:66 ; SEQ ID No:67) ; SET 31: (SEQ ID No:73 ; SEQ ID No:74 ;
SEQ ID No:75) ; SET 32: (SEQ ID No:76 ; SEQ ID No:77 ; SEQ ID
No:78) ; SET 34: (SEQ ID No:82 ; SEQ ID No:83) ; SET 49: (SEQ ID
No:118 ; SEQ ID No:119) ; SET 57: (SEQ ID No:135 ; SEQ ID No:136 ;
SEQ ID No:137) ; SET 64: (SEQ ID No:156 ; SEQ ID No:157 ; SEQ ID
15 No:158) ; SET 73: (SEQ ID No:178 ; SEQ ID No:179) ; SET 77: (SEQ ID
No:186) ; SET 81: (SEQ ID No:194 ; SEQ ID No:195) ; SET 95: (SEQ
ID No:226 ; SEQ ID No:227) ; SET 131: (SEQ ID No:308 ; SEQ ID
No:309 ; SEQ ID No:310) ; SET 138: (SEQ ID No:326 ; SEQ ID No:327
; SEQ ID No:328) ; SET 140: (SEQ ID No:331 ; SEQ ID No:332 ; SEQ
ID No:333) ; SET 149: (SEQ ID No:354 ; SEQ ID No:355) ; SET 162:
20 (SEQ ID No:385 ; SEQ ID No:386 ; SEQ ID No:387) ; SET 164: (SEQ ID
No:391 ; SEQ ID No:392 ; SEQ ID No:393) ; SET 165: (SEQ ID No:394
; SEQ ID No:395) and SET 183: (SEQ ID No:433 ; SEQ ID No:434),

 wherein said sequences are useful in
differentiating antracycline-sensitive tumors from
25 antracycline-insensitive tumors.

17. A polynucleotide library according to Claim
16 wherein said polynucleotide sequences or subsequences
thereof of said pool correspond to any combination of at
30 least one polynucleotide selected among those included in at
least 50%, preferably 75% and more preferably 100% of the
predefined sets.

18. A library according to Claim 16 wherein the
35 pool of polynucleotide sequences or subsequences correspond

substantially to any combination of at least one polynucleotide sequence selected among those included in each one of predefined polynucleotide sequences sets comprising

5 SET N° 32: (SEQ ID No:76; SEQ ID No:77; SEQ ID No:78)
; SET N°136: (SEQ ID No:322 ; SEQ ID No:323) ; SET N° 145: (SEQ ID
No:345; SEQ ID No:346) ; SET N° 149: SEQ ID No:354; SEQ ID No:355)
; SET N°169: (SEQ ID No:402 ; SEQ ID No:403)

10 and of at least one polynucleotide sequence
selected among those included in each one of predefined
polynucleotide sequences sets comprising:

15 SET No 11: (SEQ ID No:22; SEQ ID No:23 ; SEQ ID
No:24); SET No 40: (SEQ ID No:97 ; SEQ ID No:98 ; SEQ ID No:99) ;
SET No 57: (SEQ ID No:135 ; SEQ ID No:136 ; SEQ ID No:137) ; SET
No 119: (SEQ ID No:279 ; SEQ ID No:280 ; SEQ ID No:281) ; SET No
174: (SEQ ID No:414 ; SEQ ID No:415; SEQ ID No:416).

20 19. A polynucleotide library according to Claim
18 wherein said polynucleotide sequences or subsequences
thereof of said pool correspond to any combination of at
least one polynucleotide selected among those included in at
least 50%, preferably 75% and more preferably 100% of the
predefined sets.

25 20. A library according to anyone of Claims 1 or
2 wherein the pool of polynucleotide sequences or
subsequences correspond substantially to any combination of
at least one polynucleotide sequence selected among those
included in each one of predefined polynucleotide sequences
sets comprising

30 SET No 14 (SEQ ID No:30; SEQ ID No:31) ; SET No 23
(SEQ ID No:51; SEQ ID No:52; SEQ ID No:53) ; SET No 25 (SEQ ID
No:57; SEQ ID No:58) ; SET No 27 (SEQ ID No:62; SEQ ID No:63; SEQ
ID No:64) ; SET No 28 (SEQ ID No:65; SEQ ID No:66; SEQ ID No:67) ;
SET No 32 (SEQ ID No:76; SEQ ID No:77; SEQ ID No:78) ; SET No 39
35 (SEQ ID No:94; SEQ ID No:95; SEQ ID No:96) ; SET No 41 (SEQ ID

No:100; SEQ ID No:101; SEQ ID No:78) ; SET No 44 (SEQ ID No:106;
SEQ ID No:107; SEQ ID No:108) ; SET No 48 (SEQ ID No:115; SEQ ID
No:116; SEQ ID No:117) ; SET No 51 (SEQ ID No:122; SEQ ID No:78) ;
SET No 64 (SEQ ID No:156; SEQ ID No:157; SEQ ID No:158) ; SET No
5 81 (SEQ ID No:194; SEQ ID No:195) ; SET No 83 (SEQ ID No:199; SEQ
ID No:200) ; SET No 91 (SEQ ID No:216; SEQ ID No:217) ; SET No 96
(SEQ ID No:228; SEQ ID No:229) ; SET No 99 (SEQ ID No:235; SEQ ID
No:236; SEQ ID No:237) ; SET No 108 (SEQ ID No:257; SEQ ID No:258)
; SET No 110 (SEQ ID No:262; SEQ ID No:200) ; SET No 116 (SEQ ID
10 No:273; SEQ ID No:274) ; SET No 117 (SEQ ID No:275; SEQ ID No:276)
; SET No 118 (SEQ ID No:277; SEQ ID No:278) ; SET No 120 (SEQ ID
No:282; SEQ ID No:283; SEQ ID No:276) ; SET No 126 (SEQ ID No:296;
SEQ ID No:297;) ; SET No 142 (SEQ ID No:337; SEQ ID No:338; SEQ ID
No:117) ; SET No 144 (SEQ ID No:342; SEQ ID No:343; SEQ ID No:344)
15 ; SET No 149 (SEQ ID No:354; SEQ ID No:355) ; SET No 152 (SEQ ID
No:361; SEQ ID No:31) ; SET No 153 (SEQ ID No:362; SEQ ID No:363;
SEQ ID No:364) ; SET No 154 (SEQ ID No:365; SEQ ID No:366; SEQ ID
No:367) ; SET No 157 (SEQ ID No:372; SEQ ID No:373; SEQ ID No:108)
; SET No 159 (SEQ ID No:377; SEQ ID No:378; SEQ ID No:379) ; SET
20 No 162 (SEQ ID No:385; SEQ ID No:386; SEQ ID No:387) ; SET No 166
(SEQ ID No:396; SEQ ID No:397; SEQ ID No:398) ; SET No 167 (SEQ ID
No:399; SEQ ID No:400; SEQ ID No:117) ; SET No 168 (SEQ ID No:401)
; SET No 171 (SEQ ID No:406; SEQ ID No:407; SEQ ID No:408) ; SET
No 172 (SEQ ID No:409; SEQ ID No:410; SEQ ID No:411) ; SET No 173
25 (SEQ ID No:412; SEQ ID No:413) ; SET No 176 (SEQ ID No:420; SEQ ID
No:421; SEQ ID No:422) ; SET No 177 (SEQ ID No:423; SEQ ID No:424;
SEQ ID No:425) ; SET No 178 (SEQ ID No:426; SEQ ID No:427; SEQ ID
No:428) ; SET No 179 (SEQ ID No:429; SEQ ID No:408) ; SET No 184
(SEQ ID No:435; SEQ ID No:436) ; SET No 185 (SEQ ID No:437),

30 wherein said sequences are useful in classifying
good and poor prognosis primary breast tumors.

21. A polynucleotide library according to Claim
20 wherein said polynucleotide sequences or subsequences
35 thereof of said pool correspond to any combination of at
least one polynucleotide selected among those included in at

least 50%, preferably 75% and more preferably 100% of the predefined sets.

22. A library according to Claim 20 wherein the pool of polynucleotide sequences or subsequences correspond substantially to any combination of at least one polynucleotide sequence selected among those included in each one of predefined polynucleotide sequences sets comprising

SET N° 23 (SEQ ID No:51 ; SEQ ID No:52 ; SEQ ID No:53) ; SET N° 25 (SEQ ID No:57 ; SEQ ID No:58) ; SET N° 32 (SEQ ID No:76 ; SEQ ID No:77 ; SEQ ID No:78) ; SET N° 41 (SEQ ID No:100 ; SEQ ID No:101 ; SEQ ID No:78) ; SET N° 48 (SEQ ID No:115 ; SEQ ID No:116 ; SEQ ID No:117) ; SET N° 51 (SEQ ID No:122 ; SEQ ID No:78) ; SET N° 64 (SEQ ID No:156 ; SEQ ID No:157 ; SEQ ID No:158) ; SET N° 81 (SEQ ID No:194 ; SEQ ID No:195) ; SET N° 83 (SEQ ID No:199 ; SEQ ID No:200) ; SET N° 91 (SEQ ID No:216 ; SEQ ID No:217) ; SET N° 99 (SEQ ID No:235 ; SEQ ID No:236 ; SEQ ID No:237) ; SET N° 110 (SEQ ID No:262 ; SEQ ID No:200) ; SET N° 116 (SEQ ID No:273 ; SEQ ID No:274) ; SET N° 142 (SEQ ID No:337 ; SEQ ID No:338 ; SEQ ID No:117) ; SET N° 144 (SEQ ID No:342 ; SEQ ID No:343 ; SEQ ID No:344) ; SET N° 149 (SEQ ID No:354 ; SEQ ID No:355) ; SET N° 162 (SEQ ID No:385 ; SEQ ID No:386 ; SEQ ID No:387) ; SET N° 167 (SEQ ID No:399 ; SEQ ID No:400 ; SEQ ID No:117) ; SET N° 171 (SEQ ID No:406 ; SEQ ID No:407 ; SEQ ID No:408) ; SET N° 172 (SEQ ID No:409 ; SEQ ID No:410 ; SEQ ID No:411) ; SET N° 173 (SEQ ID No:412 ; SEQ ID No:413) ; SET N° 176 (SEQ ID No:420 ; SEQ ID No:421 ; SEQ ID No:422) ; SET N° 177 (SEQ ID No:423 ; SEQ ID No:424 ; SEQ ID No:425) ; SET N° 178 (SEQ ID No:426 ; SEQ ID No:427 ; SEQ ID No:428) ; SET N° 179 (SEQ ID No:429 ; SEQ ID No:408) ; SET N° 184 (SEQ ID No:435 ; SEQ ID No:436) ; SET N° 185 (SEQ ID No:437),

and at least one polynucleotide sequence selected among those included in each one of predefined polynucleotide sequences sets comprising:

SET No 14 (SEQ ID No:30 ; SEQ ID No:31) ; SET No 27 (SEQ ID No:62 ; SEQ ID No:63 ; SEQ ID No:64) ; SET No 28 (SEQ ID

No:65 ; SEQ ID No:66 ; SEQ ID No:67) ; SET No 39 (SEQ ID No:94 ;
SEQ ID No:95 ; SEQ ID No:96) ; SET No 44 (SEQ ID No:106 ; SEQ ID
No:107 ; SEQ ID No:108) ; SET No 96 (SEQ ID No:228 ; SEQ ID
No:229) ; SET No 108 (SEQ ID No:257 ; SEQ ID No:258) ; SET No 117
5 (SEQ ID No:275 ; SEQ ID No:276) ; SET No 118 (SEQ ID No:277 ; SEQ
ID No:278) ; SET No 120 (SEQ ID No:282 ; SEQ ID No:283 ; SEQ ID
No:276) ; SET No 126 (SEQ ID No:296 ; SEQ ID No:297) ; SET No 152
(SEQ ID No:361 ; SEQ ID No:31) ; SET No 153 (SEQ ID No:362 ; SEQ
ID No:363 ; SEQ ID No:364) ; SET No 154 (SEQ ID No:365 ; SEQ ID
10 No:366 ; SEQ ID No:367) ; SET No 157 (SEQ ID No:372 ; SEQ ID
No:373 ; SEQ ID No:108) ; SET No 159 (SEQ ID No:377 ; SEQ ID
No:378 ; SEQ ID No:379) ; SET No 166 (SEQ ID No:396 ; SEQ ID
No:397 ; SEQ ID No:398) ; SET No 168 (SEQ ID No:401),

wherein the combination of overexpression of the
15 genes identified by said first group of cluster sequences
with the underexpression of the genes identified by said
second group of cluster sequences are useful in classifying
good and poor prognosis primary breast tumors.

20 23. A polynucleotide library according to Claim
22 wherein said polynucleotide sequences or subsequences
thereof of said pool correspond to any combination of at
least one polynucleotide selected among those included in at
least 50%, preferably 75% and more preferably 100% of the
25 predefined sets.

24. A polynucleotide library according to anyone
of Claims 1 to 23 wherein said tumor cells are breast tumor
cells.

30 25. A polynucleotide library according to any of
Claims 1 to 23 wherein said polynucleotides are immobilized
on a solid support in order to form a polynucleotide array.

26. A polynucleotide library according to Claim 25 wherein the support is selected from the group comprising a nylon membrane, nitrocellulose membrane, glass slide, glass beads, membranes on glass support or a silicon chip.

5

27. A polynucleotide array useful for prognosis or diagnostic of tumor comprising an immobilized polynucleotide library according to Claims 1 to 3.

10

28. A polynucleotide array useful to differentiate a normal cell from a cancer cell comprising any combination of immobilized polynucleotide sequences sets according to claims 4 to 7.

15

29. A polynucleotide array useful to detect a hormone sensitive tumor cell comprising any combination of immobilized polynucleotide sequences sets according to claims 8 to 11.

20

30. A polynucleotide array useful to differentiate a tumor with lymph nodes from a tumor without lymph nodes comprising any combination of immobilized polynucleotide sequences sets according to claims 12 to 15.

25

31. A polynucleotide array useful to differentiate antracycline-sensitive tumors from antracycline-insensitive tumors comprising any combination of immobilized polynucleotide sequences sets according to claims 16 to 19.

30

32. A polynucleotide array useful to classify good and poor prognosis primary breast tumors comprising any

combination of immobilized polynucleotide sequences sets according to claim 20 to 23.

5 33. A method of detecting differentially expressed polynucleotide sequences which are correlated with a cancer, said method comprising:

a) obtaining a polynucleotide sample from a patient and

10 b) reacting said polynucleotide sample obtained in step (a) with a probe immobilized on a solid support wherein said probe comprises any combination of the polynucleotide sequences of the polynucleotide library of Claims 1 to 23 or any combination of expression products encoded by any of the polynucleotide sequences of the
15 libraries of Claims 1 to 23 and

c) detecting the reaction product of step (b).

20 34. A method for detecting differentially expressed polynucleotide sequences according to Claim 33 wherein said polynucleotide sample is labeled before its reaction step.

25 35. A method for detecting differentially expressed polynucleotide sequences according to Claim 34 wherein the label of the polynucleotide sample is selected from the group consisting of radioactive, colorimetric, enzymatic, molecular amplification, bioluminescent or fluorescent labels.

30 36. A method for detecting differentially expressed polynucleotide sequences according to Claims 33 to 35 further comprising obtaining a control polynucleotide sample, reacting said control sample with said probe

detecting a control sample reaction product and comparing the amount of said polynucleotide sample reaction product to the amount of said control sample reaction product.

5 37. A method for detecting differentially expressed polynucleotide sequences according to Claims 33 to 36 wherein the polynucleotide sample is cDNA, RNA or mRNA.

10 38. A method for detecting differentially expressed polynucleotide sequences according to Claim 37 wherein mRNA is isolated from said polynucleotide sample and cDNA is obtained by reverse transcription of said mRNA.

15 39. A method for detecting differentially expressed polynucleotide sequences according to Claims 33 to 38 wherein said reaction step is performed by hybridising the polynucleotide sample with the probe.

20 40. A method for detecting differentially expressed polynucleotide sequences according to Claims 33 to 39 wherein said method is used for detecting, diagnosing, staging, monitoring, predicting, preventing or treating conditions associated with cancer.

25 41. A method for detecting differentially expressed polynucleotide sequences according to Claims 33 to 40 wherein the cancer is breast cancer.

30 42. A method for detecting differentially expressed polynucleotide sequences according to Claims 33 to 41 wherein the product encoded by any of the polynucleotide sequences or polynucleotide sequences sets is involved in a receptor-ligand reaction on which detection is based.

43. A method for screening an anti-tumor agent comprising the method of Claim 33 wherein said polynucleotide sample is obtained from a patient treated with the anti-tumor agent to be screened.

Figure 1

Normal Breast

Figure 1A

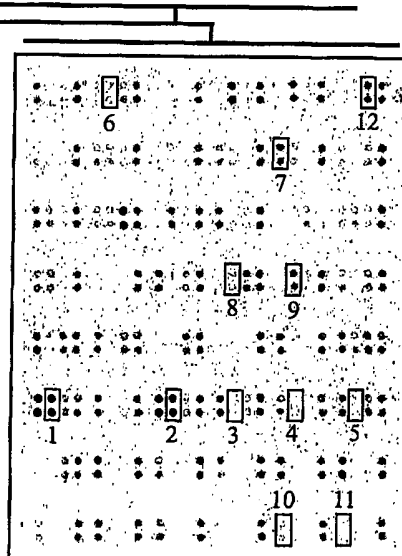
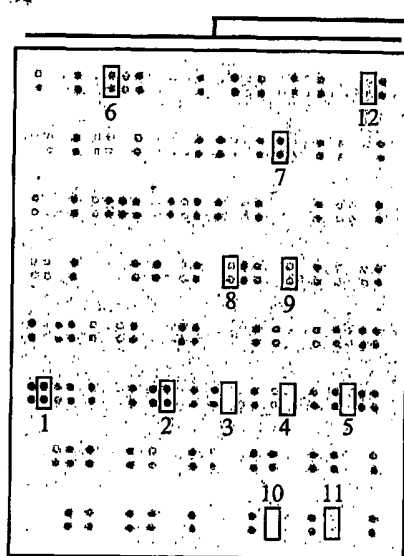
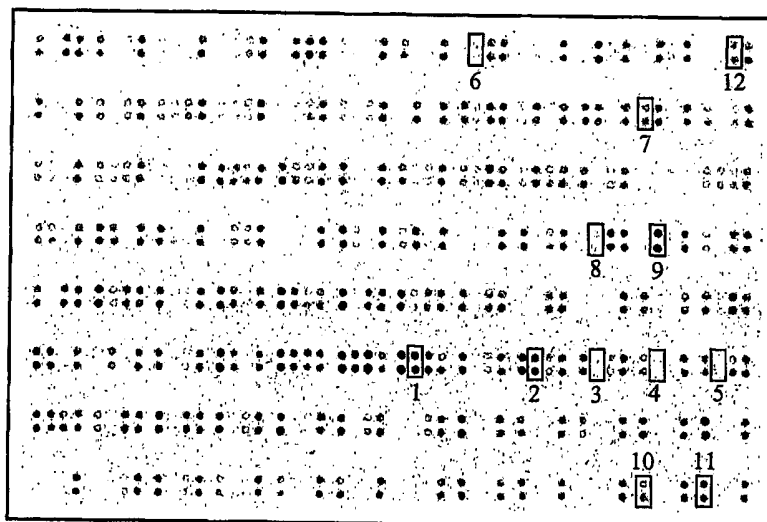


Figure 1B

ER-

ER+

Figure 1C

Breast cancer

Figure 2

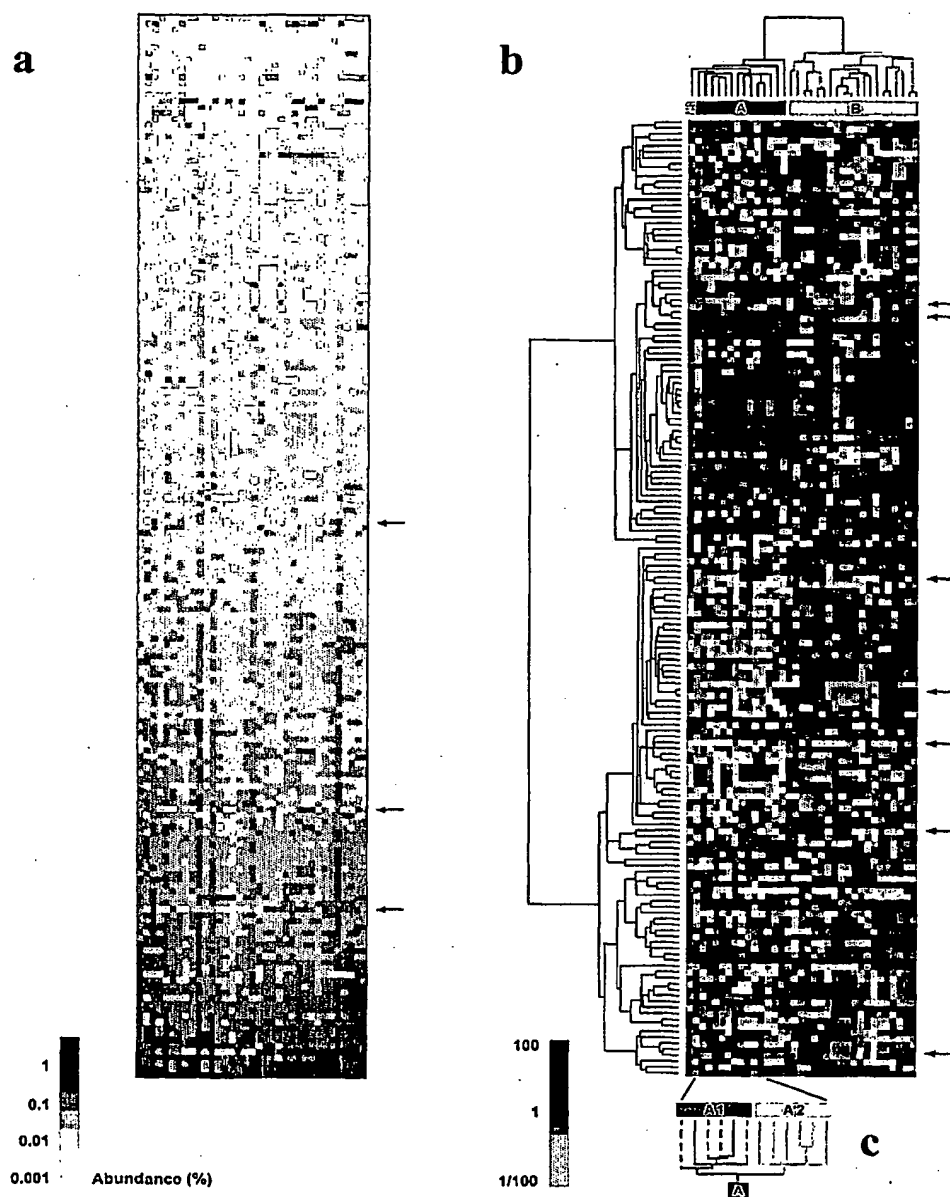


Figure 3

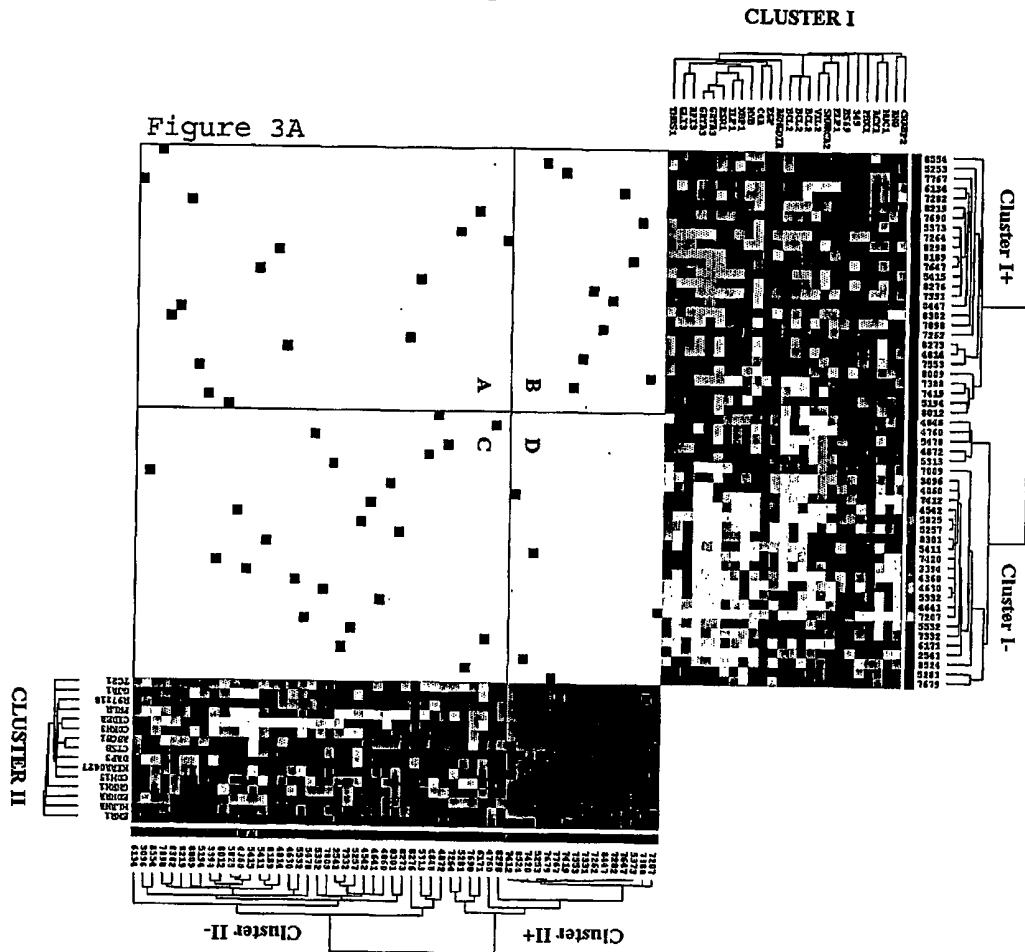


Figure 3C

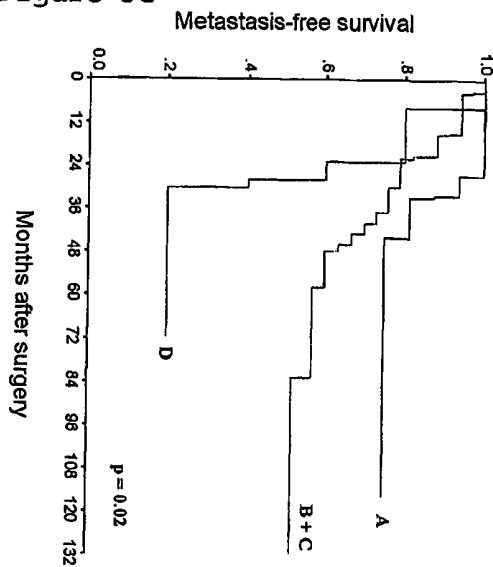


Figure 3B

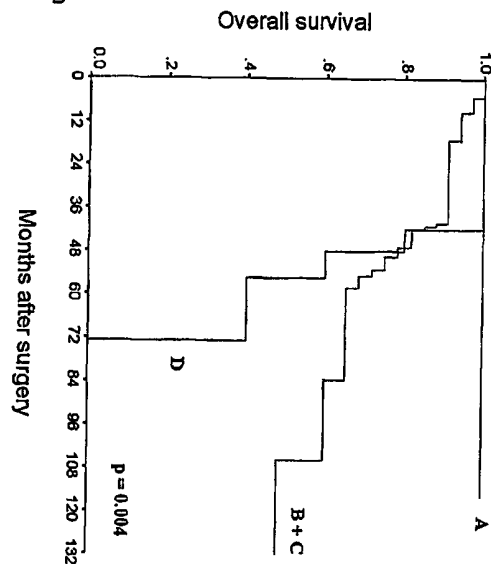


Figure 4

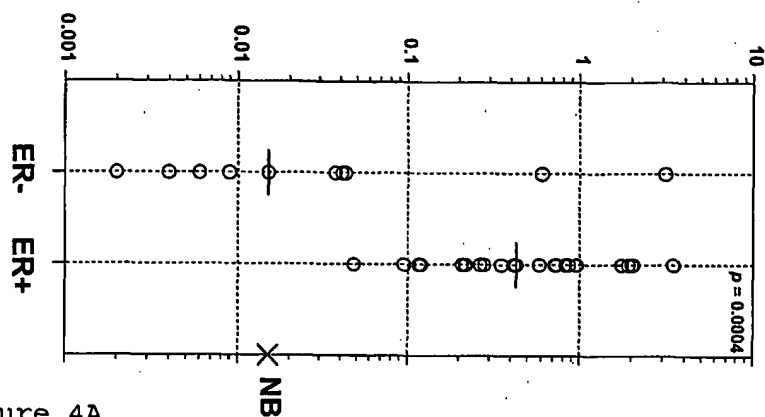


Figure 4A

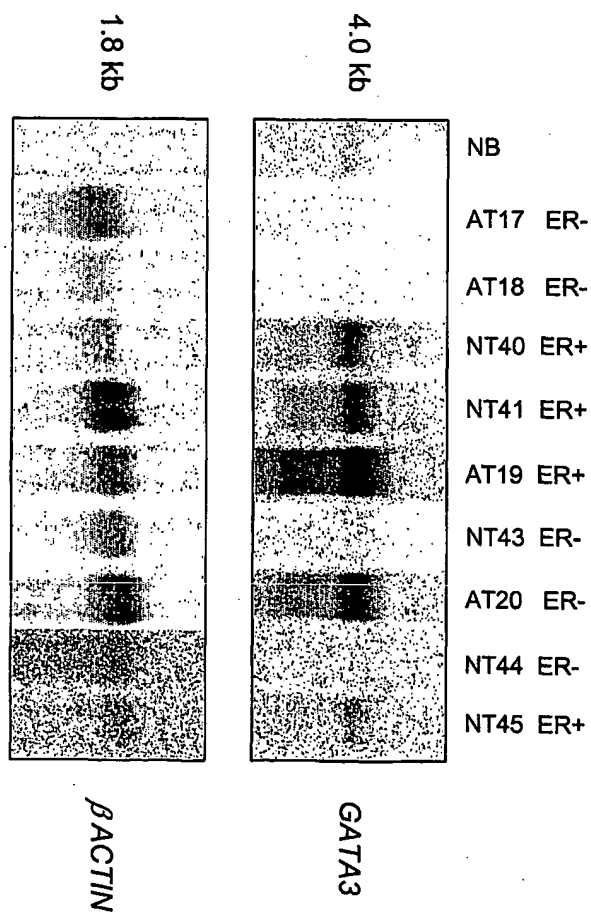


Figure 4B

SEQUENCE LISTING

<110> Ipsogen SAS

<120> cDNA arrays and their use for gene expression profiling.

<110> François Bertucci
Rémi Houlgatte
Daniel Birnbaum
Catherine Nguyen
Patrice Viens
Fert, vincent

<120> cDNA arrays and their use for gene expression profiling.

<130> 10813PCT-December-2001-ipsogen

<140> PCT/IB/xxxx
<141> 2001-12-07

<150> US-60/254,090
<151> 2000-08-12

<150> US-xx/xxxxx
<101> 2001-08-12

<160> 468

<170> PatentIn Ver. 2.1

<210> 1
<211> 317
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<220>
<221> misc_feature
<222> (1)..(317)
<223> 3' terminal sequence. hiv -1 rev binding protein (HRB) gene.

<400> 1
tttttttcac ctgcaaactg tagcaaaaca t gatcagctt tattatgcag acaggtatcc 60
ctctacattt taaaagaatt taggcatgta taaatagaag agctcttttag aaaggaaaaan 120
ttcaagantg aataaaacct tccaattttg actctgttac tttccagtag caatgggttaa 180
aatgntttta ggncattcat tccaagntat atgacagcac cttaaaagtg gctgatctat 240
ttccccagna acattttctca cataacaatg tgggttaact tncaactact gcatatgcac 300
aaatnggcta atttcta 317

<210> 2
<211> 2584
<212> DNA/RNA
<213> Artificial Sequence

2/292

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(2584)

<223> hiv-1 rev binding protein (HRB) gene.

<400> 2

```
tgccggcgccg ggccggcggtt gtccggcggtg tgccgggttg tgtggcccggt cagcccgcggt 60
accacagcgc ccgggcccgcg tcgagcccag tacagccaag ccgctgcggc cgggtccggc 120
gcggggcgccg cgcgcagacg gagggcgg cg gccgcggcca gggcgcccg tgggaccgcg 180
ggcccccgccg gcagcgctgc ccggctcccg gccctgccgg cctcctccct tggcgcccg 240
gccatggcgg ccagcgcgaa gcggaagcag gaggagaagc acctgaagat gctgcgggac 300
atgaccggcc tcccgcgcaa ccgaaagtgc ttgcactgcg accagcgcg cccacctac 360
gttaacatga cggtcggctc cttcgtgtgt acctcctgct ccggcagcct gcgaggatta 420
aatccaccac acagggtgaa atctatctcc atgacaacat tcacacaaca ggaaattgaa 480
ttcttataaa aacatggaaa tgaagtctgt aaacagattt ggctaggatt atttgatgat 540
agatcttcag caattccaga cttcagggat ccacaaaaag tgaaagag tt tctacaagaa 600
aagtatgaaa agaaaagatg gtatgtcccg ccagaacaag ccaaagtcgt ggcatacatt 660
catgcatact tttcagggtc ctctgccagt agcacaagca gcacacctga ggtcaaacca 720
ctgaaactct ttttagggga ttctgcacca acactgcact taaataaggg cacacctagt 780
cagtcgccag ttgtaggctg ttctca aggg cagcagcagg agaagaagca atttgacctt 840
ttaagtgatc tcggctcaga catctttgct gctccagctc ctcagtcaac agctacagcc 900
aattttgcta actttgcaca tttaacagt catgcagctc agaattctgc aaatgcagat 960
tttgcaaaact ttgatgcatt tggacagctt agtggttcga gtaatttttg aggtttcccc 1020
acagcaagtc actctccttt tcagccccaa actacagggtg gaagtgcctc atcagtaaat 1080
gctaattttg ctcattttga taacttcccc aaactctcca gtgctgattt tggaaccttc 1140
aataactccc agagtcacat aacagcatca gctgttagta aagtttcaac gaacaaagct 1200
ggtttacaga ctgcagacaa atatgcagca cttgctaatt ta gacaatat cttcagtgcc 1260
gggcaagggt gtgatcaggg aagtggcttt gggaccacag gtaaagctcc tgttggttct 1320
gtggtttcag ttcccagtcg gtcaagtgcg tcttcagaca agtatgcagc tctggcagaa 1380
ctagacagcg ttttcagttc tgcagccacc tccagtaatg cgtatacttc cacaagtaat 1440
gctagcagca atgtttt tgg aacagtgcga gtggttgctt ctgcacagac acagcctgct 1500
tcatacaagt tgccgtctcc atttgagcgt acgcttcca caaatccatt tgttgctgct 1560
gctggtcctt ctgtggcact ttctacaaac ccatttcaga ccaatgccag aggagcaaca 1620
gcggcaacct ttggcactgc atccatgagc atgcccacgg gattcggcac tctgc tccc 1680
tacagtcttc ccaccagctt tagtggcagc tttcagcagc ctgcctttcc agcccaagca 1740
gctttccctc aacagacagc tttttctcaa cagcccaatg gtgcaggttt tgcagcattt 1800
ggacaaacaa agccagtagt aacccctttt ggtcaagttg cagctgctgg agtatctagt 1860
aatcctttta tgactgggtc accaacagga caatttccaa caggaagctc atcaaccaat 1920
cctttcttat agccttatat agacaattta ctggaacgaa cttttatgtg gtcacattac 1980
atctctccac ctcttgcact gttgtcttgt ttcaactgac ttagctttta acacaagaga 2040
agtcttttaa aagcctgcat tgtgtattaa acaccaggta atatgtgcaa aaccgagggc 2100
tccagtaaca ccttctaacc tgtgaattgg cagaaaaggg tagcggatc atgtatatta 2160
aaattggcta atattaagtt atttcagata ccacattcat tatgtgcag tactgtacat 2220
atttttctta gaaattagct atttgtgcat atcagtattt gtaactttta cacattgtta 2280
tgtgagaaat gttactgggg aaatagatca gccactttta aggt gctgtc atatatcttg 2340
gaatgaatga cctaaaatca ttttaacct tgctactgga aagtaacaga gtcaaaattg 2400
gaagggttta ttcatctctg aatttttctt ttctaaagag ctcttctatt tatacatgcc 2460
taaattcttt taaaatgtag agggatacct gtctgcataa taaagctgat catgttttgc 2520
tacagtttgc aggtgaaaa a aaataaatat tataaaataa aaaaaaaaaa aaagaaaaaa 2580
aaaa 2584
```

<210> 3

<211> 417

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(417)

<223> 5' terminal sequence. gata-binding protein 1
(globin transcription factor 1) (GATA1) gene.

<400> 3

```
ccaggagntg cattggagtt ccttggcctg ggttccctgg ggcttcagag cccctccccc 60
agtttgtgga tctgtctctg gtgtcctcca caccagaatc aggggtttt c tccccctctg 120
ggcctgaggg cttggatgca gcagcttct cactgcccc gagcacagcc accgctgcag 180
ctgcggcact ggcctactac agggacgtg aggcctacag aactcccca gtctttcagg 240
tgtaccatt gcttcaactg tatggagggg atcccagggg gcttcacat attgccggct 300
ggggctnacg gaaaggacgg ggttnt aac ctgnctcaa ttgtgtgttc ccaaccngga 360
gaatttttct tcccagggn cttggaagat ttnggattgg naaaaggga gnaacaa 417
```

<210> 4

<211> 1498

<212> DNA/RNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(1498)

<223> gata-binding protein 1 (globin transcription
factor 1) (GATA1) gene.

<400> 4

```
gcaaaggcca aggccagcca ggacaccccc tgggatcaca ctgagcttgc cacatcccca 60
aggcgccga accctccgca accaccagcc caggttaatc cccagaggct ccatggagtt 120
ccttggcctg ggttccctgg ggacctcaga gcccctcccc cagtttgtgg atcctgctct 180
ggtgtcctcc acaccagaat caggggtttt ctccccctct gggcctgagg gcttggatgc 240
agcagcttcc tccactgccc cgagcacagc caccgtgca gctgcggcac tggcctacta 300
cagggacgct gaggcctaca gacactcccc agtctttcag gtgtacccat t gctcaactg 360
tatggagggg atcccagggg gctcaccata tgccggctgg gctacggcca agacggggct 420
ctaccctgcc tcaactgtgt gtcccacccg cgaggactct cctccccagg ccgtggaaga 480
tctggatgga aaaggcagca ccagcttctt ggagactttg aagacagagc ggctgagccc 540
agacctctg accctgggac ctgcaactgcc ttcatcactc cctgtcccca atagtgetta 600
tgggggccct gacttttcca gtaccttctt ttctcccacc gggagccccc tcaattcagc 660
agcctattcc tctcccaagc ttctgtgaac ttccccctg cctccctgtg aggccaggga 720
gtgtgtgaac tgcggagcaa cagccactcc actgtggcgg agggacagga caggccacta 780
cctatgcaac gctgcgggc tctatcacia gatgaatggg cagaacaggc cctcatccg 840
gcccagaagc cgctgattg tcagtaaacg ggcaggtact cagtgcacca actgccagac 900
gaccaccacg aactgtggc ggagaaatgc cagtgggat cccgtgtgca atgcctgcgg 960
cctctactac aagctacacc aggtgaaccg gccactgacc atgcggaagg atggtattca 1020
gactcgaac cgcaaggcat ctggaaaagg gaaaaagaaa cggggctcca gtctgggagg 1080
cacaggagca gccgaaggac cagctgggtg ctttatggtg gtggctgggg gcagcggtag 1140
cgggaattgt ggggaggtg cttcaggcct gacactgggc cccccaggta ctgccatct 1200
ttaccaaggc ctgggcctg ttgt gctgtc agggcctgtt agccacctca tgcctttccc 1260
tgaccacctc ctgggctcac ccacgggctc cttcccaca ggcccatgc cccccaccac 1320
cagcactact gtggtggctc cgctcagctc atgaggcac agagcatggc ctccagagga 1380
gggggtgtgt ccttctctc ttgtagccag aattctggac aacccaagtc tctgggcccc 144 0
aggaccccc tggcttgaac cttcaaagct tttgtaaaat aaaaccacca aagtcctg 1498
```

<210> 5

4/292

<211> 423
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<220>
<221> misc_feature
<222> (1)..(423)
<223> 5' terminal sequence. t ousled-like kinase 2
(TLK2) gene.

<400> 5
ggcacgagga gaatacgatt cttaaagcta ctgaagtgca gttcccgcca aagccagtag 60
taacacctga agcaaaggcg tttattcgac gatgcttgcc ctaccgaaag aggaccgcat 120
tgatgtccag cagctggcct gtgaccccta cttgttgcc caccatccgaa agtcagtcctc 180
tacaagtagc cctgctggag ctgctattgc atcaacctct ggggcgtcca ataacagttc 240
ttctaattga gactgactcc aaggccacaa actgttcaac acacacaaag tgggacaaat 300
gggcgtttca gcaggcgggt ttgggaacat aggcgaatcc gaatgggtac ttgatggaaa 360
cctgttacca ggtgnttttt attttatttg aattttttt t nccatnccct agaggcttgg 420
aca 423

<210> 6
<211> 3327
<212> DNA/RNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<220>
<221> misc_feature
<222> (1)..(3327)
<223> tousled-like kinase 2 (TLK2) gene.

<400> 6
ccgggcgggg ggttgcggcg ctccaggagag gccccggctc cgccccgggc ctgccaggg 60
ggagagcgga gctccgcagc cgggtcgggt cggggcccct cccgggagga gcgtggagcg 120
cggcggcggc ggccgcagca gaaatgatgg aagaattgca tagcctggac ccacgacgg c 180
aggaattatt ggaggccagg tttactggag taggtgttag taagggacca cttaatagtg 240
agtccttcaa ccagagcttg tgacgcgtcg gatccttgag tgataaagaa gtagagactc 300
ccgagaaaaa gcagaatgac cagcgaaatc ggaaaagaaa agctgaacca tatgaaacta 360
gccaagggaaggaggactcct aggggacata aaattag tga ttactttgag ttgctgggg 420
gaagcgcgcc aggaaccagc cctggcagaa gtgttccacc agttgcacga tcctcaccgc 480
aacattcctt atccaatccc ttaccgcgac gtagtagaaca gccctctat ggttttagatg 540
gcagtgtctg aaaggaggga acggaggagc agtctgtctt gccaacctc atgtcagtga 600
tgctagcaaa acctcgctt gacacagagc agctggcgca aaggggagct ggcctctgct 660
tcacttttgt ttcagctcag caaaacagtc cctcatctac gggatctggc aacacagagc 720
attcctgcag ctcccaaaaa cagatctcca tccagcacag acggaccag tccgacctca 780
caatagaaaa aatatctgca ctagaaaaca gtaagaattc tgacttagag aagaagg agg 840
gaagaataga tgatttatta agagccaact gtgatttgag acggcagatt gatgaacagc 900
aaaagatgct agagaaatac aaggaacgat taaatagatg tgtgacaatg agcaagaaac 960
tccttataga aaagtcaaaa caagagaaga tggcgtgtag agataagagc atgcaagacc 1020
gcttgagact gggccacttt actactgtcc gaca cggagc ctcatctact gaacagtgga 1080
cagatgggta tgcttttcag aatcttatca agcaacagga aaggataaat tcacagaggg 1140
aagagataga aagacaacgg aaaatgttag caaagcggaa acctcctgcc atgggtcagg 1200
cccctcctgc aaccaatgag cagaaacagc ggaaaagcaa gaccaatgga gctgaaaatg 1260
aaacgttaac gttagcagaa taccatgaac aagaagaaat cttcaaactc agattaggtc 1320
atcttaaaaa ggaggaagca gagatccagg cagagctgga gagactagaa agggttagaa 1380

```
atctacatat cagggaaacta aaaaggatac ataatgaaga taattcaciaa tttaaagatc 1440
atccaacgct aaatgacaga tatttggtgt tacatctttt gggtagag ga gggttcagt 1500
aagtttaciaa ggcatttgat ctaacagagc aaagatacgt agctgtgaaa attcaccagt 1560
taaataaaaaa ctggagagat gagaaaaagg agaattacca caagcatgca ttagagggaat 1620
accggattca taaagagctg gatcatccca gaatagttaa gctgtatgat tacttttcac 1680
tggatactga ctcgttttgt ac agtattag aatactgtga gggaaatgat ctggacttct 1740
acctgaaaca gcacaaatta atgtcggaga aagaggcccg gtccattatc atgcagattg 1800
tgaatgcttt aaagtactta aatgaaataa aacctcccat catacactat gacctcaaac 1860
caggtaatat tcttttagta aatggtacag cgtgtggaga gataaaaatt acagattttg 1 920
gtctttcgaa gatcatggat gatgatagct acaattcagt ggatggcatg gagctaacaat 1980
cacaagggtgc tggactttat tggatattac caccagagtg ttttgtggtt gggaaagaac 2040
caccaaatgat ctcaaatataa gttgatgtgt ggtcgggtgg tgtgatcttc tatcagtgtc 2100
tttatggaag gaagcctttt ggccataacc agtctc agca agacatccta caagagaata 2160
cgattcttaa agtactgaa gtgcagttcc cgccaaagcc agtagtaaca cctgaagcaa 2220
aggcgtttat tgcagcatgc ttggcctacc gaaagaggga cgcattgat gtccagcagc 2280
tggcctgtga tccctacttg ttgcctcaca tccgaaagtc agtctctaca agtagccctg 2340
ctggagctgc tattgcatca acctctgggg cgtccaataa cagttcttct aattgagact 2400
gactccaagg ccacaaactg ttcaacacac acaaagtga caaatggcgt tcagcagcgg 2460
gtttggaaca tagcgaatcc gaatggatct gatgaaacct gtaccagggt cttttatttt 2520
cttgcttttt tcccatccat agagcatgac agcatcgatt ctcatlgagg agaaaccttg 2580
ggcagctccg gccaggcctt gtaggaaaag gcccgcggcg aggttcagc gtcaacggcc 2640
actgtgtgtg gctgctctga gtgaggaaaa aattaaaaag aaaaactggt tccatgtact 2700
gtgaacttga aaacttgcat actcaggggg gtccctgatg cagtgcctca gatgaagaat 2760
gtggacttga aaatacagac tggg ctatgc cagtgtctat atttaactt gttcttttct 2820
tttaataaag tttaggtaac atctcctgaa aagctttag cacaagggt cagctgggga 2880
tgggttttga cttcggagga aaaaagtgc tattgccgt taaaggcact agagttagtg 2940
ttttatccct aaataatttc aatttttaaa aacatgcagc ttccctctcc ctttttttat 300 0
ttttgaaga atacatttg tcataaagtg aaaccgtat tagcaagtac gaggcaatgt 3060
tcattccaat cagatgcagc tttctcctcc gtctggtctc ctgtttgcaa ttgcttccct 3120
catctcagta gggaaaaaat tgagtgggag tactgagatg tgtgggtttt tgccattgga 3180
caaagaatga ggttagaaga ctgcagcttg gactctct ct aggttttcaa ctatttcttc 3240
acaatttgaa cacttgacgg ttgtcccttt taatttattt gaagtgtctat ttttttaaat 3300
aaaggttcat ctgtccatgc aaaaaaa 3327
```

<210> 7

<211> 300

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(300)

<223> 3' terminal sequence. ests, weakly similar
to alu7_human alu subfamily sq sequence
contamination warning entry [h.sapiens] (EST
T81919) gene.

<400> 7

```
tncaagagac aggggttnngc acattgccca ggatgggtctc aaactcctag agttgagcta 60
tccaccacc tttggcctnc caaagtgtc ggatcacagg cgtgagtcac tgnctccagc 120
acccatctgg aggttcttta aagcccaggc cccacgccga gcttctgagt caataaagaa 180
gtctgcattt ctaacaagct tctaggggat gctgctgctg ctgctggtcc aggggcccca 240
ctttgaagaa cactgcact gggnttttcc tctgggaccc gaatgcctgt gcttctcccc 300
```

<210> 8

<211> 369

6/292

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(369)

<223> 5' terminal sequence. ests, weakly similar
to alu7_human alu subfamily sq sequence
contamination warning entry [h.sapiens] (EST
T81919) gene.

<400> 8

cctaacgcag gtttccccgc aaatgactgg tcacgcggga ctgaacaccg cacaggcagg 60
aggcatggca agggtaagtg aa ctgaagca ctttcaatac ttcctaccta accgcgggct 120
ttccctccga gtaatgcgta aaatgggacc acgtggccca ctctgtttt tcctcttggg 180
ctctccacgt gccactcatg cttggaagag acagatttct ttctaggata aagatctctg 240
ccccatttct gtcttttaaa atggagaatt ctttaaagaa gtagggacag cttncagggt 300
cagggcagtt tgggaaagtn acaggggcct aattgtgttc cgtggaaacn ggggtaggag 360
gtttgcttt 369

<210> 9

<211> 255

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(255)

<223> 3' terminal sequence. cyclin d1 (prad1:
parathyroid adenomatosis 1) (CCND1) gene.

<400> 9

aaagacagtt tttgggtaat cttttncctt tgcttaagtc agagatggaa gggggaaaga 60
gcaaaggaaa aaacaaccaa caacaaggag aatgaagctt tcccttctgg tatcaaaatg 120
ctccggagag gagggactnt cagtggagca cctggggccg gctccgcctc gctgcgggtg 180
gcggtggcgc ccctngcctg gcgccttcag atgtccacgt cccgcacgtc ggtgggtntg 240
caagccaggt ccacc 255

<210> 10

<211> 1325

<212> DNA/RNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(1325)

<223> cyclin d1 (prad1: parathyroid adenomatosis
1) (CCND1) gene.

<400> 10

```

gcagtagcag cgagcagcag agtccgcac g ctccggcgag gggcagaaga gcgcgaggga 60
gcgcggggca gcagaagcga gagccgagcg cggacccagc caggaccac agccctcccc 120
agctgcccag gaagagcccc agccatggaa caccagctcc tgtgctgcga agtggaacc 180
atccgccgcg cgtaccccga tgccaacctc ctcaacgacc ggggtgctgcg ggccatgctg 240
aaggcggagg agacctgcgc gccctcggtg tcctacttca aatgtgtgca gaaggaggtc 300
ctgccgtcca tgcggaagat cgtcgccacc tggatgctgg aggtctgcga ggaacagaag 360
tgcgaggagg aggtcttccc gctggccatg aactacctgg accgcttctt gtcgctggag 420
cccgtgaaaa agagccgcct gcagctgctg ggggccactt gcatgttcgt ggcctctaag 480
atgaaggaga ccatccccct gacggccgag aagctgtgca tctacaccga cggctccatc 540
cggcccgagg agctgctgca aatggagctg ctctgtgtga acaagctcaa gtggaacctg 600
gccgcaatga ccccgacga ttctattgaa cacttcctct ccaaatgcc agaggcggag 660
gagaacaaac agatcatccg caaacacg cg cagaccttcg ttgcctcttg tgccacagat 720
gtgaagttca ttccaatcc gccctccatg gtggcagcgg ggagcgtggt ggccgcagtg 780
caagggctga acctgaggag cccaacaac ttctgtctt actaccgctt cacacgcttc 840
ctctccagag tgatcaagtg tgaccagac tgctccggg cctgccagga gcagatcgaa 900
gccctgctgg agtcaagcct gcgccaggcc cagcagaaca tggaccccaa ggccgccgag 960
gaggaggaag aggaggagga ggaggtggac ctggcttgca caccaccga cgtgcgggac 1020
gtggacatct gaggggcca ggcaggcggg cgccaccgcc accgcagcg agggcggagc 1080
cggccccagg tgctccacat gacagtcctt cctctccgga gcattt tgat accagaaggg 1140
aaagcttcat tctcttgtt gttggtgtt tttctcttg ctctttccc cttccatctc 1200
tgacttaagc aaaagaaaaa gattacccaa aaactgtctt taaaagagag agagagaaaa 1260
aaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 1320
aaaaa                                           1325

```

<210> 11

<211> 449

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(449)

<223> 5' terminal sequence. signal transducer and
activator of transcription 1, 91kd (STAT1) gene.

<400> 11

```

atttgaagt caaagtotta ttgataaag atgtgaatga gagaaatata gtaaaaggat 60
ttaggaagtt caacattttg ggcacgcaca caaaagtgat gaacatggag gagtccacca 120
atggcagtct ggcggctgaa ttctggcacc tgcaattgaa agaacaga aa aatgctggca 180
ccagaacgaa tgagggtcct ctcacgttta ctgaagagct tcactccott agttttgaaa 240
cccaattgtg ccagcctggg tttggtaatt gacctcgaga cgacctctct gcccgttgtg 300
ggtgatctcc aacgtcagcc agctcccag cgggtggggc ctccattcct ttgggtacaa 360
catgctgggt nggcgggaac ccgggg antc tgttccttnt ttcttgact ccaccatgtg 420
ncacggtggg gtttcagntt ttcagaagt                                           449

```

<210> 12

<211> 4003

<212> DNA/RNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(4003)

<223> signal transducer and activator of
transcription 1, 91kd (STAT1) gene.

<400> 12

```
attaaacctc tcgccgagcc cctccgcaga ctctgcgcgc gaaagtttca tttgctgtat 60
gccatcctcg agagctgtct aggttaacgt tcgcactctg tgtatataac ctgcacagtc 120
ttggcaccta acgtgctgtg cgtagctgct cctttgggtg aatccccagg cccttggttg 180
ggcacaaggt ggcaggatgt ctcaagtgtg cgaacttcag cagcttgact caaaattcct 240
ggagcagggt caccagcttt atgatgacag ttttcccatg gaaatcagac agtacctggc 300
acagtgttta gaaaagcaag actgggagca cgctgccaat gatgttt cat ttgccaccat 360
ccgttttcat gacctcctgt cacagctgga tgaatcaaat agtcgctttt ctttgagaa 420
taacttcttg ctacagcata acataaggaa aagcaagcgt aatcttcagg ataattttca 480
ggaagaccca atccagatgt ctatgatcat ttacagctgt ctgaaggaa aaaggaaaaat 540
tctggaacaa gccagagat ttaat caggc tcagtcgggg aatattcaga gcacagtgtat 600
gttagacaaa cagaagagc ttgacagtaa agtcagaaat gtgaaggaca aggttatgtg 660
tatagagcat gaaatcaaga gcctggaaga tttacaagat gaatatgact tcaaagcaa 720
aaccttgtag aacagagaac acgagaccaa tgggtgtggc aagagtgtac agaaacaaga 780
acagctgtta ctcaagaaga tgtatttaat gcttgacaat aagagaaagg aagtagttca 840
caaaataata gaggttgctga atgtcactga acttaccagc aatgccctga ttaatgatga 900
actagtggag tggaaagcga gacagcagag cgctgtattt ggggggcccgc ccaatgcttg 960
cttggtacag ctgcagaact ggttcactat agttgcggag agtct gcagc aagttcggca 1020
gcagcttaaa aagttggagg aattggaaca gaaatacacc tacgaacatg accctatcac 1080
aaaaaacaaa caagtgttat gggaccgcac cttcagtcct ttccagcagc tcattcagag 1140
ctcgtttgtg gtgaaagac agcctgtcat gccaacgcac cctcagaggc cgctggtctt 1200
gaagacaggg gtccagttca ctgtgaagtt gagactgttg gtgaaattgc aagagctgaa 1260
ttataatttg aaagtcaaaag tcttatttga taaagatgtg aatgagagaa atacagtaaa 1320
aggatttagg aagttcaaca ttttgggcac gcacacaaa gtgatgaaca tggaggagtc 1380
caccaatggc agtctggcgg ctgaatttcg gcacctgcaa ttgaaagaac agaaaaatg c 1440
tggcaccaga acgaatgagg gtccctcatc cgttactgaa gagcttccact cccttagttt 1500
tgaaacccaa ttgtccagc ctggttttgt aattgacctc gagacgacct ctctgcccg 1560
tgtgtgtatc tccaacgtca gccagctccc gagcgggttg gcctccatcc tttggtacaa 1620
catgctggtg gcggaaccca ggaatctgtc ctt cttcctg actccaccat gtgcacgatg 1680
ggctcagctt tcagaagtgc tgagttggca gttttcttct gtcacccaaa gaggtctcaa 1740
tgtggaccag ctgaacatgt tgggagagaa gcttcttggt cctaacgcca gcccgatgg 1800
tctcattccg tggacgaggt ttgtgaagga aaatataaat gataaaaatt ttccctctg 1860
gctttggaat gaaagcatcc tagaactcat taaaaaacac ctgctccctc tctggaatga 1920
tgggtgtatc atgggttca tcagcaagga gcgagagcgt gccctgttga aggaccagca 1980
gccggggacc ttctgtctgc ggttcagtga gagctcccgg gaaggggcca tcacattcac 2040
atgggtggag cgtcccaga acggaggcga acctgacttc catgagg ttg aaccctacac 2100
gaagaaagaa cttctgtct ttactttccc tgacatcatt cgcaattaca aagtcatggc 2160
tgctgagaat attcctgaga atccctgaa tatctgtat ccaaatattg acaagacca 2220
tgcttttga aagtattact ccaggccaaa ggaagcacca gagccaatgg aacttgatgg 2280
ccctaaagga actggatata t caagactga gttgatttct gtgtctgaag ttcacccttc 2340
tagacttcag accacagaca acctgtccc catgtctcct gaggagtgtg acgaggtgtc 2400
tcggatagtg ggtctgttag aattcgacag tatgatgaac acagtataga gcatgaattt 2460
ttttcatctt ctctggcgac agttttcctt ctcactctgt attccctcct gctactctgt 2520
tcttccatc cctgtgtttc tagggaaatg aaagaaaggc cagcaaatc gctgcaacct 2580
gttgatagca agtgaatttt tctctaactc agaaacatca gttactctga agggcatcat 2640
gcatcttact gaaggtaaaa ttgaaaggca ttctctgaag agtgggtttc acaagtgaag 2700
aacatccaga tacacccaaa gtatcaggac gagaa tgagg gtcctttggg aaaggagaag 2760
ttaagcaaca tctagcaaat gttatgcata aagtcagtgc ccaactgtta taggtgtgtg 2820
gataaatcag tggttattta gggaaactgt tgacgtagga acggtaaatt tctgtgggag 2880
aattcttaca tgttttcttt gctttaagt taactggcag ttttccattg gtttacctgt 2940
gaaatagttc aaagccaagt ttatatcagt cctctttcaa aggtagccat 3000
catggtctgt gtagggggaa aatgtgtatt ttattacatc tttcacattg gctattttaa 3060
gacaaagaca aattctgttt cttgagaaga gaattattgc tttactgttt gttatggctt 3120
aatgacacta gctaataatc atagaaggat gtacatttcc aaattcaca a gttgtgtttg 3180
atatccaaag ctgaatacat tctgctttca tcttggtcac atacaattat ttttacagtt 3240
ctcccaaggg agttaggcta ttcacaacca ctcatcaca agttgaaatt aacctagat 3300
gtagataaac tcagaaattt aattcatgtt tcttaaatgg gctactttgt cctttttgtt 3360
attagggttg tathtagtct att agccaca aaattgggaa aggagtagaa aaagcagtaa 3420
```

9/292

```

ctgacaactt gaataatata ccagagataa tatgagaatc agatcatttc aaaactcatt 3480
tcctatgtaa ctgcattgag aactgcatat gtttcgctga tatatgtgtt ttccacattt 3540
gcgaatgggt ccattctctc tcctgtactt tttccagaca cttttttgag tggatgatgt 36 00
ttcgtgaagt atactgtatt ttacctttt tccttcctta tcaactgacac aaaaagtaga 3660
ttaagagatg ggtttgacaa gggtcttccc ttttacatac tgctgtctat gtggctgtat 3720
cttgtttttc cactactgct accacaacta tattatcatg caaatgctgt attcttcttt 3780
gggtggagata aagattttctt gagttttgtt ttaaaat taa agctaaagta tctgtattgc 3840
attaaatata atatcgacac agtgctttcc gtggcactgc atacaatctg aggcctctc 3900
tctcagtttt tatatagatg gcgagaacct aagtttcagt tgattttaca attgaaatga 3960
ctaaaaaaca aagaagacaa cattaanaac aatattgttt cta 4003

```

<210> 13

<211> 167

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(167)

<223> 3' terminal sequence. fibroblast growth factor receptor 2 (bacteria -expressed kinase, keratinocyte growth factor receptor, craniofacial dysostosis 1, crouzon syndrome, pfeiffer syndrome, jackson-weiss syndrome) (FGFR2) gene.

<400> 13

```

ccacctctgc tcggtgaaaa ttaagaaatt atgtgtaaga acagcattta gcaaatagct 60
attaaaaaaa gagagaccaa ttttctag gt gcattgggac atccatttaa antcaatata 120
aaaaataact ccttgtaaat ntataatata ttattttatac ntaattt 167

```

<210> 14

<211> 414

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(414)

<223> 5' terminal sequence. fibroblast growth factor receptor 2 (bacteria -expressed kinase, keratinocyte growth factor receptor, craniofacial dysostosis 1, crouzon syndrome, pfeiffer syndrome, jackson-weiss syndrome) (FGFR2) gene.

<400> 14

```

ggacacagaa tggataagcc agccaactgc accaacgaac tgtacatgat gatgagggac 60
tgttggcatg cagtgcctcc cagagaccaa cggtcaagca gttggtagaa gacttggatc 120
gaattctcac tctcacaacc aatgaggaat acttggaact cagccaacct ctggaacagt 180
attcacctag ttaccctgac ac aagaagtt ctgtttcttc aggagatgat tctgtttttt 240
ctccagaccc catgccttac gaacatgcc ttcctcagta tccacacata aacgggcagt 300
gttttaaaac atgaatgact gtgtctggcc tgnccccaac acagggacag gcactggggg 360
aacctaggct acattnaggc aggggaggac ccttgccttc ccaggngttt gttt 414

```

10/292

<210> 15
<211> 4667
<212> DNA/RNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<220>
<221> misc_feature
<222> (1)..(4667)
<223> fibroblast growth factor receptor 2
(bacteria-expressed kinase, keratinocyte growth factor receptor, craniofacial dysostosis 1, crouzon syndrome, pfeiffer syndrome, jackson -weiss syndrome) (FGFR2) gene.

<400> 15
gagcgggcga gggagcgcgc gcggccgcc caaagctcgg gcgcgcggg gctgcatgcg 60
gcgtacctgg cccgcgcgcg cgactgctct c cgggctggc gggggcgcgc cgcgagcccc 120
gggggccccg aggcgcgcgc ttgcctgcgc gctctgagcc ttgcgaactc gcgagcaaag 180
tttggtggag gcaacgccaa gcctgagtc tttcttctc tcgttcccc aatccgaggg 240
cagcccgcg gcgtcatgcc cgcgctctc gcgagcctgg ggtacgcgct gaagcccggg 300
aggcttgccg ccggcgaaga cccaaggacc actcttctgc gtttgaggtt gctccccaca 360
accccgggct cgtcgtttt tccatcccg cccagccggg gcgcggggac aacacaggtc 420
gcggagagc gttgccattc aagtgactgc agcagcgcgc gcagcgctc ggttcctgag 480
cccaccgcag gctgaaggca ttgcgcgtag tccatgccc tagaggaagt g tgcagatgg 540
gattaacgct cacatggaga tatggaagag gaccggggat tggtagcgta accatggtca 600
gctggggctg tttcatctgc ctggtcgtg tcaccatggc aaccttgctc ctggcccggc 660
cctccttcag tttagttag gataccacat tagagccaga agagccacca accaaatacc 720
aaatctctca accagaagtg tacgtggctg cgccagggga gtcgctagag gtgcgctgcc 780
tggtgaaaga tgccgcctg atcagttgga ctaaggatgg ggtgcacttg gggcccaaca 840
ataggacagt gcttattggg gagtacttgc agataaagg cgccacgcct agagactccg 900
gcctctatgc ttgtactgcc agtaggactg tagacagtga aacttggtac ttcattggtga 960
atgtcacaga tgccatctca tccggagatg atgaggatga caccgatggt gcggaagatt 1020
ttgtcagtga gaacagtaac aacaagagag caccatactg gaccaacaca gaaaagatgg 1080
aaaagcggt ccatgctgtg cctgcggcca aactgtcaa gtttcgctgc ccagccgggg 1140
ggaacccaat gccaaccatg cgggtgctga aaaacgggaa ggagttt aag caggagcatc 1200
gcattggagg ctacaaggta cgaaccagc actggagcct cattatggaa agtggtgtcc 1260
catctgacaa gggaaattat acctgtgtgg tggagaatga atacgggtcc atcaatcaca 1320
cgtaccacct ggatgttg gacgcatgc ctaccggcc catcctcaa gccggactgc 1380
cggcaaatgc ctccacagt g tcggaggag acgtagagtt tgtctgcaag gtttacagt 1440
atgcccagcc ccacatccag tggatcaagc acgtggaaaa gaacggcagt aaatacgggc 1500
ccgacgggt gccctacctc aaggttctca aggttctcaa ggccgcgggt gttaacacca 1560
cggacaaa gattgaggtt ctctatattc ggaatgtaac ttttgaggac gctggggaat 1620
atacgtgctt ggcgggtaatt tctattggga tatcctttca ctctgcatgg ttgacagttc 1680
tgccagcgcc tggaagagaa aaggagatta cagcttcccc agactacctg gagatagcca 1740
tttactgcat aggggtcttc ttaatcgct gtatggtggt aacagtcac ctgtgccgaa 1800
tgaagaacac gaccaagaag ccagacttca gcagc cagcc ggctgtgcac aagctgacca 1860
aacgtatccc cctgcggaga caggtttcgg ctgagtcacg ctctccatg aactccaaca 1920
ccccgctggt gaggataaca acacgcctct cttcaacggc agacaccccc atgctggcag 1980
gggtctccga gtagtaactt ccagaggacc caaatggga gtttccaaga gataagctga 2040
cactgggcaa gccctggga gaaggtgct ttgggcaagt ggtcatggcg gaagcagtg 2100
gaattgcaa agacaagccc aaggaggcgc tcaccgtggc cgtgaagatg ttgaaagatg 2160
atgccacaga gaaagacctt tctgatctgg tgcagagat ggagatgatg aagatgattg 2220
ggaaacacaa gaatatcata aatcttctt gagcctgcac acaggatgg g cctctctatg 2280
tcatagttga gtatgcctc aaaggcaacc tccgagaata cctccgagcc cggaggccac 2340
ccgggatgga gtactcctat gacattaacc gtgttcctga ggagcagatg accttcaagg 2400
acttggtgct atgcacctac cagctggcca gaggcagatg gtacttggct tcccaaaaat 2460
gtattcatcg agatttagca gcc agaaatg ttttggtaac agaaacaat gtgatgaaa 2520

11/292

```

tagcagactt tggactcgcc agagatatca acaatataga ctattacaaa aagaccacca 2580
atgggcggtc tccagtcaag tggatggctc cagaagccct gtttgataga gtatacactc 2640
atcagagtga tgtctggtcc ttccgggtgt taatgtggga gatcttcact ttagggggct 27 00
cgccctaccc agggattccc gtggaggaaac tttttaagct gctgaaggaa ggacacagaa 2760
tggataagcc agccaactgc accaacgaac tgtacatgat gatgaggagc tgttggcatg 2820
cagtgccttc ccagagacca acgttcaagc agttggtaga agacttggat cgaattctca 2880
ctctcacaac caatgaggaa tacttggaac tcagtca gcc tctogaaccg tattcacctt 2940
gttatcctga cccaagatga aataaaacgt ctctcttccc ttctttcagg aatacttgga 3000
cctcagccaa cctctcgaac agtattcacc tagttaccct gacacaagaa gttcttgttc 3060
ttcaggagat gattctgttt tttctccaga ccccatgcct tacgaaccat gccttctca 3120
gtatccacac ataaacggca gtgttaaaac atgaatgact gtgtctgcct gtcccaaac 3180
aggacagcac tgggaacctc gctacactga gcaggagagc catgcctccc agagcttgtt 3240
gtctccactt gtatatatgg atcagaggag taaataattg gaaaagtaat cagcatatgt 3300
gtaaagattt atacagttga aaacttgtaa tcttcccag gaggagaaga aggtttctgg 3360
agcagtggac tgccacaagc caccatgtaa cccctctcac ctgccgtgcg ttctggctgt 3420
ggaccagtag gactcaaggt ggacgtgcgt tctgccttcc ttgttaattt tgtaataatt 3480
ggagaagatt tatgtcagca cacttaca gagcacaat gcagtatata ggtgctggat 3540
gtatgtaaat atattcaaat tatgt ataaa tatatattat atatttaca ggagttattt 3600
tttgtattga ttttaaatgg atgtcccaat gcacctagaa aattgggtctc tcttttttta 3660
atagctattt gctaaatgct gttcttacac ataatttctt aattttcacc gagcagaggt 3720
ggaaaataac ttttgctttc agggaaaatg gtataacgtt aatttattaa taaattggta 3780
atatacaaaa caattaatca tttatagttt tttttgtaat ttaagtggca tttctatgca 3840
ggcagcacag cagactagtt aatctattgc ttggacttaa ctagtatatca gatcctttga 3900
aaagagaata tttacaatat atgactaatt tggggaaaat gaagttttga tttatttgtg 3960
tttaaatgct gctgtcagac gattgttctt agacctcct a aatgccccat attaaaagaa 4020
ctcattcata ggaaggtgtt tcatttttgt gtgcaaccct gtcattacgt caacgcaacg 4080
tctaactgga ctcccaaga taaatggtac cagcgtcttc ttaaaagatg ccttaatcca 4140
ttccttgagg acagacctta gttgaaatga tagcagaatg tgcttctctc tggcagctgg 4200
ccttctgctt ctgagttgca cattaatcag attagcctga ttctcttcag tgaattttga 4260
taatggcttc cagactcttt gcgttgaga cgctgttag gatcttcaag tcccatcata 4320
gaaaattgaa acacagagtt gttctgctga tagttttggg gatacgtcca tctttttaag 4380
ggattgcttt catctaattc tggcaggacc tcacaaaag atccagcctc at acctacat 4440
cagacaaaat atcgccgttg ttcttctgt actaaagtat tgtgttttgc tttggaaca 4500
cccactcact ttgcaatagc cgtgcaagat gaatgcagat tacactgatc ttatgtgtta 4560
caaaattgga gaaagtattt aataaaacct gttaattttt atactgacaa taaaaatgtt 4620
tctacagata ttaatgttaa caagaca aaa taaatgtcac gcaactt 4667

```

<210> 16

<211> 483

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(483)

<223> 3' terminal sequence. ests (EST T89980)
gene.

<400> 16

```

gtgttgagct cccaaaaggc ttaaaacttg ctttgtgaat gaatgatctt aaatcactag 60
tgaagatgat catggggcat ttgcacatta aagaactaaa atgaaatgaa aaagccatga 120
ctcctcactt aatgctatta aaaaaaatac tgatttggtt aattaacccc acttctcata 180
gtttaattgg gtaatcaacg ttcttgggaa ttc aggttct catgggcacc ctaatagtgt 240
ttagggccgg gggtcctgag gctgctgggg gtgatccga ggaacaagaa gctgccctat 300
taaaagtaat ctacttgagt ttttcccgag tctttgggag ttgttcccta ctgtggggct 360
acttataggg taggggcccc ccaaaccct cacacttagg tcggccctgc tggttgcgtg 420
tggggctctg aaangcagcc gctaggangt cccaagcct naacttacc attttctggc 480

```

12/292

ctg

483

<210> 17
<211> 400
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<220>
<221> misc_feature
<222> (1)..(400)
<223> 3' terminal sequence. protein phosphatase 3
(formerly 2b), catalytic subunit, gamma isoform
(calcineurin a gamma) (PPP3CC) gene.

<400> 17
ntttatatat attgaacata aattaaaaga atttataaaa cagccacctt ttacagaat 60
aaatgcagac tgaattataa atgcacctcc acgttgaagt tgttttgagt tgcttttcat 120
tttccaataa taaataaata gaatttgttc ttgagtttta gatccacctg agccacggca 180
ggactctaag tcatgaatgg gctttcttcc cttgggtcgt cctgtgcgca gatgntgagt 240
gtgctgaggt tacagatttc attggccccc cagcgtgtat gc tatecttt cgggggtggg 300
cattcgctca ttaattcggg ccagncctt cgcgctttct ttcaaaactc cgggatcttg 360
tgcntggagg cgaggnaccc ctctgatggg cttcccgggg 400

<210> 18
<211> 490
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<220>
<221> misc_feature
<222> (1)..(490)
<223> 5' terminal sequence. protein phosphatase 3
(formerly 2b), catalytic subunit, gamma isoform
(calcineurin a gamma) (PPP3CC) gene.

<400> 18
cttgagcac tatacccaca aactgtccg aggggtgctt tatttctaca gttaccctgc 60
agtttgtgaa tttttgcaga acaataattt actatcaatt atcagagccc atgaagccca 120
agatgctggg tatcgaatgt acaggaagag ccaagccaca ggttttccat cacttattac 180
aattttctct gcccacaatt acctagatgt ctataacaat aaagctgctg tgttgaaata 240
tgaaaacaat gtcataaata tcaggcagtt taactgttct ccacaccctt actgggcttc 300
caaactttat gggatgtttt cacatgggtc ttgacctttt gttgggggga ccccgacac 360
agaggatggc tgggtaaatg tggntcaaca ttatggntct ggatggacgg aactgatttt 420
ctggatgat ggaagcngga tgggaaggca cttacngttt cgtaaggng g ttcttcggg 480
gnttagttc 490

<210> 19
<211> 2134
<212> DNA/RNA
<213> Artificial Sequence

<220>

13/292

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(2134)

<223> protein phosphatase 3 (formerly 2b),
catalytic subunit, gamma isoform (calcineurin a
gamma) (PPP3CC) gene.

<400> 19

```
gggccaccct tagcagcggg cgcggtcggg gccgaagcgg tgttccccgc cttagccgct 60
gcgcctccca agagagcggc cgggtgggccc tcgtcctgtc agtggcgctg gaggc cggcc 120
tgcggtggcc gcgcccttct ggtgctcgga caccgctgag gagccggggc cgggcacggc 180
tggtgacggc ctccgggcag ctaaggctgc ccgaggagaa ggcggcggcc gcggcgtagg 240
cgacgctccg gcgggctcct ggagcctgga ggaggccgag ggaccatgt ccgggaggcg 300
cttcaccttc tccaccaccg accgcgtcat caa agctgtc ccctttcctc caacccaacg 360
gcttactttc aaggaagtat ttgagaatgg gaaacctaaa gttgatgttt taaaaaacca 420
tttggtaaag gaaggacgac tggaagagga agtagcctta aagataatca atgatggggc 480
tgccatcctg aggcaagaga agactatgat agaagtagat gctccaatca cagtatgtgg 540
tgatattcat ggacaattct ttgacctaat gaagttattt gaagttggag gatcacctag 600
taacacacgc tacctctttc tgggtgacta tgtggacaga ggctatttca gtatagagtg 660
tgtgtgtgat ttatggagtt taaagattaa tcatcccaaa acattgtttc tgcttcgggg 720
aaatcatgaa tgcaggcatc ttacagacta ttccaccttc aaacaggaat gtc gaatcaa 780
atattcgga caggtgtatg atgcctgtat ggagacattt gactgtcttc ctcttgctgc 840
cctcttaaac cagcagtttc tctgtgtaca tggaggaatg tcacctgaaa ttacttcttt 900
agatgacatt aggaaattag acaggtttac ggaacctccc gcctttggac ctgtgtgtga 960
cctgctttgg tctgatccct cagagatta t ggcaatgag aagaccttgg agcactatac 1020
ccacaacact gtccgagggt gctcttattt ctacagttac cctgcagttt gtgaattttt 1080
gcagaacaat aatttactat caattatcag agcccatgaa gcccaagatg ctgggtatcg 1140
aatgtacagg aagagccaag ccacaggcct tccatcactt attacaattt tctctgcccc 1200
caattaccta gatgtctata acaataaagc tgctgtgttg aaatatgaaa acaatgtcat 1260
gaatatcagg cagtttaact gttctccaca ccctactgg cttccaaact ttatggatgt 1320
tttcacatgg tctttgcctt ttgttgggga aaaagtcaca gagatgctgg taaatgtgct 1380
caacatatgc tctgatgacg aactgatttc tgatgatgaa gcaga aggaa gcactacagt 1440
tcgtaaggag atcatcagga ataagatcag agccattggg aagatggcac gggctctttc 1500
aattcttcgg caagaaagtg agagtgtgct gactctcaag ggcctgactc ccacaggcac 1560
actccctctg ggcgtcctct caggaggcaa gcagactatc gagacagcca tcagagggtt 1620
ctcgcttcag cacaagatcc ggagttttga agaagcgcgga ggtctggacc gaattaatga 1680
gcgaatgcc cccgaaagg atagcatata ccctggtggg ccaatgaaat ctgtaacctc 1740
agcacactca catgtgcgc acaggagcga ccaagggaag aaagccatt catgacttag 1800
agtctgtccg tgctcagggt gatctaaaac tcaagaacaa attctattta ttattatt g 1860
gaaaatgaaa agcaactcaa acaacttca acctggaggt gcatttataa ttcagtctgc 1920
atatttctg taaaagggtg actgttttat aaattctttt aatttatgtt caatatatat 1980
aaaaagtgca tctgttttgt ttttcccttt tttctccata attttaagaa atgaatctga 2040
ttgtgtgcaa cacatttgtg aagtcttgtg cta taaaggg gaacttcccc taataaaagg 2100
gccttgaaa cctcaaacct gggtttctga cccc 2134
```

<210> 20

<211> 248

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(248)

<223> 3' terminal sequence. ests (EST T90726)
gene.

<400> 20
atccatttat tatatccaat gctaaacact accacttgga ctctaagata tgtttatgcc 60
tctctgttta ttctagtttt ttaaaaatca aatatacaag atctacaatt atttatatcc 120
aagatgtcta caccactgcc taagaagcta ttaaaatat t tgtatttgtg caatggnacc 180
cattattcac atgggcctag gattaaaaag tcaatttata ttgngaataa atttntccaa 240
aaaaacca 248

<210> 21
<211> 427
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<220>
<221> misc_feature
<222> (1)..(427)
<223> 5' terminal sequence. ests (EST T90726)
gene.

<400> 21
taagatacga acgagaaacc tgatttattg ctcatccttc ccttgccctcc ctaatggcaa 60
gcaaaactct gaacatctga aaaggatgta gttctggaca aatcct gact acccagagga 120
aactcactgt gagattgctg ttgatttgaa ggggtgcttc actaaggcta tattttaaag 180
tagaataaca catgctgagt gtaaactggg ctttggtatg gtcagctgca gtagtacaaa 240
aacagcatag aatttgagga aaactaaaac tgctatgaga taggctatga ggaaaactta 300
aaactggcta tgtggtagga aatg atgtta aanttatgtg gggaaagttt ttcccctccn 360
tattacttca cattacaggc ctttngaggg gcntctgggc tctgnaccn gtttgatggg 420
cctttga 427

<210> 22
<211> 294
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<220>
<221> misc_feature
<222> (1)..(294)
<223> 3' terminal sequence. sry (sex determining
region y)-box 4 (SOX4) gene.

<400> 22
tttcttgttt ttcttttttt ttttcgaaa ccaactgccc tccactgact gccctgtac 60
cacatcaaac agtctcctct cctccacgcc tccgggtctt gggaagtctc acctcactga 120
tttcacgtag aaaagaaggc ggaggccagc agccgcgcgc ncaagctccc caacgtgcaa 180
atccatttca gtttgaccgt gaacccctt cagttcgtg tctcctccg cccccgccc 240
tagctccgc tgctggnttc caacggggtt ntccgggtcat ttcctagcgc cggc 294

<210> 23
<211> 362
<212> DNA
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(362)

<223> 5' terminal sequence. sry (sex determining region y)-box 4 (SOX4) gene.

<400> 23

```
ttccggactt gtctgcaccc ccagcaagaa ggcgagttag ttttctagag acttgaagga 60
gtctccccct tcctgcatca ccaccttggg tttgttttat tttgcttctt ggtcaagaaa 120
ggaggggaga acccagcgca cccctcccc ctttttttaa acgctgatg aagacagaag 180
gtctccgggt gacgaatttg gccgatggag nat gtttttg gggaacgccg ggactgagag 240
actccacggc agggcgaatt cccgtttggg gcttttttt tcctccctct ttttccctt 300
gccccttttg canccggngg agggagntgt tnaaggggag ggagggccag ccagtgttga 360
cc                                     362
```

<210> 24

<211> 2797

<212> DNA/RNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(2797)

<223> sry (sex determining region y) -box 4 (SOX4) gene.

<400> 24

```
ttccccagca ttcgagaac tcctctctac tttagcacgg tctccagact cagccgagag 60
acagcaaact gcagcgcggt gagagagcga gagagagga gagagagact ctccagcctg 120
ggaactataa ctctcttcgc agaggcggag aactccttcc ccaaattctt tggggacttt 180
tctctcttta cccactccg cccctgcgag gaggttgagg gccagttcgg ccgcccgcgcg 240
cgtcttcccg ttccgctgtg gcttgcccg gggaaccggg agggcccggc gatcgcgcg 300
cggccgcgcg gagggtgtga gcgcgcgtgg gcgcccgcg agccgaggcc atggtgcagc 360
aaaccaacaa tgccgagaac acggaagcgc tgctggccgg cgagagctcg gactcggggc 420
ccggcctcga gctgggaate gcctcctccc ccacgccgg ctccaccgcc t ccacgggcg 480
gcaaggccga cgaccgcagc tgggtcaaga ccccgagtgg gcacatcaag cgacccatga 540
acgccttcat ggtgtggtcg cagatcgagc ggcgcaagat catggagcag tcgcccagaca 600
tgacacaacg cgagatctcc aagcggctgg gcaaacgctg gaagctgctc aaagacagcg 660
acaagatccc ttctattoga gaggcggagc ggctgcgcct caagcacatg gctgactacc 720
ccgactacaa gtaccggccc aggaagaagg tgaagtccgg caacgccaac tccagctcct 780
cggccgcgcg ctctccaag ccgggggaga agggagacaa ggtcgggtggc agtggcgggg 840
gcggccatgg gggcggcggc ggcgcgggga gcagcaacgc ggggggagga ggcgcggtg 900
cgagtggcgg cggcgccaac tccaaaccgg cgcagaaaaa gagctgcggc tccaaagtgg 960
cggcgcgcgc gggcggtggg gttagcaaac cgcacgccaa gctcatcctg gcaggcggcg 1020
gcggcgcgcg gaaagcagcg gctgcgcgcg ccgcctcctt cgccgccgaa caggcggggg 1080
ccgcgcctct gctgccctcg ggcgcgcgcg ccgaccacca ctgcgtgt ac aaggcgcgga 1140
ctcccagcgc ctccggcctc gcctcctcgg cagcctcggc ctccgcagcg ctccgcggcc 1200
cggccaagca cctgcgggag aagaaggtag agcgcgtcta cctgttcggc ggccctgggca 1260
cgtcgtcgtc gccgtgggc ggcggtggcg cgggagccga cccagcgac cccctgggce 1320
tgtacgagga ggagggcgcg gg ctgctcgc ccgacgcgc cagcctgagc ggccgcagca 1380
gcgcgcctc gtccccgcgc gcgggccgct cgcccgccga ccaccgggc tacgccagcc 1440
tgcgcgcgcg ctgcgccgc ccgtccagcg cgccctcgca cgcgtcctc tcggcctcgt 1500
ccaactctc ctcttctctc tcctcgggct cctcgtcctc cgacgacgag ttcgaagacg 1 560
acctgctcga cctgaacccc agctcaaaact ttgagagcat gtccctgggc agcttcagtt 1620
```


16/292

```

cgctcgctggc gctcgaccgg gacctggatt ttaacttcga gcccggtcc ggctcgact 1680
tcgagttccc ggactactgc acgcccagg tgagcgagat gatctcgga gactggctcg 1740
agtccagcat ctccaacctg gttttcacct actgaa ggc gcgcaggcag ggagaagggc 1800
cggggggggg aggagaggag aaaaaaaaaa tgaaaaaaaa aaacgaaaag gacagacgaa 1860
gagtttaaag agaaaaggga aaaaagaaag aaaaagtaag cagggctcgt tcgcccgcgt 1920
tctcgtcgtc ggatcaagga gcgcggcggc gttttggacc cgcgctcca tccccacct 1980
tcccgggccg gggaccact ctgccagcc ggagggacgc ggaggaggaa gagggtagac 2040
agggggcacc tgtgattgtt gttattgatg ttgttgttga tggcaaaaaa aaaaagcgac 2100
ttcagatttg ctcccccttg cttgaagaga cccctcccc cttccaacga gcttccggac 2160
ttgtctgcac cccagcaag aaggcgagtt agttttctag agacttgaag gacttcccc 2220
cttctcgcac caccaccttg gttttgtttt attttgcttc ttggtcaaga aaggagggga 2280
gaaccagcg caccctccc cccctttttt taaacgcgtg atgaagacag aaggctccgg 2340
ggtgacgaat ttggccgatg gcagatgttt tgggggaacg ccgggactga gagactccac 2400
gcagcggaat tcccgtttgg gccc tttttt tctccctct tttcccttg cccctctgc 2460
agccggagga ggagatgtt aggggaggag gccagccagt gtgaccggcg ctaggaaatg 2520
acccgagaac cccgttgga ggcgcagcgc gggagctagg ggcggggcg gaggaggaca 2580
cgaactggaa gggggttcac ggtcaaatg aaatggattt gcacgttggg gagctggcg 264 0
cggcgctgc tgggcctccg cttcttttc tacgtgaaat cagtgggtg agacttcca 2700
gaccccgag gcgtggagga gaggagactg tttgatgtg tacaggggca gtcagtggag 2760
ggcgagtgtt ttcggaaaaa aaaaagaaa aaaaggg 2797

```

<210> 25

<211> 352

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(352)

<223> 5' terminal sequence. ring finger protein 5 (RNF5) gene.

<400> 25

```

acggggggcc caacnanant cgcgagcngg gcgtggcggg cgcgaccttc gaatgt anta 60
tatgtttgga gactgctcgg gaagctgttg tcagtgtgtg tggccacctg tactgttggc 120
catgtcttca tcagtggctg gagacaaggc cagaacggca agagtgtcca gtatgtaaag 180
ctgggatcag cagagagaag gttgtccgcg tttatgggag agggagccag aagccccagg 240
atcccagatt aaaaactcca ccccgcccc aggcc agaga ccagctccgg agagcagagg 300
gggattccag ccatttggtg ataccggggg cttccacttn ttcatttggg gt 352

```

<210> 26

<211> 543

<212> DNA/RNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(543)

<223> ring finger protein 5 (RNF5) gene.

<400> 26

```

atggcagcag cggaggagga ggacgggggc cccgaagggc caaatcgca gcggggcggg 60
gcgggcgcga ccttcgaatg taatatatgt ttggagactg ctcgggaagc tgtgttcagt 120

```

17/292

gtgtgtggcc acctgtactg ttggccatgt cttcatcagt ggctggagac acggc cagaa 180
cggcaagagt gtccagtatg taaagctggg atcagcagag agaaggttgt cccgctttat 240
gggcgagggg gccagaagcc ccaggatccc agattaaaaa ctccaccccg ccccagggc 300
cagagaccag ctccggagag cagaggggga ttccagccat ttggtgatac cgggggcttc 360
cactttctcat ttggtgttgg tgcttttccc ttt ggctttt tcaccaccgt cttcaatgcc 420
catgagcctt tccgccgggg tacagggtg gatctgggac agggtcaccc agcctccagc 480
tggcaggatt cctcttctct gtttctcgcc atcttcttct ttttttggct gctcagtatt 540
tga 543

<210> 27

<211> 397

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(397)

<223> 3' terminal sequence. axl receptor tyrosine
kinase (AXL) gene.

<400> 27

gccgtggggg gggaaagtgg gaag gtggag ttttccccag tggcagtgt tagcttggat 60
cctgagaggg agtaccaggt ggaggttgt ctcaggcacc atcctcctgc cctgggctgc 120
tggggagccc ctatcagcag gctgagcggg gctaggggtt ttggaagggc agaggacata 180
gcntccagca ggatggacct cagccgcagt naggcagcta caggaatcct tagggctctgg 240
ctgggttggg gggtcagctc ctctgcagc tccaggggnt tcaggataac ctccaccctc 300
atccatntn acatagagga tttcgtcagg ctctgggggc aggangcaan gcctttcagt 360
ntgttctcca aatcttccn caactctnta aaacttt 397

<210> 28

<211> 418

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(418)

<223> 5' terminal sequence. axl receptor tyrosine
kinase (AXL) gene.

<400> 28

ctgaatgaga acatgtccgt gtgtgtggcg gacttcgggc tctccaagaa gatctaca at 60
ggggactact accgccagga ccgtatcgcc aagatgccag tcaagtggat tgccattgag 120
agtctagctg accgtgtcta caccagcaag agcgatgtgt ggtccttcgg ggtgacaatg 180
tgggagattg ccacaagagg ccaaacccca tatccggggc gtggagaaca gcgagattta 240
tgantatctg cgccagggaa atcgccctgaa gcagcct ncg gactgtcttg gatgggantg 300
ttatgccttg atgttcggcg tncctgggga gcttaaattc cccaggggnc ccgnccaatt 360
ttttacaaag cttncgggga agatttttgg gagnacacac ttttaagggc tttncctt 418

<210> 29

<211> 5015

<212> DNA/RNA

18/292

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(5015)

<223> axl receptor tyrosine kinase (AXL) gene.

<400> 29

```
gagtgaggatt ctggaggaat gtttaccaga cacagagccc agagggacag cgcccagagc 60
ccagatagag agacacggcc tcaactggctc agcaccaggg tccccttccc cctcctcagc 120
tccctccctg gcccttttaa gaaagagctg atcctctcct ctcttgagtt aaccctgat 180
tgtccagggt gcccttggtt gggcgaggc aaagggggag ccaggggagg 240
agaaaggggt gcccaagtct gggagtgagg gaaggaggca ggggtgctga gaaggcggt 300
gctgggcaga gccggtggca agggcctc cc ctgccgctgt gccaggcagg cagtgcacaa 360
tccggggagc ctggagctgg ggggagggcc ggggacagcc cgcccgcgtg ccccctccc 420
cgctgggagc ccagcaactt ctgaggaaaag tttggcaccc atggcggtgc ggtgccccag 480
gatgggcagg gtcccgtagg cctggtgctt ggcgctgtgc ggctgggctg gcatggcccc 540
caggggacag caggctgaag aaagtccctt cgtgggcaac ccagggaata tcacaggtgc 600
ccggggactc acgggcaccc ttccggtgtca gctccagggt caggagagag cccccgaggt 660
acattggctt cgggatggac agatcctgga gctcgcggac agcaccaga cccaggtgcc 720
cctgggtgag gatgaacagg atgactggat agtggtcagc cagctcag aa tcacctccct 780
gcagctttcc gacacgggac agtaccagtg tttggtgttt ctgggacatc agaccttcgt 840
gtcccagcct ggctatgttg ggctggaggg cttgccttac ttccctggagg agcccgaaga 900
caggactgtg gccgccaaca cccccttcaa cctgagctgc caagctcagg gacccccaga 960
gcccggtggc ctactctggc tccagg atgc tgtcccctg gccacggctc caggtcacgg 1020
ccccagcgc agcctgcatg ttccagggtt gaacaagaca tcccttttct cctgcgaagc 1080
ccataacgcc aaggggttca ccacatcccg cacagccacc atcacagtgc tccccagca 1140
gccccgtaac ctccacctgg tctcccgcca accacaggag ctggaggtgg cttggactcc 1200
aggectgagc ggcatctacc cctgaccca ctgcaccctg caggctgtgc tgtcagacga 1260
tgggtgggag atccaggcgg gagaaccaga cccccagag gagccccca cctcgcaagc 1320
atccgtgccc ccccatcagc ttccggtagg cagcctccat cctcaccctt cttatcacat 1380
ccgcgtggca tgcaccagca gccaggggcc ctcactctgg acccactggc ttccctgtgga 1440
gacgccggag ggagtgcctc tgggcccccc tgagaacatt agtgctacgc ggaatgggag 1500
ccaggccttc gtgcattggc aagagccccg ggcgcccctg cagggtaccc tgttagggta 1560
ccggtctggc tatcaaggcc aggacacccc agaggtgcta atggacatag ggctaaggca 1620
agaggtgacc ctggagctgc agggggagcg gtctgtgtcc aatctgacag tgtgtgtggc 1680
agcctacact gctgctgggg atggaccctg gagcctccca gtaccctgg aggcctggcg 1740
ccaggggaa gcacagccag tccaccagct ggtgaaggaa ccttcaactc ctgccttctc 1800
gtggccctgg tggatgtgac tgctaggagc agtcgtggcc gctgcctgtg tcc tcattctt 1860
ggctctcttc cttgtccacc ggcgaaagaa ggagaccctg tatggagaag tgtttgaacc 1920
aacagtggaa agaggtgaac tggtagtcag gtaccgctg cgcaagtcct acagtcgtcg 1980
gaccactgaa gctaccttga acagcctggg catcagtga gagctgaagg agaagctgcg 2040
ggatgtgatg gtggaccggc acaaggtg gc cctggggag actctgggag agggagagtt 2100
tggagctgtg atggaaggcc agctcaacca ggacgactcc atcctcaagg tggctgtgaa 2160
gacgatgaag attgccatct gcacgaggtc agagctggag gatttcctga gtgaagcggg 2220
ctgcatgaag gaatttgacc atcccaacgt catgaggctc atcgggtgtct gtttccaggg 2280
ttctgaacga gagagcttcc cagcacctgt ggtcatctta cctttcatga aacatggaga 2340
cctacacagc ttctcctctt attcccggct cggggggccag ccagtgtacc tgcccactca 2400
gatgctagtg aagtcatgag cagacatcgc cagtggcatg gagtatctga gtaccaagag 2460
attcatacac cgggacctgg cgccaggaa ctgcatgctg a atgagaaca tgtccgtgtg 2520
tgtgcggagc ttccggctct ccaagaagat ctacaatggg gactactacc gccagggagc 2580
tatgcgcaag atgccagtc agtggattgc cattgagagt ctagnetacc gtgtctacac 2640
cagcaagagc gatgtgtggt ccttcggggg gacaatgtgg gagattgcca caagaggcca 2700
aaccacatat ccgggcgtgg agaacagcga gatttatgac tatctgcgcc agggaaatcg 2760
cctgaagcag cctgcggact gtctggatgg actgtatgcc ttgatgtcgc ggtgctggga 2820
gctaaatccc caggaccggc caagttttac agagctgcgg gaagatttgg agaacacact 2880
gaaggccttg cctcctgccc aggagcctga cgaaatcctc tatgtcaaca tggat gaggg 2940
tggaggttat cctgaacccc ctggagctgc agggaggagc gaccccccaa cccagccaga 3000
```

```

ccctaaggat tctgttagct gcctcactgc ggctgaggtc catcctgctg gacgctatgt 3060
cctctgccct tccacaaccc cttagcccccgc tcagcctgct gataggggct cccagcagc 3120
cccagggcag gaggatgggt cctgagacaa ccctccacct ggtactccct ctgaggatcc 3180
aagctaagca ctgccactgg gggaaactcc accttcccac ttcccaccc cagccttat 3240
cccacttgc agccctgtct tctacctat cccacctcca tcccagacag gtccctggcc 3300
ttctctgtgc agtagcatca ccttgaaagc agtagcatca ccatctgtaa aaggaagggg 3360
ttggattgca atatctgaag ccctcccagg tgtaaacatt ccaagactct agagtccaag 3420
gtttaaagag tctagattca aaggttctag gtttcaaaga tgctgtgagt ctttggttct 3480
aaggacctga aattccaaag tctctaattc tattaagtg ctaaggttct aaggcctact 3540
tttttttttt tttttttttt tttttttttt ttgtcgatag agt ctactg tgtcaccag 3600
gctggagtgc agtgggtgca tctgcctca ctgcaacctt cacctaccga gttcaagtga 3660
ttttcctgct ttggcctccc aagtagctgg gattacaggt gtgtgccacc acaccgggt 3720
aatttttata ttttttagtag agacaggggt tcacctgtt ggccaggctg gtctaaaact 3780
cotgacctca agtgatctgc ccacctcagc ctcccagggt gctgagatta caggcatgag 3840
ccactgcact caaccttaag acctactgtt cttaaagctct gacattatgt ggttttagat 3900
tttctggttc taacattttt gataaagcct caaggtttta ggttctaaag ttctaagatt 3960
ctgatttttag gagctaaggc tctatgagtc tagatgttta ttcttctaga gttcaga gtc 4020
cttaaaatgt aagattatag attctaaaga ttctatagtt ctgacatgg aggttctaag 4080
gcctaggatt ctaaaatgtg atgttctaag gctctgagag tctagattct ctggctgtaa 4140
ggctctagat cataaggctt caaaatgtta tcttctcaag ttctaagatt ctaatgatga 4200
tcaattatag tttctgaggc tttatgataa t agattctct tgtataagat cctagatcct 4260
aagggctgaa agctctagaa tctgcaattc aaaagttcca agagtctaaa gatggagttt 4320
ctaaggtccg gtgttctaag atgtgatatt ctaagactta ctctaagatc ttagattctc 4380
tgtgtctaag attctagatc agatgctcca agattctaga tgattaaata agattctaac 4440
ggctgttctt gtttcaaggc actctagatt ccattgggtc aagattccgg atcctaagca 4500
tctaagttat aagactctca cactcagttg tgactaacta gacaccaaag ttctaataat 4560
ttctaagtgt ggacaccttt aggttctttg ctssattctg cctctctagg accatgggtt 4620
agagtccaag aatccacatt tctaaaatct tatagttcta ggcac tgtag ttctaagact 4680
caaagtgtct aagtttctaa gattctaaag gtccacaggt ctgactatt aggtgcaatt 4740
tcaaggttct aacctatac tgtagtattc tttgggggtc ccctctcctt cttagctatc 4800
attgcttctt cctcccacac tgtgggggtg tgccccttc aagcctgtgc aatgcattag 4860
ggatgcctcc tttccgcagg ggatggacga tctcccacct ttccgggccat gttgcccccg 4920
tgagccaatc cctcaccttc tgagtacaga gtgtggactc tgggtgcctcc agaggggctc 4980
aggtcacata aaactttgta tatcaacgaa aaaaa 5015

```

<210> 30

<211> 439

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(439)

<223> 5' terminal sequence. cathepsin b (CTSB) gene.

<400> 30

```

aacacgtcac cggagagatg atgggtggcc atgcacccgc atcctgggct ggggagtgga 60
gaatggcaca ccctactggc tgg ttgcaa ctcctgggac actgactggg gtgacaatgg 120
cttctttaaa atactcagag gacaggatca ctgtggaatc gaatcagaag tgggtgctgg 180
aattccacgc accgatcagt actgggaaaa gatctaattc gccgtgggct tgtcgtgcca 240
gtcctggggg gcgagatcgg ggtagaaatg cattttattc tttaagttca cgtaaggat 300
acaagttttc agacagggtc tgaaagggan tgggatttng gccaaacatc agacctgttc 360
tttccaagg gaggaccaag ttcttgggct aacattcccc agcctnttgg tttaacagtt 420
gncaggacag ggcctgtt

```

439

20/292

<210> 31
<211> 1996
<212> DNA/RNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<220>
<221> misc_feature
<222> (1)..(1996)
<223> cathepsin b (CTSB) gene.

<400> 31
tccggcaacg ccaacgcgtc cgctgcgcgc aggctgggct gcaggctctc ggctgcagcg 60
ctgggtctgg gtgcagtggt gcgaccacg g ctacaggcag cctcagccac ccagatgtaa 120
gcgatctggt tcccacctca gcctcccgag tagtgatct aggatccggc ttccaacatg 180
tggcagctct gggcctccct ctgctgcctg ctgggtgttg ccaatgcccg gagcaggccc 240
tctttccatc cctgtcgga tgagctggtc aactatgtca acaaacggaa taccacgtgg 300
caggccgggc acaacttcta caacgtggac atgagctact tgaagaggct atgtggtacc 360
ttcctgggtg ggcccaagcc accccagaga gttatgttta ccgaggacct gaagctgcct 420
gcaagcttcg atgcacggga acaatggcca cagtgtccca ccatcaaaga gatcagagac 480
cagggtcctc gtggctcctg ctgggccttc ggggctgtgg aagccatct c tgaccggatc 540
tgcattccaca ccaatgcgca cgtcagcgtg gaggtgtcgg cggaggacct gctcacatgc 600
tgtggcagca tgtgtgggga cggtgtaat ggtggctatc ctgctgaagc ttggaacttc 660
tggacaagaa aaggcctggg ttctgtgtgc ctctatgaat cccatgtagg gtgcagaccg 720
tactccatcc ctccctgtga gcaccac gtc aacggctccc ggcccccatg cacgggggag 780
ggagatacc ccaagtgtag caagatctgt gagcctggct acagcccgac ctacaacag 840
gacaagcact acggatacaa ttctacagc gtctccaata gcgagaagga catcatggcc 900
gagatctaca aaaacggccc cgtggaggga gctttctctg tgtattcgga cttcctgctc 960
tacaagtcag gagtgtacca acacgtcacc ggagagatga tgggtggcca tgccatccgc 1020
atcctgggct ggggagtgga gaatggcaca ccctactggc tggttgcaa ctcctggaac 1080
actgactggg gtgacaatgg cttctttaaa atactcagag gacaggatca ctgtggaate 1140
gaatcagaag tgggtggctg aattccacgc accgatcagt actg gaaaaa gatctaact 1200
gccgtgggcc tgcgtgcca gtcctgggg cgagatcggg gttagaaatgc attttattct 1260
ttaagttcac gtaagataca agtttcaggc agggctctgaa ggactggatt ggccaaacat 1320
cagacctgtc ttccaaggag accaagtcct ggctacatcc cagcctgtgg ttacagtgc 1380
gacaggccat gtgagccac c gctgcagca cagagcgtcc ttccccctgt agactagtgc 1440
cgtgggagta cctgtgccc agctgctgtg gccccctccg tgatccatcc atctccaggg 1500
agcaagacag agacgcagga tggaaagcgg agttcctaac aggatgaaag ttcccccatc 1560
agttccccc gtaacctcaa gcaagtagct ttccacattt gtcacagaaa tcagagga ga 1620
gatgtgttg ggagcccttt ggagaacgcc agtctccagg tccccctgca tctatcgagt 1680
ttgcaatgtc acaacctctc tgatcttgtg ctcagcatga ttctttaata gaagttttat 1740
ttttcgtgca ctctgcta at catgtgggtg agccagtga acagcgggag cctgtgctgg 1800
tttgagatt gcctcta at gacgcggctc aa aaggaaac caagtgggtca ggagttgttt 1860
ctgaccact gatctctact accacaagga aaatagtta ggagaaacca gcttttactg 1920
tttttgaaaa attacagctt caccctgtca agttaacaag gaatgcctgt gccataaaaa 1980
ggtttctcca acttga 1996

<210> 32
<211> 492
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<220>
<221> misc_feature
<222> (1)..(492)

21/292

<223> 3' terminal sequence. protein phosphatase 4
(formerly x), catalytic subunit (PPP4C) gene.

<400> 32

```
ttccattttt cttcttttat tagaattttt tcattttttt tctcaaaatt tttatctaaa 60
aacaacaga aaaaagaagg aaaaaaagaa aaaaaaatta ttggaaactt catggttcaa 120
gtggggagag aggaggagga acatggagct aggtctccag gcctctccag agaagtcctc 180
accctcgaag caccctcttg ggggacagca gageccagg ga cagccccccc ccacgccag 240
cctccgtctg agggaagatg ggcagagtca cagtgggtgc gaggggccag aagggttggg 300
aggngggcag gggcgggcgg ggtcacagga agtagttcgg ccacggcttt ctttgggagg 360
gggatncccc gtgtcttctt ttgggggagc agccttcaaa gatgatgaaa tctttttctt 420
gggagatgct tcgttc cagc ttnccaagat tggcttncca cattttccca cagcgggtaca 480
agttagtttt tg                                         492
```

<210> 33

<211> 330

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(330)

<223> 5' terminal sequence. protein phosphatase 4
(formerly x), catalytic subunit (PPP4C) gene.

<400> 33

```
ctnttcatgg gggactttgt ggaccgtggc ttctatagcg tcgaaacggt nctnctgctg 60
ctggcactta aggttcgcta tcttgatcgc atcacactga tccgggg caa ccatgagagt 120
cgccagatca cgcaggctca tggcttctac gatgagtgcc tgcgcaagta acggctcggg 180
gactgtgtgg cgctactgca ctgagatctt tgactacctc agcctgtcag ccatcatcga 240
tngaaagaat cttctgcgtg caggggggcc tctccccctc catccagacc ctgggatcca 300
gattcggaca atcgaccgaa agcaa gaggt                                         330
```

<210> 34

<211> 1429

<212> DNA/RNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(1429)

<223> protein phosphatase 4 (formerly x),
catalytic subunit (PPP4C) gene.

<400> 34

```
gccacgaagg ccggagagcc ggaaccggag tcgcagcggc ggagaccctt gtgcggtgcg 60
gagggggcgg cggcccgac tctgaccgc gccgggggtg ggccatggcg gagatcagcg 120
acctggaccg gcagatcgag cagctgcgtc gctgcgagct catcaaggag agcgaagtca 180
aggccctgtg cgctaaggcc agagagatct tggtagagga gagcaacgtg cagaggttgg 240
actcggcagt cacagtgtgc ggcgacatcc atggacaatt ctatgacctc aaagagctgt 300
tcagagtagg tggcgacgtc cctgagacca actacctt catgggggac tttgtggacc 360
gtggcttcta tagcgtcgaa acgttcctcc tgctgctggc acttaagggt t cgctatcctg 420
atcgcatcac actgatccgg ggcaaccatg agagtcgcca gatcacgcag gtctatggct 480
```

22/292

```

tctacgatga gtgcctgcgc aagtaaggct cggtagactgt gtggcgctac tgcactgaga 540
tctttgacta cctcagcctg tcagccatca tcgatggcaa gatcttctgc gtgcacgggg 600
gcctctcccc ctccatccag accctgg atc agattcggac aatcgaccga aagcaagagg 660
tgccatcatga tgggcccattg tgtgacctcc tctggtctga ccagaagac accacaggct 720
ggggcgtag ccccgaggga gccggctacc tatttggcag tgacgtggtg gccagttca 780
acgcagccaa tgacattgac atgatctgcc gtgcccacca actggtgatg gaaggttaca 840
agtggcactt caatgagacg gtgctcactg tgtggtcggc acccaactac tgctaccgct 900
gtgggaatgt ggcaagccatc ttggagctgg acgagcatct ccagaaagat ttcatcatct 960
ttgaggtgctg tccccaagag acacggggca tccccccaa gaagcccggtg gccgactact 1020
tctgtgacc cgcggcgcc cctgccccct ccaacccttc tggccc tcgc accactgtga 1080
ctctgccatc ttctcagac ggaggtggg cgtggggggg gctgtcctgg ctctgctgtc 1140
ccccaaagg gtgcttcgag ggtgaggact tctctggaga ggcctggaga cctagctcca 1200
tgttcctcct cctctctccc cacttgaacc atgaagtctc caataatttt ttttctttt 1260
tttcttctt ttttctgttt gtttttagat aaaaattttg agaaaaaaa tgaaaaaatt 1320
ctaataaaag aagaaaaatg aaaaaaaaa aaaaaaaaa aaaaaaaaa aaaaaaaaa 1380
aaaaaaaaa aaaaaaaaa aaaaaaaaa aaaaaaaaa aaaaaaaaa 1429

```

<210> 35

<211> 493

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(493)

<223> 3' terminal sequence. ests (EST T79867)
gene.

<400> 35

```

tttttttggc acttcagctc caaagggtgaa acggcacagt taaaagcaag aaattttgtg 60
tcccttcccc aagctagctt tggaa taaat ccacttttct tgtaccagac cccactcttg 120
ttaattggac tctacatgtg gnaagcaact aacttgattt tcggttacaa tataatattc 180
aacttcagta aatcaaagac aattttgaaa gaagccaaag ggaaaaaaat gacctgaaga 240
gtcctgttta anttttagatt tctgaacaca aatctctggc gactaggact gaagcttgac 300
ctnttcctac ccaggaccn ttcccacctc actagggnac tttggantgg gatatatgtg 360
gggaaactct tgggctttcc ccattgtggc accatttcat atcttatggc aaatggtgcc 420
tcctacctcc cttgggncac tcccngttg gatgggntt gggggaggag ncctgntggg 480
gntttttccc at 493

```

<210> 36

<211> 354

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(354)

<223> 3' terminal sequence. fibroblast growth
factor receptor 4 (FGFR4) g ene.

<400> 36

```

tttttgtttt ttatttcaaa aaaataattt ataaaacgcc atttgctcct gttttcggca 60
ggcttccagc ttctctgggc tcaggggcaa tgctcccgtc aagacgctgg ggcagcagca 120

```

23/292

gcagggggag gtnntggggaa aggggggttca gaggcccaga acctcctgct ggtattggga 180
ggcaggaggt ttagcatagc agctctcca g ccaggctcag ccaaaccg gatggggact 240
aagcgccaag gtccaagaag ccgagcagaa ccctgacatt tggggccatc aggacanagg 300
cacggcagct cccaagggca aggggcacgg ccttngggac angggcacag caac 354

<210> 37

<211> 336

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(336)

<223> 5' terminal sequence. fibroblast growth
factor receptor 4 (FGFR4) gene.

<400> 37

atcggatgga ccgaccccc cactgcccc cagagctgta cgggctgatg cgtgagtgt 60
ggcagcagcg ccctcccaga ggcctacctt caagcagctg gtggaggcgc tggacaaggt 120
ctgctggccg tctctgagga gtacctcgac ctccgcctga ccttcggacc ctattcccc 180
tctggtgggg aagccagca gcacctgctt cctccagcga ttctgtcttc agccacgacc 240
cctgccatt ggggattcag ctcttccct ttgggtctng ggggtgcagac atga gcaagg 300
ctnaagggtt ttgcaaggga catagggttg gtgggc 336

<210> 38

<211> 3015

<212> DNA/RNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(3015)

<223> fibroblast growth factor receptor 4 (FGFR4)
gene.

<400> 38

ccgaggagcg ctcgggctgt ctgcggaccc tgccgcgtgc aggggtcgcg gccggctgga 60
gctgggagtg aggcggcgga ggagccaggt gaggaggagc caggaaggca gttggtggga 120
agtccagctt gggctccctga gagctgtgag aaggagatgc ggctgctgct gg ccctgttg 180
ggggtcctgc tgagtgtgcc tgggcctcca gtcttgtccc tggaggcctc tgaggaagt 240
gagcttgagc cctgcctggc tccagcctg gagcagcaag agcaggagct gacagtagcc 300
cttgggcagc ctgtgcggct gtgctgtggg cgggctgagc gtggtggcca ctggtacaag 360
gagggcagtc gcctggcacc tgctggccgt gtacggggct ggaggggccc cctagagatt 420
gccagcttcc tacctgagga tgctggccgc tacctctgcc tggcacgagg ctccatgatc 480
gtcctgcaga atctcacctt gattacaggt gactccttga cctccagcaa cgatgatgag 540
gaccccaagt cccataggga cctctcgaat aggcacagtt acccccagca agcaccctac 600
tggaacacac cccagcgcat ggagaagaaa ctgcatgcag tacctgcggg gaacaccgtc 660
aagttccgct gtccagctgc aggaacccc acgcccacca tccgctggct taaggatgga 720
caggccttcc atggggagaa ccgcattgga ggcattcggc tgcgccatca gcaactggag 780
ctcgtgatgg agagcgtggt gccctcggac cgcgccacat acacctgcct ggtagagaac 840
gtctggtggc gcatccgcta taactacctg ctatagtgtc tggagcggtc ccgcaccgg 900
cccattcctg aggcggggct cccggccaac accacagccg tgggtggcag cgacgtggag 960
ctgctgtgca aggtgtacag cgatgccag ccccatatcc agtggctgaa gcacatcgtc 1020

24/292

```

atcaacggca gcagcttcgg agccgacg gt tccccctatg tgcaagtcct aaagactgca 1080
gacatcaata gctcagaggt ggaggtcctg tacctgcgga acgtgtcagc cgaggacgca 1140
ggcgagtaca cctgcctcgc aggcaattcc atcggcctct cctaccagtc tgcttggtc 1200
acgggtgtgc cagaggagga cccacatgg accgcagcag cgcgcgaggc caggtatacg 1260
gacatcatcc tgtacgcgtc gggctccctg gccttggtg tgctcctgct gctggccggg 1320
ctgtatcgag ggcaggcgct ccacggccgg caccgccgcc cgcccgccac tgtgcagaag 1380
ctctcccgtt tccctctggc ccgacagttc tccctggagt caggctcttc cggcaagtca 1440
agctcatccc tggtagcagg cgtgcgtctc tctccagcg g cccgcctt gctgcgcggc 1500
ctcgtgagtc tagatctacc tctcgaccca ctatgggagt tcccccgga caggctggtg 1560
cttgggaagc ccctaggcga gggctgcttt ggccaggtag tacgtgcaga ggcctttggc 1620
atggaccctg ccggcctga ccaagccagc actgtggccg tcaagatgct caaagacaac 1680
gcctctgaca aggacc tggc cgacctggc tcggagatgg aggtgatgaa gctgatcggc 1740
cgacacaaga acatcatcaa cctgcttggt gtctgcaccc aggaagggcc cctgtacgtg 1800
atcgtggagt gcgcgcgcaa gggaaacctg cgggagttcc tgccggcccg gcgccccca 1860
ggccccgacc tcagccccga cgtcctcgg agcagtgagg ggccgctctc ctcc cagtc 1920
ctggctcctt gcgcctacca ggtggccga ggcattgcagt atctggagtc ccggaagtgt 1980
atccaccggg acctggctgc ccgcaatgtg ctggtgactg aggacaatgt gatgaagatt 2040
gctgactttg ggctggcccg cggcgtccac cacattgact actataagaa aaccagcaac 2100
ggccgcctgc ctgtgaagtg gatggcggc gaggccttgt ttgaccgggt gtacacacac 2160
cagagtgcag tgtgtcttt tgggatcctg ctatgggaga tcttcaccct cgggggctcc 2220
ccgtatcctg gcatcccggt ggaggagctg ttctcgtgc tgccggaggg acatcggtg 2280
gaccgacccc cacactgccc ccagagctg tacgggctga tgcgtgagtg ctggcacgca 2340
gcgcctctcc agaggcctac cttcaagcag ctggtggagg cgttggaaca ggtcctgctg 2400
gccgtctctg aggagtacct cgacctccgc ctgaccttcg gacctattc cccctctggt 2460
ggggacgcca gcagacctg ctctccagc gattctgtct tcagccacga cccctgcca 2520
ttgggatcca gtccttccc cttcgggtct ggggtgcaga cat gagcaag gctcaaggct 2580
gtgcaggcac ataggctggt ggcttgggc cttggggctc agccacagcc tgacacagtg 2640
ctcgaccttg atagcatggg gcccttgcc cagagttgct gtgcccgtgc caagggccgt 2700
gcccttgccc ttggagctgc cgtgcctgtg tctgatggc ccaaattgca gggttctgct 2760
cggcttcttg gaccatgg cg cttagtcccc atccccgggt tggctgagcc tggctggaga 2820
gctgctatgc taaacctct gcctccaat accagcagga ggttctggc ctctgaaccc 2880
cctttcccca cactccccc tgctgctgct gcccagcgt cttgacggga gcattggccc 2940
ctgagcccag agaagctgga agcctgccga aaacaggagc aaatggcgtt ttataaa tta 3000
tttttttgaa ataaa

```

3015

<210> 39
 <211> 252
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:primer

<220>
 <221> misc_feature
 <222> (1)..(252)
 <223> 3' terminal sequence. ectonucleotide
 pyrophosphatase/phosphodiesterase 2 (autotaxin)
 (ENPP2) gene.

```

<400> 39
gtgtgattta ttatgtttta gattggttta taaggcttaa atatatctgt catagttaac 60
agttaacagc aaataaaggc aactttacaa aatcagtggt tccatacagt acaggactaa 120
atgtggcaac tgtgcattgg aaaattaata ttctctcaat gcaaatntca aatctgcagc 180
accatttaga agcttccact aaaaactcaa gctgcagtat ttattacang ctctactcng 240
aacacanggc ta

```

252

<210> 40
 <211> 382

25/292

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(382)

<223> 5' terminal sequence. ectonucleotide
pyrophosphatase/phosphodiesterase 2 (autotaxin)
(ENPP2) gene.

<400> 40

```
ctnacnttca aacgganntg gaa ttatttc caaagggtat tggatgaagaa atatgcttcg 60
gaaagaaatg gagttaacgt gataagtga ccaatcttcg actatgacta tgatggctta 120
catgacacag aagacaaaat aaaacagtac gtggaaggca gttccattcc tgttccaact 180
cactactaca gcatcatcac cagctgtctg gattttactc agcctgccga caagtgtgac 240
ggccctctct ctgtgtcctc cttcatcctg cctcaccggc ctgacaacga ggagagctgc 300
aatagctcag aggacgnatt caaaatgggt agnaggaact catgaaggnt gcacacagct 360
agggtnctgt gacctttgna cc                                     382
```

<210> 41

<211> 2592

<212> DNA/RNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(2592)

<223> ectonucleotide
pyrophosphatase/phosphodiesterase 2 (autotaxin)
(ENPP2) gene.

<400> 41

```
atggcaagga ggagctcggt ccagtcgtgt ca gataatat ccctgttcac ttttgccgtt 60
ggagtcaata tctgcttagg attcaactgca catcgaatta agagagcaga aggatgggag 120
gaaggtcctc ctacagtgtc atcagactcc ccctggacca acatctccgg atcttgcaag 180
ggcaggtgct ttgaacttca agaggctgga cctcctgatt gtcgctgtga caacttgtgt 240
aagagctata ccagttgctg ccatgacttt gatgagctgt gtttgaagac agcccgtgcg 300
tgaggagtga ctaaggacag atgtggggaa gtcagaaatg aagaaaatgc ctgtcactgc 360
tcagaggact gcttggccag gggagactgc tgtaccaatt accaagtggg ttgcaaagga 420
gagtcgcatt gggttgatga tgactgtgag gaaataaagg ccgcagaatg ccc tgcaggg 480
tttgttcgcc ctccattaat catcttctcc gtggatggct tccgtgcac atacatgaag 540
aaaggcagca aagtcattgc taatattgaa aaactaaggc cttgtggcac aactctccc 600
tacctgaggc cgggtgtacc aactaaaacc tttcctaact tatacacttt ggccactggg 660
ctatatccag aatcacatgg aattgttggc a attcaatgt atgacctgt atttgatgcc 720
acttttcac tgcgagggcg agagaaattt aatcatagat ggtggggagg tcaaccgcta 780
tgattacag ccaccaagca aggggtgaaa gctggaacat tcttttggtc tgttgtcatc 840
cctcacgagc ggagaatatt aaccatattg cagtggctca ccctgccaga tcatgagagg 900
ccttcggtct atgccttcta ttctgagcaa cctgatttct ctggacacaa atatggccct 960
ttcgccctg agatgacaaa tcctctgagg gaaatcgaca aaattgtggg gcaattaatg 1020
gatggactga aacaactaaa actgcatcgg tgtgtcaacg tcatctttgt cggagaccat 1080
ggaatggaag atgtcacatg tgatagaact gagttcttga gtaattacct aactaatgtg 1140
gatgatatta ctttagtgcc tggaaactcta ggaagaattc gatocaaatt tagcaacaat 1200
gctaaatatg accccaaagc cattattgcc aatctcacgt gtaaaaaacc agatcagcac 1260
ttaagcctt acttgaaaca gcaccttccc aaacgtttgc actatgcaa caacagaaga 1320
```

26/292

```

attgaggata tccatthatt ggtg gaacgc agatggcatg ttgcaaggaa acctttggat 1380
gtttataaga aaccatcagg aaaatgcttt ttccagggag accacggatt tgataacaag 1440
gtcaacagca tgcagactgt tttgttaggt tatggcccaa catttaagta caagactaaa 1500
gtgcctccat ttgaaaacat tgaactttac aatgttatgt gtgatctcct gggattgaag 156 0
ccagctccta ataattgggac ccatggaagt ttgaatcatc tcctgcgcac taataccttc 1620
aggccaacca tgccagagga agttaccaga cccaattatc cagggattat gtaccttcag 1680
tctgattttg acctgggctg cacttgtgat gataaggtag agcceaagaa caagttggat 1740
gaactcaaca aacggcttca taaaaagggt tctacaga ag agagacacct cctctatggg 1800
cgacctgcag tgctttatcg gactagatat gatattctat atcacactga ctttgaaagt 1860
ggttatagtg aaatattcct aatgccactc tggacatcat atactgtttc caaacaggct 1920
gaggtttcca gcgttcctga ccatctgacc agttgcgtcc ggcctgatgt ccgtgtttct 1980
ccgagtttca gt cagaactg tttggcctac aaaaatgata agcagatgtc ctacggattc 2040
ctctttcctc cttatctgag ctcttcacca gaggtctaat atgatgcatt ccttgtaacc 2100
aatatgggtc caatgtatcc tgctttcaaa cgggtctgga attatttcca aagggtattg 2160
gtgaagaaat atgcttcgga aagaaatgga gttaacgtga taagtggacc a atcttcgac 2220
tatgactatg atggcttaca tgacacagaa gacaaaataa aacagtacgt ggaaggcagt 2280
tccattcctg ttccaactca ctactacagc atcatcacca gctgtctgga tttcactcag 2340
cctgccgaca agtgtgacgg ccctctctct gtgtcctcct tcactcctgc tcaccggcct 2400
gacaacgagg agagctgcaa tagctc agag gacgaatcaa aatgggtaga agaactcatg 2460
aagatgcaca cagctagggt gcgtgacatt gaacatctca ccagcctgga cttcttccga 2520
aagaccagcc gcagctaccc agaaatcctg acactcaaga catacctgca tacatatgag 2580
agcgagattt aa 2592

```

<210> 42

<211> 467

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(467)

<223> 3' terminal sequence. v-rel avian
reticuloendotheliosis viral oncogene homolog a
(nuclear factor of kappa light polypeptide gene
enhancer in b-cells 3 (p65)) (RELA) gene.

<400> 42

```

acagatttat tagttcagag tagaaagagc aagagtccaa gtgctttgat tgttcagtaa 60
aaactatgcc tccngactgg agagctgcca gcctgctctc cccactctt aacaacttac 120
cctactatta aggcacttga gaagagggag agcaaggaag tcccagacca aacccttct 180
ggatccnggg ngagagccag tgctgttgcg tggntttcct tcagccatgg ttgagcaagg 240
aaagagccgg cagagacctc tgtagggcag gaaggccagc ccctcaaacg ctggtnttag 300
ggcacagggg acaatgccag tgccatacag gggctggtat ctgggggcgt tattttgatt 360
aagctgtaat gaatccatga tgggaaggac acttgataag gctttntggg gctcaaaggn 420
ctttacctcc agcctgcttc tntctctag gngagtaccc agaagct 467

```

<210> 43

<211> 2444

<212> DNA/RNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

27/292

<222> (1)..(2444)

<223> v-rel avian reticuloendotheliosis viral
oncogene homolog a (nuclear factor of kappa light
polypeptide gene enhancer in b-cells 3 (p65))
(RELA) gene.

<400> 43

```
ggcacgagggc ggggcccgggt cgcagctggg cccgcggcat ggacgaactg ttccccctca 60
tcttcccggc agagcagccc aagcagcggg gcatgcgctt ccgctacaag tgcgaggggc 120
gctccgcggg cagcatccca ggcgagagga gcacagatac caccaagacc caccaccacca 180
tcaagatcaa tggctacaca ggaccaggga cagtgcgcat ctccctgggc a ccaaggacc 240
ctcctcaccg gcctcaccac cagcagcttg taggaaagga ctgccgggat ggcttctatg 300
aggctgagct ctgcccggac cgctgcatcc acagtittcca gaacctggga atccagtgtg 360
tgaagaagcg ggacctggag caggctatca gtcagcgcat ccagaccaac aacaaccct 420
tccaagttcc tatagaagag cagcgtgggg actacgacct gaatgctgtg cggctctgct 480
tccaggtgac agtgccggac ccatcaggca ggccccctcg cctgccgcct gtcccttctc 540
atcccatctt tgacaatcgt gccccaaca ctgccgagct caagatctgc cgagtgaacc 600
gaaactcttg cagctgcctc ggtggggatg agatcttct actgtgtgac aaggtgcaga 660
aagaggacat tgagggtgat ttcacgggac caggctggga ggcccagggc tccttttctc 720
aagctgatgt gcaccgacaa gtggccattg tgttccggac cctccctac gcagacccca 780
gcctgcaggc tctgtgcgt gtctccatgc agctgcggcg gccttccgac cgggagctca 840
gtgagcccat ggaattccag tacctgccag atacagacga tcgtcaccgg attgaggaga 900
aacgtaaaag gacatatgag accttcaaga gcatcatgaa gaagagtcct ttcagcggac 960
ccaccgaccc ccggcctcca cctcgacgca ttgctgtgcc ttcccgagc tcagcttctg 1020
tccccaagcc agcaccaccg ccctatccct ttacgtcatc cctgagcacc atcaactatg 1080
atgagtttcc caccatggtg tttcct tctg ggcagatcag ccaggccctg gccttggccc 1140
cggcccttcc ccaagtctg cccaggtc cagccctgc ccctgctcca gccatggtat 1200
cagctctggc ccaggcccca gccctgtcc cagtcctagc ccaggccct cctcaggctg 1260
tgccccacc tgcccccaag cccaccagg ctggggaagg aacgctgtca gaggccctgc 1320
tgcagctgca gtttgatgat gaagacctgg gggccttgct tggcaacagc acagaccag 1380
ctgtgttcac agacctggca tccgtcgaca actccgagtt tcagcagctg ctgaaccagg 1440
gcatacctgt ggccccccac acaactgagc ccagctgat ggagtaccct gaggctataa 1500
ctcgctagt gacagcccag aggccccccg acccagctcc tgcctcactg ggggcccccg 1560
ggctcccca tgccctcctt tcaggagatg aagacttctc ctccattgcg gacatggact 1620
tctcagccct gctgagtcag atcagctcct aagggggtga cgcctgccct cccagagca 1680
ctggttgtag gggattgaag ccctccaaa gcacttacgg attctggtg ggtgtgttcc 1740
aactgcccc aactttgtg atgtcttct tggaggggg agccatattt tattctttta 1800
ttgtcagtat ctgtatctct ctctctttt ggaggtgctt aagcagaagc attaacttct 1860
ctggaaaggg gggagctggg gaaactcaaa cttttccct gtctgatgg tcagctccct 1920
tctctgtagg gaactgtggg gtccccatc ccctcctcc agcttctggt act ctctag 1980
agacagaagc aggtcggagg taaggccttt gagccacaa agccttatca agtgtcttcc 2040
atcatggatt cattacagct taatcaaaat aacgccccag ataccagccc ctgtatggca 2100
ctggcattgt ccctgtgcct aacaccagcg tttgaggggc tgccttctg ccctacagag 2160
gtctctcgcg gctcttctct tgctcaac ca tggctgaagg aaacagtga acagcactgg 2220
ctctctccag gatccagaag gggtttggtc tggacttct tgcctctccc tcttctcaag 2280
tgccttaata gtagggtaag ttgttaagag tgggggagag caggctggca gctctccagt 2340
caggaggcat agtttttagt gaacaatcaa agcacttga ctcttgcct ttctactctg 2400
aactaataaa gctgttgcca agctggacgg cagagctcg tgcc 2444
```

<210> 44

<211> 381

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(381)

28/292

<223> 5' terminal sequence. il2 -inducible t-cell
kinase (ITK) gene.

<400> 44

```
aactctttcc tttggttgtg ctaagaggtg atgcccgaag tgcaccacct ttcaagaact 60
ggatcatgaa caactttatc ctcttggaag aacagctcat caagaaatcc caacaagaga 120
agaacttctc cctcgaaactt taaagtccgc ttctttgtgt taaccaaagc cagcctgg ca 180
tactttgaag atcgtcatgg gaagaagcgc acgctgaagg ggtccattga gctctcccg 240
attcaaatgt gttgaggttg tgaaaagtga catcagcatc ccatgccact attaaatacc 300
cgttttcagg tnggtgcatg acaacttacc tcctnttatg gtgtttgntt ccagntcgtg 360
aggaggccgg ncagcgttng g                                     381
```

<210> 45

<211> 6381

<212> DNA/RNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(6381)

<223> il2-inducible t-cell kinase (ITK) gene.

<400> 45

```
cgcgccgctgct atatataatg cagcatcaca ccatgtaggg catttactct tattttatcac 60
attcagatat gtttgaacaa ttcttaaggc tacaaaacag aacatagaaa aataaacagg 120
aataatattca aactttacaa aaagtgatat gataaagaat ataaagtact agtttccttt 180
taacacttca aaagatatgt atatatactt ttttttacaa gtaacatcac aaatgctcac 240
atcttcacat gctcttaaag tattatttgt actcagtgtg aggctattat cgtttttcat 300
acataaaaatt ttctagctct gtaacacaat gcaattttta atccattcag taagtccaac 360
cccaaagttg ccgcttccca gcatcaagac atgcaccac cctcttcta agattttcta 420
aacttgtatt tcggggagaa agacctct tt taaaaaataa tccaattagt gggagagtaa 480
atggctgaca ttagtagcaa aaccttagtt atctgaaaat aacatatttg aaatgagaca 540
ttattagatg tttaaacaaa caatagcatt tagacataaa gtaggaagca aaatacagta 600
aacagaaaata gtgtagccaa atatcattct ctccagctac ctttaagtaa agacaaaaca 660
tttacctcat ctaaaaatga aggtaaaacg aaagaggcaa aaataaataat tgctagtttc 720
taggatggct gaatgttttc taaaccagaa atgggttagaa aggaacttta ttgcaccaag 780
tcaatcataa gcaagtttgc agttcacagg cattttaatt caaccttgag tcacaaagga 840
gaacaacacg ctgcgagaat acagtctaca gtctgcatta aataagaa ta tatcagcatt 900
gtggtctggg aaaacctatg cttgccagga caaggcaggg tgctgagctt aggtcatgcc 960
atgaaaatga atttgtgggt tatcagtaaa cagtatgagg actacacaga tgccagcatc 1020
ctgctgccaa ggagacatgg ggcaagagtt gaagatttga gaggaatga agagacatac 1080
acaacaccaa aggaaaaggg ggct ggaatc aagttcagcc aaagcaccta acacaaaaaa 1140
caggtgagct ttggtcagtc tgttcttcaa aatatgtatg atcatatggt aatgaagttt 1200
cataatttcc aactcaaaaa tacaaatgat cctcagttct atacttttgc ctctattctc 1260
ttataaagaa atatgtcaac ataacagtat gacataacag ttaaaataag gacaaaagct 132 0
tgcttatctt agtttgacct cagcataagg caaaatcccc tggagaatac atttaaaaac 1380
aaacttaaaa ggaaaaaaag cgaaaccaac ttcattgcaa gattcctttt aaaactatca 1440
aaagtcagtt cttttattcc agaggtcact gagaaaagta ccatctgcta aaattctctt 1500
tcaagcactt cttccatcat atcctagagg tgagatat gg gaaacagaaa gcaaatcagt 1560
gttccctcagg agctatatct gttactcaat tgagggttag acaaagtgc aatgaagata 1620
tgagttagat ttccttccaa tttttaaaga ttttcagaag ctgagatcaa acccactca 1680
ataaaatgca ggagactaga agcaacaact tattttggac tcctgagatc aaacacattg 1740
aactttcaaa tctgggtgtt tctatcaaaa tgtgattttc ataaaatcag taagctagtc 1800
ctacataaaa aagcatgagc tgaaagtgga ggacctcta tcttctcatt ccttaactga 1860
gccaccgatg ttaagaaaaa aatggcttaa gcggtacctt caacaactat tctagttaag 1920
aaggtgacaa caaattgagg ccgcgaattc ggcgaaaact ctttcctttg g ttgtgctaa 1980
gaggtgatgc ccaaggtgca ccacctttca agaactggat catgaacaac tttatcctcc 2040
```

tggaagaaca gctcatcaag aaatcccaac aaaagagaag aacttctccc tcgaacttta 2100
 aagtcgcgtt ctttgtgtta accaaagcca gcctggcata ctttgaagat cgtcatggga 2160
 agaagcgcac gctgaagggg tccatt gagg tctcccgaat caaatgtgtt gagattgtga 2220
 aaagtgcacat cagcatccca tgccactata aatacccggt tcaggtgggtg catgacaact 2280
 acctcctata tgtgtttgct ccagatcgtg agagccggca gcgctgggtg ctggccctta 2340
 aagaagaaac gaggaataat aacagtttgg tgcctaaata tcatcctaatt ttctggatgg 2400
 atgggaagtg gaggtgctgt tctcagctgg agaagcttgc aacaggctgt gcccaatatg 2460
 atccaacca gaatgcttca aagaagcctc ttcctcctac tctgaagac aacaggcgac 2520
 cactttggga acctgaagaa actgtgtgtca ttgccttata tgactacca accaatgac 2580
 ctcaggaact cgcactgcgg cgcaacgaag agtactgcct gctggacagt tctgagattc 2640
 actggtggag agtccaggac aggaatgggc atgaaggata tgaaccaagc agttatctgg 2700
 tggaaaaatc tccaaataat ctggaaacct atgagtggta caataagagt atcagccgag 2760
 acaaagctga aaaacttctt ttggacacag gcaaagaagg agccttcagt gtaagggatt 2820
 ccaggactgc agga acatac accgtgtctg ttttcaccaa ggctgttcta agtgagaaca 2880
 atccctgtat aaagcattat cacatcaagg aaacaaatga caatcctaag cgatactatg 2940
 tggctgaaaa gtatgtgttc gattccatcc ctcttctcat caactatcac caacataatg 3000
 gaggaggcct gtggactcga ctccggtatc cagtttgttt tgggaggcag aaa gccccag 3060
 ttacagcagg gctgagatac gggaaatggg tgatcgacct ctacagagctc acttttgtgc 3120
 aagagattgg cagtgggcaa tttgggttgg tgcattctgg ctactggctc aacaaggaca 3180
 aggtggctat caaaaccatt cgggaagggg ctatgtcaga agaggacttc atagaggagg 3240
 ctgaagtaat gatgaaactc tctcatcc ca aactgtgtga gctgtatggg gtgtgcctgg 3300
 agcaggcccc catctgcctg gtgtttgagt tcatggagca cggctgcctg tcagattatc 3360
 tacgcacca gcggggactt tttgctgcag agacctgct gggcatgtgt ctggatgtgt 3420
 gtgaggcat ggcctacctg gaagaggcat gtgtcatcca cagagacttg gctgccagaa 3480
 attgtttggt gggagaaaac caagtcatca aggtgtctga ctttgggatg acaaggttcg 3540
 ttctggatga tcagtacacc agttccacag gcaccaaatt cccgggtgaag tgggcatccc 3600
 cagaggtttt ctctttcagt cgctatagca gcaagtcga tgtgtgttca tttgtgtgc 3660
 tgatgtggga agttttcagt gaaggcaaaa tccggtatga a aaccgaagc aactcagagg 3720
 tgggtggaaga catcagtacc ggatttcggt tgtacaagcc cgggctggcc tccacacacg 3780
 totaccagat tatgaatcac tgctggaaag agagaccaga agatcgcca gccttctcca 3840
 gactgctgcg tcaactggct gaaattgcag aatcaggact ttagtagaga ctgagtacca 3900
 ggccacgggc tcagat cctg aatggaggaa ggatatgtcc tcattccata gagcattaga 3960
 agctgccacc agcccaggac cctccagagg cagcctggcc tgtactcagt ccctgagtca 4020
 ccatggaagc agcatcctga ccacagctgg cagtcaagcc acagctggag ggtcagccac 4080
 caagctggga gctgagccag aacaggagtg atgtctctgc ccttctctca gcctc ttgtc 4140
 acatgtgtg cacaacctc aacctgacag ctttcagaca gcattcttgc acttcttagc 4200
 aacagagaga gacatgacgt aagaccaga ttgtattttt tattgttatt tttcaacagt 4260
 gaatctaaag tttatggttc cagggaactt ttatttgacc caacaacaca gtatcccagg 4320
 atatggaggc aagggaaca agagcatgag tgtttttcca agaaactggg gagttaagta 4380
 agattagagt gagtgtgctc tgtgtctg atgtctcag ccacagcttc ctgccgtaga 4440
 gaatgataga gcagctgctc acacaggagg ccgatatct gataagcagc ttatgagggt 4500
 tttacagagt atgtgtctac ctctctcctt gaaggagca tggcagacct a ttggatgga 4560
 ttgggtgaa cagttcaggt ccatgtctt gagcattggg tatctgatgt ctgccaccaga 4620
 acaagagaac ctctgacggt ggagaacctat gtggtgtaag aagagatctt aggtctcttc 4680
 tttataccaa gctcatgttt tataccaagc tcatctttta tacciaagctg tgcagggtgac 4740
 tatgcctct ctctgcaca gaatgcttcc accagcatcc tga gaagaaa tgattacttc 4800
 tgtaaaacat ctttttttcc agcctctgg aatcagcccc cccctctctg cactatccga 4860
 tctcatcaa cagagggcag cattgtgttg gtcagtgttc ccttggcgag caattgaaac 4920
 ttgtttaggc cctagggttg agcaatttta aggttgagac tccaagtctc ctaaaattct 4980
 aggagagaaa taaagagt ct gtttttgctc aaacctcag gatgaaaca gtcaggcact 5040
 gactggggtg ctccaagag gcatgagagt gcctactctg gcttgagcac ttctatatgc 5100
 aagtggaata tgtactgagc taggagactt ccctgcaaaa tctctgttca ccctgggttc 5160
 acatcccat gaggtaatat tttttacaaa taatgtaact gaggctt taa 5220
 aaagccaaga catctgcccc aagtgatgga actagaaagt ctagagctgg tattctagcc 5280
 caaatctgtc tgaccgcaat acacagatta tttattccta ttagacactg gcttctactg 5340
 aaaatgaaac ttattgcaga ggaataaat acaaagatgg aaagccagta aagaagtcag 5400
 tatagaacca ctagegatag tgttgcctg g cacagacca ctgtgttgta tgcattggccc 5460
 tccaacttgg aataggattt tcttttctc attctgtatc cttaccttgg tcatgttaat 5520
 gactttggag ttattcagtt cctgacctt taattctcac aaccaaccag tcatgttgc 5580
 tgaagccatt atagacgagc ttcaaagcaa ctttaaaaga ttgttatgta gaagtatgag 5640
 ttcttctctt aattatcatt ccaactttca gctgtagtct tctgaacac ttatgaggag 5700

30/292

ggaggacatt ccctgatata agagaggatg gtgttgcaat tggctctttc taaatcatgt 5760
gacgttttga ctggccttgag attcagatgc ataattttta attattgtga agtggagagc 5820
ctcaagataa aactctgtca ttacgaagat gattttactc agctt atcca aaattatctc 5880
tgtttacttt ttagaatttt gtacattatc ttttgggatc cttaattaga gatgatttct 5940
ggaacattca gtctagaaag aaaacattgg aattgactga tctctgtggg ttgggtttaga 6000
aaattccctt gtgcatggta ttaccttttt caagctcaga ttcatctaat cctcaactgt 6060
acatgtgtac attcttcacc tcctgggtgcc ctatcccgcg aaatgggctt cctgcctggg 6120
ttttctcttt ctacattttt ttaaatgggc cctgtgttt gtagagaact cccttatata 6180
gagttttggg tctagtttta tttcgtagat ttgcatttt gtaccttttg agactatgta 6240
tttatatttg gatcagatgc atatttatta atgtacagtc actgctagtg ttcaaaata a 6300
aaatgttaca aatacctgtt atcctttgta gagcacacag agttaaaggt tgaatatagc 6360
aatattaaag ctgcatttta a 6381

<210> 46

<211> 274

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(274)

<223> 5' terminal sequence. tenascin xb (TNXB)
gene.

<400> 46

ctgagntctc ggtccgaggc tttgaggaga gtgagcctct cacaggcttc ctcaccaagg 60
ttcctgaagg tcccacacag ttgcgtgcac tgaacttgac cgagggatc gccgtgctgc 12 0
actggaagcc ccccagaat cctgtggaca cctatgacgt ccaggtcaca gcctggggcc 180
ccggctntgc aggcggagga cccagggcag gcgcgggtgga cttacccctt gcattgacct 240
gtccttccac atcaacttac accgncacag tgc 274

<210> 47

<211> 13268

<212> DNA/RNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(13268)

<223> tenascin xb (TNXB) gene.

<400> 47

ggtcctcccc ttctcctccc ctgctcgctg cagactccct cctcactgtc gctgcogaga 60
tccacagtgc gttgtggctc agcc cctgtt gcaggggaca agtgaggag acttccctgt 120
cctgcctga gacgcgcgcc tcccggggtt ggggacagag cagggtcaga ggcactgcag 180
ctgctcggtt gccagcctc ctgaatgat ccagcccagt atgctctaac ctccagcctg 240
gttctcctgg tgctgtgag cacagccaga gcaggccctt tctcttcacg gtccaatgtg 300
acactgccag ccccccggcc cctccccag ccagggggcc acacagtggg ggctggagtg 360
ggaagccctt cttctcagct ttacgagcac acagtggag gaggggagaa gcagggtgta 420
ttcaccacc gcattaacct gccccttcc actggctgtg gctgtcccc aggcaccgag 480
ccccagtc ttgcttcaga ggtacaggcc ctgagggtcc gtct agagat cctggaggag 540
ttggtgaagg ggctcaagga acagtgcact gggggatgtt gtcctgcctc tgccaagct 600
ggcacaggtc agacagatgt gcggaccctc tgcagtctcc atggtgtgtt tgatctgagc 660

cgtgtcacct gttcctgtga gccaggtggt ggtgggcca cctgtcaga cccacagat 720
 gctgagatcc ctccctcttc cc caccctca gcctcgggt cctgcccaga tgactgcaat 780
 gatcagggtc gctgtgtccg tggctgttgc gtgtgcttcc cggctacac tggcccagc 840
 tgtgtgtggt catcctgtcc cggggactgc caaggcgtg ggcgtgctg gcaggcgtg 900
 tgtgtgtggt gggcaggctt ctacggcccc gactgcagcc agcgtcctg ccctcgaggt 960
 tgcagccaga ggggacgctg tgagggtggg cgctgcgtgt gtgaccaggt ctacactggt 1020
 gacgactgtg gcatgaggag ctgccctcgc ggttgagtc agagggggcg ctgtgagaat 1080
 gggcgctgct tgtgtaaccc cggctacact ggcgaggact gtgggtgag gagctgccct 1140
 cggggctgca gccagcgggg acgctgcaag gacgggctg gcgtgtgtga ccccggtac 1200
 actggcgagg actgtgttac gcggagctgc ccctgggact gtggcgaggg cggcgctgc 1260
 gtggacggcc gctgcgtgtg ctggccccggg tacacaggcg aggactgcag caccgagca 1320
 tgtccgaggg actgccgggg ccgcgggcgc tgcgaggac gcgaatgcat ttgcgacacg 1380
 ggctacagcg ggga cgtactg cgcgctgctg agctgccctg gcgactgcaa ccaaaggggc 1440
 cgctcgaggg acggccgctg cgtgtgtctg cgggggtaca ctggaaccga ttgggctcg 1500
 cgcgcctgcc cagcgactg tagaggtcgc ggcgctgctg agaacggcg gtgtgtttgc 1560
 aatgggggct acagcggcga ggactgcgtg gtgcgagct gtccgtggga ctg tctgtgc 1620
 cggggcgtg gtgagagtgg ccgctgcctg tgttgccgg ggtacacagg ccgggactgc 1680
 ggcacgcgcg cctgtcctgg cgactgtcgc gggcgcgggc gctgcgtgga tggcgctgc 1740
 gtgtgcaacc cgggcttcac cggtgaggac tgtgggagcc gtgctgtcc cggggactgc 1800
 cgtgggcacg gcctttgcga ggatggcg tg tgcgtgtgtg acgcaggcta ctacgggaa 1860
 gactgcagca cgcgcagctg ccccgggggc tgcgaggcc gcggccagt cctagatggg 1920
 cgggtgtgtg gcgagcagg ctactctgca gaggattgc gtgtgaggca gtgccgaat 1980
 gactgcagcc agcacggcgt gtgccaggac ggtgtgtgca tctgttggga aggtacgtg 2040
 agtgaggact gcagcatccg cactgcccc tccaactgcc acgggagggg ccgctgtgag 2100
 gaaggcgctg gcctgtgcga cccaggctac accggcccta cctgtgccac ccgcatgtg 2160
 ccggctgact gccggggacg tggcggtgt gtgcaaggag tgtgcctgt ccacgtggg 2220
 tatggcggtg aggactgcg gcaggaagag cctccagcca g cgcctgcc tggaggctgc 2280
 gggccccggg aactgtgccc ggcaggccag tgtgtgtgt tagagggct ccgaggccct 2340
 gactgtgcca tccagacatg cccaggggac tgcctggcc gaggagagt tcaogatggc 2400
 agctgtgtct gcaaagatgg gtatgtgtgc gaagactgc gagaagcac ggttccaagc 2460
 tctgcctcag cctatg acca gagaggactg gccctggac agagtacca ggtcactgtc 2520
 cgagcccttc gagggaccag ctggggcctt cctgcctcca agaccatcac caccatgatc 2580
 gatgggcccc aggacctccg agtgggtggt gtgacaccga caactctgga gcttggctgg 2640
 ctgcgtcccc aggtgaggt ggaccgatt gtgtgtctt acgtcagtgc cggca accag 2700
 aggtgtgggc tggaaagtgc ccctgaagca gacgggagc tctgactga cctgatgcca 2760
 ggcgtagaat atgtgtgtgac tgtcacagcg gacggggcc gggcagtcag ctaccagct 2820
 tctgtcaggg ccaacacaga ggaaggag gagagtccc cggccaggcc aagcctgtcc 2880
 cagccccac ggcggccttg gggcaacctg acggccgagc tgagccgtt ccgggcacg 2940
 gtgcaggacc tggagcgcca cctgcgggt caccgctacc cactgcgggc caaccagact 3000
 tacacgtcgg tggcgcgcca catccatgaa tacttgagc ggcaggtgt gggcagttcc 3060
 gccgatggcg gcctctcgt gtctctgcac ggcctcgcg gccagttcga gcgctgggtg 3120
 ctgcgtgtgc ggcctcagcc gcctgcagag ggcctcgcg gtgagctgac tgtgcgggc 3180
 accacgcgca ccgtcagcct gcccgacctc agggccggca ccactacca cgtggaggtc 3240
 cacgggtgtg gggcggggca gacctccaag tctacgcct tcatcaccac cacaggcccc 3300
 tcgacgacgc aaggggccca ggctcctctc ctgcagcagc gcc cccagga gctgggagag 3360
 ttgagggtgc tgggcagaga tgagacagg cgctcctgt tggctgtggc cggccagcct 3420
 gaacctttg cctacttcca actgcgcat cggtgccc agggggccgg ggcacatgag 3480
 gaagtgtcgc caggggacgt ccgccaggct ctggtgcct caccctctc tggaaacctg 3540
 tatgagctgt cacttcat gg ggtccctct gggggcaagc cctctgacct catcatctac 3600
 caaggcatta tggacaagga tgaggagaag cctgggaagt cctcaggccc accacgctg 3660
 ggtgagctga cggtagacaga caggacctcc gactccttgc tctgcgtg gacggtcccc 3720
 gaggcgaggt ttgactcctt cgtgatccag tacaagaca gggacgggca gcccag gtg 3780
 gtgcccgtg aaggacccca gcgtcggcc gtcacacct ccctggatcc tggccgcaag 3840
 tacaaattgt tctgtatgg gttgtgtggc aagaaggagc atggtccgt ggtggtgaa 3900
 gccaaatct tgcctcagag tgaccacaagt ccagggact caccacct gggaaacctg 3960
 tgggtgacag acctacccc agattcactg c acctctct ggactgtccc tgaggggcag 4020
 tttgacacct tcatggtcca gtacagggac agggatggac ggccccaggt ggtacctgtg 4080
 gaaggggccg agcgttcatt tgtgtctcc tcttgagac ctgaccaca gtacagattc 4140
 actctgtttg gaattgcgaa caagaagcgg tatggcccc tccagggcca tggcaccact 4200
 gctccagaga ggaaagagga gccccccgc cctgagttcc tggagcagc cctcctgggg 4260
 gaactgacag tgaccggcgt gacccagac tcttgcgtc tctcatggac agtggcccag 4320

ggcccccttcg actcattcat ggtccagtag aaggatgcac aggggcagcc ccaggcagtg 4380
 cctgtttgcgg gggatgagaa tgaggttact gtccccggcc tggat cccga ccggaagtat 4440
 aagatgaacc tctacgggct tctgtggcagg cagcgtgttg ggcccgagtc tgtggtggcc 4500
 aagactgctc ctcaggagga tgtggacgag acccccagcc ccacagaact gggcacggag 4560
 gccccggagt cccccgagga gccgctcctg ggggagctga cagtgcagag atcctccccct 4620
 gattcgctga gcctcttctg gaccgtcccc cagggcagct tcgactcttt caccgtgcag 4680
 tacaaggaca gggatgggag gccccgggag gtgcgtgttg ggggcaagga gagtgcagtc 4740
 accgtgggag gcctagagcc cgggcacaag tacaagatgc acctgtacgg cctccacgag 4800
 gggcagcgag tgggccccgt gtccgcccgt ggcgtgacag ccccaacaaga agaagagac c 4860
 cctccagcca ctgagtcctc gctggagcca cgcctaggag agctgcagat gacagatgtg 4920
 accccaact ctgtgggctc ctctgggaca gtccccgagg gccagtttga ctcttcata 4980
 gtccagtaca aggacaagga cgggcagccc cagggtggtg cgggtggcggc agaccagcga 5040
 gaggtcacag tctacaacct ggagcctgag aga aatatata agatgaacat gtatggacta 5100
 catgatgggc aacgcatggg cccctgtctc gtggtcatcg tgacggcccc agccacagag 5160
 gcctccaagc cctccctgga gccacgcta ggggagctga cagtgcagga tataaccctc 5220
 gactctgttg gcctctcatg gacagtcctc gaggggtgaat tcgactcctt tgtggttcag 5280
 tacaaggaca gggcagggca gcccagggtg gtgcccgttg ctgcagatca gcgggaggtc 5340
 actatccctg acctggaacc ctcccgcaag tacaagttcc tgctcttttg gatccaggat 5400
 gggaaacgac gcagcccagt ctctgtggag gcaaagacgg ttgcccaggg tgacgccagc 5460
 ccaggggccc caccgccctc tggggagctg ttgggtgacag accccac ccc agactcactg 5520
 cgctctcctt ggagcgttcc tgagggccag ttcgactctt ttgtggtcca gttcaaggac 5580
 aaagacgggc cccaggtggt gcccggtgag ggcctagac gctctgtcac tgtaccctc 5640
 ctggatgccg gccgcaagta cagattcctc ctctatggcc tcctgggcaa gaagcgccat 5700
 ggccctctca ctgcccagcg c accacggaa gcccgagtg ctatggatga tactggaaca 5760
 aagcgtcccc caaaaccocg tctgggggag gacgtgcagg tgaccaccgt gaccagaaac 5820
 tccgtgggccc tctcctggac agtccctgag ggccagtttg actcctttgt ggtccagtag 5880
 aaagacaggg acgggcagcc ccaggtggtg cccgtggagg gcagcctcag ggaggtcagc 5940
 gtgcccgggc tggaccctgc ccacaggtac aagctgctgc tctacgggct gcaccacggc 6000
 aagcgtgttg gcccctctc gcccgctgcc attactgccg gcagggaga aacggaaact 6060
 gagaccacgg ccccgacccc tccagcgcct gagccccacc tcggggagtt gacagtgag 6120
 gaggccacgt cacacacctc gcctctctcc tggat ggtga ctgagggaga attgactcc 6180
 ttgaaatcc agtacacaga tagagacggg caactccaaa tgggtccgcat aggaggtgac 6240
 cggaatgaca tcacctctc tggcctgga tccgaccaca gatacctggt gaccctgtat 6300
 ggtttcagtg atgggaagca tgtaggtcct tccatgtcg aggcctgac agtcccgag 6360
 gaggagaagc cttcagaacc tcccacgca accccgagc ccccatcaa gcctcgccct 6420
 ggggagctga ccgtgacaga tgccacctc gactccctca gcctgtcctg gacagttccc 6480
 gagggacagt ttgaccactt cctggtccag tacaggaatg gagatgggca gccaaggca 6540
 gtgaggggtg cagggcacga ggaaggggtc accatctcgg gcctggagc c agaccataaa 6600
 tacaagatga acctgtacgg ctccaacggg ggccagcgca tgggcccctgt gtctgtcgtc 6660
 ggggtgacag aaccagcat ggaggcccc gagcccgtg agggaccact cctgggggag 6720
 ctaacagtga caggatcctc cctgactcg ctgagcctc cctggaccgt ccccagggc 6780
 cgcttcgact ccttcaccgt gca gtacaag gacagggagc ggcgccccca ggtggtgcgt 6840
 gttgggggag aggagagtga agtcaccgtg gggggcctgg agcctgggag caagtacaag 6900
 atgcacctgt acggcctcca cgaggggagg cgcgtgggag cagtgtctgc tgtgggagtc 6960
 acggcccccg aagaggagtc cctgatgtc cctcttgcaa agctgcgcct agggcagatg 70 20
 acagtgcag acatcacctc cgactccctc agcctctcct ggacagtccc cgagggccag 7080
 tttgaccatt tcttggtcca gtttaagaat ggggacgggc agcccaaggc ggtgcgggtg 7140
 ccgggacagc aggtgggggt caccatctcg ggcctggagc cagaccacaa gtacaagatg 7200
 aacctgtacg gcttccacgg tggccagcgc gtgggccc cgtgtctgctgt tggtttaact 7260
 gcctcgacag aacctcccac cctgaacc cccatcaagc ctgcctgga ggagctgacc 7320
 gtgacagatg cgaccctga ctccctcagc ctgtcctgga cggttcccga gggacagttt 7380
 gaccacttcc tgggtccagta caagaatggg gatgggcagc ccaaggcaac acgggtgcca 7440
 ggacatgagg acagggtcac catctccggc ctggagccag acaacaagta caagatgaac 7500
 ctgtacggct tccacgggtg ccagcgtgtg ggcccgtgt ctgccatcg ggtgacagag 7560
 gaagagaccc ccagccccac atggaggccc cggagcccc tgaggagccg 7620
 ctctggggg agctaacagt gacaggatcc tcccctgact cgctgagcct ctctggacc 7680
 gtccccagg gccgcttoga ctcttcacc gtgcagtaca aggacaggga cgggcggccc 7740
 cagggtggtg gtgtggggg cgaggagagc gaggtcaccg tggggggcct ggagcctggg 7800
 cgcaaataca agatgcacct gtacggcctc cacgaggggc ggcgtgtggg cccggtgtcc 7860
 accgtgggag tgactgcccc acaag aggat gtggacgaga cccccagccc tacagaacca 7920
 ggcacagagg ccccagagcc ccccaggag cctctcctgg gggagctgac agtgacagga 7980

tcctcccctg actcgetgag cctttcctgg accgtccccc agggccgctt tgactccttc 8040
 accgtgcagt acaaggacag ggacgggcgg cccagggcgg tgcgtgttgg gggccaggag 8100
 agcaagggtca ctgtgagggg cctggagcct gggcgcaagt acaagatgca cctgtacggc 8160
 ctccacgagg ggccggcgct agggccggtg tctgccgtgg gcgtcacaga ggatgaagcc 8220
 gagaccaccc aagcagtgcc taccatgacc cctgagcccc ccatcaagcc tcgcctgggg 8280
 gagctgacca tgacagatgc caccctgac tccctcagc c tgcctggac ggttcccag 8340
 ggccagtttg accacttctt ggtccagtac aggaatgggg atgggcagcc caaggcggtg 8400
 cgggtgcccg ggacagagga cggggtcacc atctcaggcc tggagccaga ccataaatac 8460
 aagatgaacc tgtacggctt ccacggtggc cagcgcgtgg gcccacatct tgctattggg 8520
 gtgacggagg aagagacccc cagccccacg gaactcagca ctgaggcccc ggagccccct 8580
 gaggagccgc tctgggggga gctgacagtg acaggatcct cccctgactc gctgagcctc 8640
 tcttgacca tccccaggg ccacttcgac tcttcaccg tgcagtacaa ggacagggac 8700
 gggcgccccc aggtgatgag tgtagggggc gagagagcgg aggtcaccgt gg ggggcctg 8760
 gagccccggc gcaaatataca gatgcacctg tacggcctcc acgaggggag gcgtgtgggc 8820
 ccggtgtcca ccgtgggtgt gacagtgcgc accacaaccc ctgagcccc caacaagcct 8880
 cgctcgggg agctgaccgt gacagatgcc acccctgact cctcagcct gtcttgatg 8940
 gtccccgagg gccagtttga ccacttc ctg gtccagtaca ggaatgggga tgggcagccc 9000
 aagggtggtc ggggtgccggg gcacgaggac ggggtcacca tctcaggcct ggagccagac 9060
 cacaagtata agatgaacct gtacggcttc caggtggcc agcgcgtggg cccatctct 9120
 gtcaattggg tgacagagga agaaactccc gccccacag aaccagcac ggaggccccg 9180
 gagccccctg aggagccgct cctgggggag ctgacagtga caggatcctc cctgactcg 9240
 ctgagcctct cctggaccat cccccagggc cgttcgact ccttactgt gcagtacaag 9300
 gacagggacg ggcggcccca ggtggtgctg gtcaggggag agggagagcga ggtcaccgtg 9360
 gggggcctgg agcccggtg caaatacaag atgcacctgt acggcctcca cgaggggag 9420
 cgctgaggcc cagtgtccgc tgtgggtgtg acagctccaa aggatgaagc cgagaccacc 9480
 caagcagtgc ctaccatgac ccctgagccc cccatcaagc ctgcctggg ggagctgacc 9540
 gtgacagatg ccacccccga tccctcagc ctgtcctgga tggttccga gggcagttt 9600
 gaccacttcc tggtc cagta caggaatggg gatgggcagc ccaaggcggt gcgggtgccc 9660
 gggcacgagg acgggtcac catctcaggc ctggagccag accataaata caagatgaac 9720
 ctgtacggct tccacgggtg ccagcggtg ggcctgtgt ctgccattgg ggtgacggag 9780
 gaagagaccc ccagccccac agaaccagc actgaggccc cggaggcccc tgag gagccg 9840
 ctctggggg agttgacagt gacaggatcc tccctgact cgtgagcct ctctggacc 9900
 gtccccagg gccgcttoga tccctcacc gtgcagtaca aggacagga cgggcagccc 9960
 caggtggtgc gtgtcagggg caggagagc gaggtcaccg tggggggcct ggagccggg 10020
 cgcaaatata agatgcatct gtacggcc tc cagggggg agcgcgtggg cccagtgtcc 10080
 accgtgggca tcacggcgcc cctgcccaca ccactgccg tggagccccg cctgggggag 10140
 ctggcggtgg cggcggtgac ctcggaactca gtgggcctct catggacggt ggcccagggc 10200
 ccctttgact ccttctcgtt acagtacagg gacgcgcagg ggcagcccca ggcagtgcct 1026 0
 gtgagcggag acctccgagc ggtcgccgtc tcggggctgg acccgccccg caagtacaag 10320
 ttctgtctct ttggactcca gaatgggaaa cgcacggccc cagtccctgt ggaggccagg 10380
 accgccccag acaccaaacc gtctccccgc ctgggggagc tgactgtgac agatgagacc 10440
 cctgactccg tgggcctctc gtggacggtc cctga gggcg aattcgactc ctctgtggtc 10500
 cagtacaagg ataaggatgg tcggctccag gtggtgcccg tggcagccaa ccagcgggag 10560
 gtcacagtcc agggcctgga gccagtagg aaatacaggt tctgtctcta tggctgtca 10620
 ggcaggaac gactgggccc catctctgct gacagacca cagctcccc ggagaaggag 10680
 ctacctccc acctggggga actgaccgtg gctgaggaga cctccagctc tctgcgctg 10740
 tcttgagcgg tagccaggg ccctttgac tcttctgtg tccagtacag ggacacggac 10800
 gggcagccca gggcagtgcc tgtggccgca gaccagcga cagtaccgt agaggacctg 10860
 gagcctggca agaaatacaa gtttctgtc tacgggctcc tt gggggaaa gcgcctgggc 10920
 ccggtctctg cctgggaat gacagcccca gaagaggaca caccagcccc agagtttagc 10980
 ccagaggccc ctgagcctcc tgaagagccc cgcctaggag tgcagaccgt gaccgacaca 11040
 accccagact ccattgcctc ctctggagc gtggcccagg gcccttttga tctctctgt 11100
 gtccagtatg agtcacgaa cgggcagccc caggccttgc tegtggacgg cgaccagagc 11160
 aagatcctca tctcaggcct ggagcccagc accccctaca ggttctctct ctatggcctc 11220
 catgaaggga agcgcctggg gccctctca gctgagggca ccacagggt ggtcctgtct 11280
 ggtcagacct cagaggagtc aaggccccgc ctgtccagc tgtctgtgac tgacgtgacc 11340
 accagttcac tgaggctcaa ctgggagggc ccaccgggg ccttcgactc ctctctgtc 11400
 cgctttggg ttccatcacc aagcactctg gagccgcatc cgcgtccact gctgcagcgc 11460
 gagctgatgg tgccggggac gggcactcg gccgtgtcc gggacctgcg ttccgggact 11520
 ctgtacagcc tgacactgta tgggtgcca ggacccaca aggccagac catccaggga 11580
 accgcccga ccctcagccc agttctggag agccccgtg acctccaatt cagtgaatc 11640

34/292

```

agggagacct cagccaaggt caactggatg cccccacat cccgggcgga cagcttcaaa 11700
gtctcctacc agctggcgga cggaggggag cctcagagtg tgcaggtgga tggccag gcc 11760
cggaccacaga aactccaggg gctgatccca ggcgctcgct atgaggtgac cgtgggtctcg 11820
gtccgaggct ttgaggagag tgagcctctc acaggcttcc tcaccacggt tcctgacggt 11880
cccacacagt tgcgtgcaact gaacttgacc gagggattcg ccgtgctgca ctggaagccc 11940
ccccagaatc ctgtggacac ctatgacg tc caggtcacag cccctggggc cccgcctctg 12000
caggcgagga cccagggcag cgcggtggac taccctctgc atgacctgt cctccacacc 12060
aactacaccg ccacagtgcg tggcctgcgg ggccccaacc tcacttcccc agccagcatc 12120
accttcacca cagggtctaga ggccctcgg gacttggagg ccaaggaagt gacccccgc 1218 0
accgccctgc tcacttggac tgagcccca gtccggcccg caggctacct gctcagcttc 12240
cacaccctg gtggacagaa ccaggagatc ctgctcccag gagggatcac atctcaccag 12300
ctccttgccc tctttccctc cacctcctac aatgcacggc tcaggccat gtggggccag 12360
agcctcctgc cgcctgtgc cacctctttc accac gggtg ggctgcggat ccccttcccc 12420
agggactgcg gggaggagat gcagaacgga gccggtgcct ccaggaccag caccatcttc 12480
ctcaacggca accgcgagcg gccctgaac gtgttttgcg acatggagac tgatggggg 12540
ggctggctgg tgtccagcg ccgcatggat ggacagacag acttctggag ggactgggag 12600
gactatgccc atggttttgg gaacatctct ggagagttct ggctgggcaa tgaggccctg 12660
cacagcctga cacaggcagg tgactactcc atgcgcgtgg acctgcgggc tggggacgag 12720
gctgtgttcg ccagtagca ctcttccac gtagactcgg ctgcggagta ctaccgcctc 12780
cacttgagg gctaccacgg caccgcagg gactccatga gc taccacag cggcagtgtc 12840
ttcttgccc gtgatcgga cccaacagc ttgctcatc cctgcgctgt ctctaccga 12900
ggggcctggt gttacaggaa ctgccactac gccaacctca acgggctcta cgggagcaca 12960
gtggaccatc agggagttag ctggtaccac tggaaagggt tcgagttctc ggtgcccttc 13020
acggaaatga agctgagacc aagaaacttt cgctccccag cggggggagg ctgagctgct 13080
gccacctct ctgcacccc agtatgactg ccgagcactg aggggtcgcc ccgagagaag 13140
agccagggtc cttcaccacc cagccgctgg aggaagcctt ctctgccagc gatctcgag 13200
cactgtgttt acagggggga ggggaggggt tcgtacagga gcaataaagg agaaactgag 13260
gtaccgcg 13268

```

<210> 48

<211> 438

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(438)

<223> 3' terminal sequence. colony stimulating factor 1 (macrophage) (CSF1) gene.

<400> 48

```

ttttgcagct tgtgcacttc ttttattatt aaatatataa gcagcttccat atctttttaa 60
tagatattta aatgacttta tataaaataa ttcaccactt ccaagtataa aaacaaaatc 120
tcacagtgcg tgancaatgt cctctc ttga cttctcagag aacagaaggg gttcctgagc 180
aggtagcctg gggggacacc agaggngcct ctggggctcc tcctgctctg atgccaccaa 240
gtgctcaaaa agagcttctg cagtggggtt gggattgctt ttttgacctt taaaatatta 300
tatgtttaag gtaggggggg atgaaggggg gaatgccctt tttatttttc ttccattttt 360
aaaaatatgt gttttctagg catccaaata tagggggctg tggcctggga gggctaggcc 420
ccctttgccca ggttcact 438

```

<210> 49

<211> 390

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(390)

<223> 5' terminal sequence. colony stimulating factor 1 (macrophage) (CSF1) gene.

<400> 49

```
ggcaccgagggc gagctctgac tgaagatggg cctttgaaat ataggtatgc acctgaggtt 60
gggggaggggt ctgcactccc aaaccccagc gcagtgtcct ttccctgc tg ccgacagaac 120
ctggggctga gcaggttata cctgtcagga gccctgggac tgggctgcat ctacgcccc 180
cctggcatgg tatccagctc ccattccatt cttcaccctt ctttcctcct gaccttgggt 240
caacagtgat ggaccttcca actcttcacc caccctctct accattcacc tctaaaccag 300
gggaagccag gggtngggag agcant cagg gagagccagg gcttcagttt tccaattgct 360
ggggangggc ttccattttn tggggccagc 390
```

<210> 50

<211> 2475

<212> DNA/RNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(2475)

<223> colony stimulating factor 1 (macrophage) (CSF1) gene.

<400> 50

```
agccgtctctc cgcattccag gacagcgggtg cggccctcgg ccggggcgcc cactccgag 60
caccagcgga gcgagcgagc gacgcagggc ggccgacgcg ccgggcccgg acccagctgc 120
ccgtatgacc gcgcccggcg ccgcccggcg ctgccctccc acgacatggc tgggctccct 180
gctgttgttg gtctgtctcc tggcgagcag gactatcacc gaggaggtgt cggagtactg 240
tagccacatg attgggagtg gacacctgca gtctctgcag cggctgattg acagtcagat 300
ggagaccctg tgccaaatta catttgagtt ttagaccag gaacagttga aagatccagt 36 0
gtgctacctt aagaaggcat ttctcctggt acaagacata atggaggaca ccattgcgctt 420
cagagataac accccaatg ccattgccat tgtgcagctg caggaactct ctttgaggct 480
gaagagctgc ttcaccaagg attatgaaga gcatgacaag gcctgcgtcc gaactttcta 540
tgagacacct ctccagtgct tggagaaggc caagaatgtc tttaatgaaa caaagaatct 600
ccttgacaag gactggaata ttttcagcaa gaactgcaac aacagcttg ctgaatgctc 660
cagccaagat gtggtgacca agcctgattg caactgcctg taacccaaag ccattccctag 720
cagtgaaccc gcctctgtct cccctcatca gccctcgcgc ccttccatgg cccctgtggc 780
tggcttgacc tgggaggact ctgagggaaac tgagggcagc tcctcttgc ctggtgagca 840
gccctgcac acagtggatc caggcagtg ccaagcagcg ccaccagga gcacctgcca 900
gagctttgag ccgccagaga cccagttgt caaggacagc accatcggtg gctcaccaca 960
gcctcgcccc tctgtcgggg ccttcaaccc cgggatggag gatattcttg actctgcaat 1020
gggcactaat tgggtcccag aagaagcctc tggagaggcc agtgagattc ccgtacocca 1080
agggacagag ctttccccct ccaggccagg agggggcagc atgcagacag agcccgcag 1140
accagcaac ttctctctag catcttctcc actccctgca tcagcaaagg gccaacagcc 1200
ggcagatgta actggtaccg ccttgcccag ggtgg gccc gtgaggcca ctggccagga 1260
ctggaatcac acccccaga agacagacca tccatctgcc ctgctcagag acccccgga 1320
gccaggctct ccaggatct catcaccgcg ccccagggc ctcagcaacc cctccacct 1380
ctctgctcag ccacagcttt ccagaagcca ctctcgggc agcgtgctgc ccttgggga 1440
gctggagggc aggaggagca ccagggatcg gaggagcccc gcagagccag aaggaggacc 1500
agcaagtga ggggcagcca ggcccctgcc ccgttttaac tccgttcctt tgactgacac 1560
acatgagagg cagtccgagg gatcctccag ccgcagctc caggagtctg tcttccacct 1620
gctggtgccc agtgtcatcc tggcttctgt ggcgctcgga ggcctcttg t tctacaggtg 1680
```

36/292

```

gaggcggcgg agccatcaag agcctcagag agcggattct cccttgagc aaccagaggg 1740
cagccccctc actcaggatg acagacaggt ggaactgccg gtgtagaggg aattctaaga 1800
cccctcacca tcctggacac tctcgtttgt caatgtccct ctgaaaatgt gacgcccagc 1860
cccgacacac gtactccaga tgttgtctga ccagctcaga gagagtacag tgggactgtt 1920
accttccttg atatggacag tattcttcta tttgtgcaga ttaagattgc attagttttt 1980
ttcttaacaa ctgcatcata ctgttgatcat atgttgagcc tgtggtctat aaaacccta 2040
gttcatttc ccataaactt ctgtcaagcc agaccatctc taccctgtac ttggacaact 21 00
taactttttt aaccaaagtg cagtttatgt tcacctttgt taaagccacc ttgtggtttc 2160
tgcccatcac ctgaacctac tgaagtgtg tgaatccta attctgtcat ctccgtagcc 2220
ctccagttg tgctcctgc acattgatga gtgcctgctg ttgtctttgc ccatgttgtt 2280
gatgtagctg tgacctatt gtctctcacc cctgccc ccc gccaaaccca gctggccccc 2340
ctctccccc tcccacccaa gccacagcc agcccatcag gaagccttc tggtctctc 2400
acaaccttct gactgtctt tcagtcatgc cccctgctt tttgtattg gctaatagta 2460
tatcaatttg cactt                                     2475

```

<210> 51

<211> 397

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(397)

<223> 3' terminal sequence. villin 2 (ezrin)
(VIL2) gene.

<400> 51

```

atcngttgaa tagttgattc catacatttc cagg tcttga gcaatcttca ggtattccaa 60
catagcatta tctttgagca tcccacgggtg ttccgcatgc cacacctgga tccggtcctc 120
ccactgggtcc ctggttaagtt tgtgctggtc catcactctt tgagggatca nccgctcaga 180
gctgagggtac ccagacttgt gcacttcttt gttgtagtcc ccaaacttgg cctgcacagc 240
gtagggaccc caagagcacg gcagtctcag ggggggcagt agatctcatc gctaagggat 300
tcctttcctt cacttnggag ggaggaaaag tttctggggt gatgtcctgg ggatgagctt 360
ccttcagcca catctttcag ggnaggact ttnggcc                                     397

```

<210> 52

<211> 468

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(468)

<223> 5' terminal sequence. villin 2 (ezrin)
(VIL2) gene.

<400> 52

```

ggacgaggca gggcgggagg gcgtctaaag ggttctgctc tgactccagg ttgggacagc 60
gtcttcgctg ctgctggata gtcgtgtttt cggggatcga ggatactcac cagaaaccga 120
aaatgccgaa accaatcaat gtccgagtta ccaccatgga tgcagagctg gagtttgcaa 180
tccagccaaa tacaactgga aaacagcttt ttgatcaggt ggtaaagact atcggcctcc 240
gggaagtgtg gtactttggc ctccactatg tggatnaata aaggatttcc tacctgg gct 300
gaagctggat aagaaggtgt ctgccaggga ggtcagggaag gagaatcccc tccagttcaa 360

```

37/292

gttccggggc caagttctac cctgaagatg tgggctgagg agctcattcc agggacattc 420
accagaaat tttntttcnt ccaagtgaag gaagggattc ttaggcgn 468

<210> 53

<211> 3064

<212> DNA/RNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(3064)

<223> villin 2 (ezrin) (VIL2) gene.

<400> 53

aggcagggcg ggcgggcgct ctaagggttc tgctctgact ccaggttggg acagcgtctt 60
cgctgctgct ggatagtcgt gttttcgggg atcgaggata ctcaccagaa accgaaaatg 120
ccgaaaccaa tcaatgtccg agttaccacc atggatgcag agctggagtt tgcaatccag 180
ccaaatacaa ctggaaaaca gctttttgat cagggtggtaa agactatcgg cctccgggaa 240
gtgtggtact ttggcctcca ctatgtggat aataaaggat ttctacctg gctgaagc tg 300
gataagaagg tgtctgcccc ggaggtcagg aaggagaatc cctccagtt caagttccgg 360
gccaaagtct accctgaaga tgtggtgag gagctcatcc aggacatcac ccagaaactt 420
ttcttctccc aagtgaagga aggaatcctt agcgtatgaga tctactgcc ccctgagact 480
gccgtgctct tggggtccta cgctgtgcag gccaaag ttg gggactacaa caaagaagtg 540
cacaagtctg ggtacctcag ctctgagcgg ctgatccctc aaagagtgat ggaccagcac 600
aaacttacca gggaccagtg ggaggaccgg atccagggtg ggcatgcgga acaccgtggg 660
atgctcaaag ataatgctat gttggaatac ctgaagattg ctcaggacct ggaaatgtat 720
ggaatcaact atttcgagat aaaaaacaag aaaggaacag acctttggct tggagttgat 780
gcccttgagc tgaatattta tgagaaagat gataagttaa ccccaaagat tggctttcct 840
tggagtgaat tcaggaacat ctctttcaat gacaaaaagt ttgtcattaa acccatcgac 900
aagaaggcac ctgactttgt gttttatgcc ccacgtctga gaatcaacaa gcggat cctg 960
cagctctgca tgggcaacca tgagttgtat atgcgccgca ggaagcctga caccatcgag 1020
gtgcagcaga tgaaggccca ggcccgagg gagaaagcat agaagcagct ggagcggcaa 1080
cagctggaaa cagagaagaa aaggagagaa accgtggaga gagagaaaga gcagatgatg 1140
cgcgagaagg aggagttgat gctgcggctg caggactatg aggagaagac aaagaaggca 1200
gagagagagc tctcgagcga gattcagagg gccctgcagc tggaggagga gaggaagcgg 1260
gcacaggagg aggccgagcg cctagaggct gaccgtatgg ctgcactgcg ggctaaggag 1320
gagctggaga gacaggcggg ggatcagata aagagccagg agcagctggc tgcggagctt 1380
gcagaatata cagccaagat tgccctctcg gaagaggcgc ggaggcgcaa ggagatgaa 1440
gttgaagagt ggcagcacag ggccaaagaa gcccaggatg acctggtgaa gaccaaggag 1500
gagctgcacc tggatgatgac agcaccctcg ccccccacc ccccggtgta cgagccgggtg 1560
agctaccatg tccaggagag ctgagaggat gagggcgag agccc acggg ctacagcgcg 1620
gagctgtcta gtgagggcat ccgggatgac cgcaatgagg agaagcgcat cactgaggca 1680
gagaagaacg agcgtgtgca gcggcagctc gtgacgctga gcagcgagct gtcccaggcc 1740
cgagatgaga ataaggagac ccacaatgac atcatccaca acgagaacat gaggaaggc 1800
cgggacaagt acaagacgct gcggcagatc cggcagggca acaccaagca gcgcatcgac 1860
gagttcgagg cctgtaaca gccaggccag gaccaagggc agaggggtgc tcatagcggg 1920
cgctgccagc cccgccacgc ttgtctttag tgctccaagt ctaggaaact cctcagatcc 1980
cagttccttt agaagcagat taccacaacag aacattctg ggctgggaac cagggaggc g 2040
ccctggtttg ttttccccag ttgtaatatg gccaaagcag cctgattctc gcgattattc 2100
tcgaatcacc tcctgtgttg tgctgggagc aggactgatt gaattacgga aaatgcctgt 2160
aaagtctgag taagaaactt catgctggcc tgtgtgatac aagagtcagc atcattaaag 2220
gaaacgtggc aggaattcca tctgtgccat acttgtctg tattcgaaat gagtcaaat 2280
tgattttttt aatttctatg aaggatccat ctttgtatat ttacatgctt agaggggtga 2340
aaattatttt ggaaattgag tctgaagcac tctgcacac acagtgatcc cctcctcccg 2400
tcactccacg cagctggcag agagcacagt gatcaccagc gtgagtgggt gagggaggca 2460
cttgatattt tttttagttc tttttttttt ggcttaacag ttttagaata cattgtactt 2520
atacacctta ttaatgatca gctatatact atttatatac aagtataat acagatttgt 2580

38/292

```
aacattagtt ttaaaaaggg aaagttttgt tctgtatatt ttgttacctt ttacagaata 2640
aaagaattac atatgaaaaa ccctctaaac catggcactt gatgtga tgt ggcaggaggg 2700
nagtgggtga gctggacctg cctgctgcag ctgcagtcac gtgtaaagac gattattatt 2760
agtgttttat gcatgtaatg gactatgcac acttttaatt ttgtcagatt cacacatgcc 2820
actatgagct ttcagactcc agctgtgaag agactctgtc tgcttgtgtt tgtttgcagt 2880
ctctctctgc catggccttg g caggctgct ggaaggcagc ttgtggaggc cgttggttcc 2940
gccactcat tccttctcgt gactgcttt ctccttcaca gctaagatgc catgtgcagg 3000
tggattccat gccgcagaca tgaaataaaa gctttgcaaa ggcaaagaaa aaaaaaaaaa 3060
aaaa 3064
```

<210> 54

<211> 435

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(435)

<223> 3' terminal sequence. adenomatosis polyposis
coli (APC) gene.

<400> 54

```
tgcataaata ccaatttttc cctgatgtaa gtttagtcag tttataatct agaaatgatt 60
gataacagca atatatcata ttttctatct gtagtggtca ttattttaag acaagcaata 120
attaaaaggaa gttgggatgg gatgctactt taaatacatg taaaacatac tgtacaaaca 180
tacttggctt tactattttt ttctaacca tcaagagtgc ctcccaaat aa gnccagt 240
aagacaaagt atactatcaa atatgggctt ccnggaacaa aaaccctctt aacaaggnt 300
ccaaacccta tttacaaaaa tttcccggt cttttaaggt ttccatttgg aaaccaaaat 360
gtctatatgg ccggttggtg attancatgg ggnttttctt gggnttcctt ctcccnct 420
ctttttaacc ggtgg 435
```

<210> 55

<211> 414

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(414)

<223> 5' terminal sequence. adenomatosis polyposis
coli (APC) gene.

<400> 55

```
agaaaaatgaa ttttctccca caaatagtac ttctcagacc gtttcctcag gtgctacaaa 60
tggtgctgaa tcaaagactc taatttatca aatggcacct gctgtttcta aaacagagga 120
tgtttgggtg agaattgagg actgtcccat taacaatcct agatctggaa gatctccac 180
aggtaatact ccccgggtga ttg acagtgt ttcagaaaag gcaaatccaa acattaaaga 240
ttcaaaagat aatcagggca aaacaaaatg tggggtaatn ggcagtgttc ccatgncgta 300
ccgtgggggt tnggaaaatc gcctggaact cctttatttc aggtgggatg cccctgacca 360
aaaaggganc ttnnggttna aaccggggnc aaattattcc tgttccctgt tttc 414
```

<210> 56

<211> 10383

<212> DNA/RNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(10383)

<223> adenomatosis polyposis coli (APC) gene.

<400> 56

attgaggact cggaatgag gtccaagggt agcc aaggat ggctgcagct tcatatgata 60
agttgttataa gcaagttgag gcaactgaaga tggagaactc aaatcttcga caagagctag 120
aagataattc caatcatctt acaaaactgg aaactgagga atctaataatg aaggaagtac 180
ttaacaact acaaggaagt attgaagatg aagctatggc ttcttctgga cagattgatt 240
tattagagcg tottaaagag cttaacttag atagcagtaa tttccctgga gtaaaactgc 300
ggtcaaaaat gtccctccgt tcttatggaa gccgggaagg atctgtatca agccgttctg 360
gagagtgcag tcctgttctt atgggttcat ttccaagaag aggggtttgta aatggaagca 420
gagaaagtac tggatattta gaagaacttg agaaagagag gtcattgctt cttgc tgatc 480
ttgacaaaga agaaaaggaa aaagactggt attacgtca acttcagaat ctactaaaa 540
gaatagatag tcttcttcta actgaaaatt tttccttaca aacagatatg accagaaggc 600
aattggaata tgaagcaagg caaatcagag ttgcgatgga agaacaacta ggtacctgcc 660
aggatatgga aaaacgagca cagcgaagaa tag ccagaat tcagcaaatc gaaaaggaca 720
tacttcgtat acgacagctt ttacagtccc aagcaacaga agcagagagg tcatctcaga 780
acaagcatga aaccggctca catgatgctg agcggcagaa tgaagggtcaa ggagtgggag 840
aaatcaacat ggcaacttct ggtaattggtc aggggttcaac tacacgaatg gaccatgaaa 900
cagccagtgt tttgagttct agtagcacac actctgcacc tcgaaggctg acaagtcac 960
tggaaccaa ggtggaatg gtgtattcat tgtgtcaat gcttgggtact catgataagg 1020
atgatattgc gcgaactttg ctatgatgt ctatgtccca agacagctgt atatccatgc 1080
gacagtctgg atgtcttctt ctctcatcc agcttttaca tggcaatgac a aagactctg 1140
tattgttggg aaattcccgg ggcagtaaag aggtcggggc cagggccagt gcagactcc 1200
acaacatcat tcaatcacag cctgatgaca agagaggcag gcgtgaaatc cgagtccctc 1260
atcttttggg acagatacgc gcttactgtg aaacctgttg ggagtggcag gaagtcctg 1320
aaccaggcat ggaccaggac aaaaat ccaa tgccagctcc tgttgaaatc cagatctgtc 1380
ctgctgtgtg tgttctaatt aaactttcat ttgatgaaga gcatagacat gcaatgaatg 1440
aactagggg actacaggcc attgcagaat tattgcaagt ggactgtgaa atgtacgggc 1500
ttactaatga ccaatcacag attacactaa gacgatatgc tggaaatgct ttgacaaact 1560
tgacttttgg agatgtagcc aacaaggcta cgctatgctc tatgaaaggc tgcagtagag 1620
cacttgtggc ccaactaaaa tctgaaagtg aagacttaca gcaggttatt gcaagtgttt 1680
tgaggaattt gtcttggcga gcagatgtaa atagtaaaaa gacgttgcga gaagtggaa 1740
gtgtgaaagc attgatgga tgtgcttttag aagttaaaaa ggaatcaacc ctcaaaagcg 1800
tattgagtgc cttatggaat ttgtcagcac attgcactga gaataaagct gatatatgtg 1860
ctgtagatgg tgcacttgca tttttggttg gcactcttac ttaccggagc cagacaaaca 1920
ctttagccat tattgaaagt ggaggtggga tattacggaa tgtgtccagc ttgatagcta 1980
caaatgagga ccacaggcaa atcctaagag agaacaactg tctacaaact ttattacaac 2040
acttaaaatc tcatagtttg acaatagtca gtaatgcatg tggaaactttg tggaaatctc 2100
cagcaagaaa tcctaaagac caggaagcat tatgggacat gggggcagtt agcatgctca 2160
agaacctcat tcattcaaag cacaaaatga ttgctatggg aagtgtgca gct ttaagga 2220
atctcatggc aaataggcct gcgaagtaca aggatgccaa tattatgtct cctggctcaa 2280
gcttgccatc tcttcatgtt aggaacaaaa aagccctaga agcagaatta gatgctcagc 2340
acttatcaga aacttttgac aatatagaca atttaagtcc caaggcatct catcgtagta 2400
agcagagaca caagcaaagt ctctatgg tg attatgtttt tgacaccaat cgacatgatg 2460
ataataggtc agacaatttt aatactggca acatgactgt cctttcacca tatttgaata 2520
ctacagtgtt acccagctcc tcttcatcaa gaggaagcct agatagttct cgttctgaaa 2580
aagatagaag ttggagaga gaacgcggaa ttggtctagg caactacat ccagcaacag 2640
aaaatccagg aacttcttca aagcgaggtt tgcagatctc caccactgca gccagattg 2700
caaagtcat ggaagaagtg tcagccatc atacctctca ggaagacaga agttctgggt 2760
ctaccactga attacattgt gtgacagatg agagaaatgc acttagaaga agctctgctg 2820
ccatacaca ttcaaacact tacaatttca ctaagtcgga a aattcaaat aggcattgtt 2880

ctatgcctta tgccaaatta gaatacaaga gatcttcaaa tgatagttaa aatagtgtca 2940
gtagtagtga tggttatggt aaaagaggtc aaatgaaacc ctcgattgaa tcctattctg 3000
aagatgatga aagtaagttt tgcagttatg gtcaataccc agccgaccta gcccataaaa 3060
tacatagtgc aaatca tatg gatgataatg atggagaact agatacacca ataaattata 3120
gtcttaaata ttcagatgag cagtngaact ctggaaggca aagtccttca cagaatgaaa 3180
gatgggcaag acccaaacac ataatagaag atgaaataaa acaaagtgaag caaagacaat 3240
caaggaatca aagtacaact tatcctggtt atactgagag cactgatgat aaaca cctca 3300
agttccaacc acattttgga cagcaggaat gtgtttctcc atacaggta cggggagcca 3360
atgggtcaga aacaaatcga gtgggttcta atcatggaat taatcaaat gtaagccagt 3420
ctttgtgtca agaagatgac tatgaagatg ataagcctac caattatagt gaacgttact 3480
ctgaagaaga acagcatgaa gaagaagaga gaccaacaaa ttatagcata aaatataatg 3540
aagagaaacg tcatgtggat cagcctattg attatagttt aaaatatgcc acagatatc 3600
cttcatcaca gaacagtcata ttttcattct caaagagttc atctggacaa agcagtaaaa 3660
ccgaacatat gtcttcaagc agtgagaata cgtccacacc ttcattctaat gccaaagggc 3720
agaatcagct ccattccaagt tctgcacaga gtagaagtgg tcagcctcaa aaggctgcca 3780
cttgcaaaagt ttcttctatt aaccaagaaa caatacacagc ttattgtgta gaagatactc 3840
caatatgttt ttcaagatgt agttcattat catctttgtc atcagctgaa gatgaaatag 3900
gatgtaatca gacgacacag gaagcagatt ctgctaatac cct gcaaata gcagaaataa 3960
aagaaaagat tggaactagg tcagctgaag atcctgtgag cgaagttcca gcagtgtcac 4020
agcaccctag aaccaaattc agcagactgc agggttctag tttatcttca gaatcagcca 4080
ggcacaagc tgttgaattt tcttcaggag cgaaatctcc ctccaaaagt ggtgctcaga 4140
cacccaaaag tccacttg aa cactatgttc aggaagcccc actcatgttt agcagatgta 4200
cttctgtcag ttcacttgat agttttgaga gtctgtcgat tgccagctcc gttcagatg 4260
aaccatgcag tggaatggta agtggcatta taagccccag tgatcttcca gatagccctg 4320
gacaaaccat gccaccaagc agaagtaaaa cacctccacc acctcctcaa acagctc aaa 4380
ccaagcgaga agtacctaaa aataaagcac ctactgctga aaagagagag agtggaccta 4440
agcaagctgc agtaaatgct gcagttcaga gggctccagg tcttccagat gctgatactt 4500
tattacattt tgccacggaa agtactccag atggattttc ttgttcatcc agcctgagt 4560
ctctgagcct cgatgagcca ttatacaga a agatgtgga attaagaata atgcctccag 4620
ttcaggaaaa tgacaatggg aatgaaacag aatcagagca gcctaaagaa tcaaatgaaa 4680
accaagagaa agaggcagaa aaaactattg attctgaaaa ggacctatta gatgattcag 4740
atgatgatga tattgaaata ctagaagaat gtattatttc tgccatgcca acaaagtc 4800
cacgtaaaagc aaaaaagcca gccagactg ctccaaaatt acctccacct gtggcaagga 4860
aaccaagtca gctgcctgtg tacaaaactc taccatcaca aaacagggtg caaccccaaa 4920
agcatgttag ttttacaccg gggatgata tgccacgggt gtattgtgtt gaaggacac 4980
ctataaactt ttcacagct acatctctaa gtgatctaac aatcg aatcc cctccaaatg 5040
agttagctgc tggagaagga gttagaggag gacacagtc aggtgaattt gaaaaacgag 5100
ataccattcc tacagaaggc agaagtacag atgaggctca agggagaaaa acctcatctg 5160
taaccatacc tgaattggat gacaataaag cagaggaagg tgatattctt gcagaatgca 5220
ttaattctgc tatgccccaa gggaaaagtc acaagccttt ccgtgtgaaa aagataatgg 5280
accagtgcca gcaagcatct gcgtcgtctt ctgcacccaa caaaaatcag ttatagtgga 5340
agaaaaagaa accaacttca ccagtataac ctataccaca aaatactgaa tataggacac 5400
gtgtaagaaa aatgcagac tcaaaaaata atttaaatgc tgagagagtt ttctcagac a 5460
acaaagattc aaagaaacag aatttgaaaa ataattccaa ggacttcaat gataagctcc 5520
caaataatga agatagagtc agaggaagtt ttgcttttga ttcacctcat cattacacgc 5580
ctattgaagg aactccttac tgtttttcac gaaatgattc tttgagttct ctatgatttg 5640
atgatgatga tgttgacctt tccagggaaa agg ctgaatt aagaaaggca aaagaaaata 5700
aggaatcaga ggctaaagtt accagccaca cagaactaac ctccaaccaa caatcagcta 5760
ataagacaca agctattgca aagcagccaa taaatcgagg tcagcctaaa ccatacttc 5820
agaaacaatc cacttttccc cagtcatcca aagacatacc agacagaggg gcagcaactg 5880
atgaaaagtt acagaatttt gctattgaaa atactccagt ttgcttttct cataattcct 5940
ctctgagttc tctcagtgac attgaccaag aaaacaacaa taaagaaaat gaacctatca 6000
aagagactga gccccctgac tcacaggag aaccaagtaa acctcaagca tcaggctatg 6060
ctcctaatac atttcatggt gaagataccc cagtttggtt ctcaaga aac agttctctca 6120
gttctcttag tattgactct gaagatgacc tgttgacgga atgtataagc tccgcaatgc 6180
caaaaaagaa aagccttca agactcaagg gtgataatga aaaacatagt cccagaaata 6240
tggttgatc attaggtgaa gatctgacac ttgatttgaa agatatacag agaccagatt 6300
cagaacatgg tctatccct g attcagaaa attttgattg gaaagctatt caggaagggtg 6360
caaattccat agtaagtagt ttacatcaag ctgctgctgc tgcattgtta tctagacaag 6420
cttctgtctga ttcagattcc atcctttccc tgaaatcagg aatctctctg ggatcccat 6480
ttcatcttac acctgatcaa gaagaaaaac cctttacaag taataaaggc ccacgaattc 6540

taaaaccagg ggagaaaagt acattggaaa ctaaaaagat agaattctgaa agtaaaggaa 6600
 tcaaggagg aaaaaaagtt tataaaagtt tgattactgg aaaagttcga tctaattcag 6660
 aaatttcagg ccaaatgaaa cagccccttc aagcaaacat gccttcaatc tctcgaggca 6720
 ggacaatgat tcatattcca ggagttcgaa atagc tcctc aagtacaagt cctgtttcta 6780
 aaaaaggccc accccttaag actccagcct ccaaaagccc tagtgaaggc caaacagcca 6840
 ccacttctcc tagaggagcc aagccatctg tgaatcaga attaagccct gttgccaggc 6900
 agacatccca aataggtggg tcaagtaaag caccttctag atcaggatct agagattcga 6960
 ccccttcaag acctgcccag caaccattaa gttagacctat acagtctcct ggccgaaact 7020
 caatttcccc tggtagaaat ggaataagtc ctccatacaa attatctcaa cttccaagga 7080
 catcatcccc tagtactgct tcaactaagt cctcaggttc tggaaaaatg tcatatacat 7140
 ctccaggtag acagatgagc caacagaacc ttaccaaaca aacaggttt a tccaagaatg 7200
 ccagtagtat tccaagaagt gagtctgcct ccaaaggact aatcagatg aataatggta 7260
 atggagccaa taaaaggta gaactttcta gaatgtcttc aactaaatca agtggaagtg 7320
 aatctgatag atcagaaaga cctgtattag tacgccagtc aactttcatc aaagaagctc 7380
 caagcccaac cttagaagaa aaa ttggagg attctgcttc atttgaatct ctttctccat 7440
 catctagacc agcttctccc actagggtccc aagcacaaac tccagtttta agtccttccc 7500
 ttctgatgat gtctctatcc acacattcgt ctgttcaggc tgggtgatgg cgaaaactcc 7560
 cacctaactc cagtcacct atagagtata atgatggaag accagcaaag cgccatgata 76 20
 ttgcacggtc tcatctgaa agtcttcta gacttccaat caataggta ggaacctgga 7680
 aacgtgagca cagcaaacat tcatcatccc ttctcagat aagcacttg agaagaactg 7740
 gaagttcatc ttcaattctt tctgttcat cagaatccag tgaaaaagca aaaagtgagg 7800
 atgaaaaaca tgtgaactct atttcaggaa ccaaaca aag taaagaaaac caagtatccg 7860
 caaaaggaa atggagaaaa ataaaagaaa atgaattttc toccacaaat agtacttctc 7920
 agaccgtttc ctcagggtgct acaaatgggt ctgaatcaaa gactctaatt tatcaaatgg 7980
 cacctgctgt ttctaaaaca gaggatgttt gggtagaat tgaggactgt cccattaaca 8040
 atcctagatc tgggaagatc cccacaggta atactcccc ggtgattgac agtgtttcag 8100
 aaaaggcaaa tccaaacatt aaagattcaa aagataatca ggcaaaaaca aatgtgggta 8160
 atggcagtggt tcccattgct accgtgggtt tggaaaaatc cctgaactcc tttattcagg 8220
 tggatgcccc tgacaaaaaa ggaactgaga taaaaccagg acaaaataat cctgtccctg 8280
 tatcagagac taatgaaagt tctatagtgg aacgtacccc attcagttct agcagctcaa 8340
 gcaaacacag ttacacctagt gggactgttg ctgccagagt gactcctttt aattacaacc 8400
 caagccctag gaaaagcagc gcagatagca cttcagctcg gccatctcag atcccaactc 8460
 cagtgaataa caacacaaaag aagcg agatt ccaaaactga cagcacagaa tccagtggaa 8520
 cccaaagtcc taagcgccat tctgggtctt acctgtgac atctgtttta aagagaggaa 8580
 gaatgaaact aagaaaattc tatgttaatt acaactgcta tatagacatt ttgtttcaaa 8640
 tgaaacttta aaagactgaa aaattttgta aatagggttg attctgttta gaggtttttt 8700
 gttctggaag ccatatttga tagtatactt tgtcttcaact ggtcttattt tgggaggcac 8760
 tcttgatggt taggaaaaaa atagtaaagc caagtatgtt tgtacagtat gttttacatg 8820
 tattttaaagt agcaccatc ccaacttctt ttaattattg cttgtcttaa aataatgaac 8880
 actacagata gaaaatatga tatattgctg ttatcaatc a tttctagatt ataaactgac 8940
 taactttaca tcagggaaaa attggtattt atgcaaaaa aaatgttttt gtccttgtga 9000
 gtccatctaa catcataatt atcatgtgg ctgtgaaatt cacagtaata tggttcccga 9060
 tgaacaagtt taccagcct gtttgcttna ctgcatgaat gaaactgatg gttcaatttc 9120
 agaagtaatg attaacagtt atgtgggtcac atgatgtgca tagagatagc tacagtgtaa 9180
 taattttacac tattttgtgc tccaaacaaa acaaaaatct gtgtaactgt aaaacattga 9240
 atgaaactat ttacactgaa ctgattttta tctgaaaagta ggtagaattt ttgctatgct 9300
 gtaatttgtt gtatatctg gtatttgagg tgagatggct gctcttnatt aa tgagacat 9360
 gaattgtgct tcaacagaaa ctaaatgaac atttcagaat aaattattgc tgtatgtaaa 9420
 ctgttactga aattggattt tgtttgaagg gtnttgtttc acatttgat taattaattg 9480
 tttaaaatgc ctcttttaaa agcttatata aattttttnc ttcagcttct atgcattaag 9540
 agtaaaattc ctcttactgt aataaaa aca attgaagaag actgttgcca cttaccatt 9600
 ccatgcgttg gcacttatct attcctgaaa ttcttttatg tgattagctc atcttgattt 9660
 ttaacatttt tccacttaaa cttttttttc ttactccact ggagctcagt aaaagtaaat 9720
 tcatgtaata gcaatgcaag cagcctagca cagactaagc attgagcata ataggccac 9780
 ataatttctc ctttcttaat attatagaaa ttctgtactt gaaattgatt cttagacatt 9840
 gcagtctctt cgaggcttta cagtgtaaac tgtctgccc cttcatcttc ttgttgcaac 9900
 tgggtctgac atgaacactt tttatcacc tgtatgttag ggcaagatct cagcagtga 9960
 gtataatcag actttgccat gctcagaaaa ttcaaatcac atggaacttt agaggtagat 10020
 ttaatacgtat taagatatc agaagtatat tttagaatcc ctgcctgtta aggaaacttt 10080
 atttgtggta ggtacagttc tggggtacat gttaagtgtc cccttatata gtggaggga 10140
 gtcttcttc ctgaaggaaa ataaactgac acttattaac taagataatt tacttaatat 10200

42/292

atctnccctg atttgtttta aaagatcaga gggtgactga tgatacatgc atacatattt 10260
 gttgaataaa tgaaaattta ttttttagtga taagattcat aactctgtga tttggggaga 10320
 gaaaaccttt ttaagcatgg tggggcactc agataggagt gaatacacct acctggtggt 10380
 cat 10383

<210> 57

<211> 404

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(404)

<223> 5' terminal sequence. mucin 1, transmembrane
(MUC1) gene.

<400> 57

aaacggaagc agcctctcga tataaactga cgatctcaga cgtcagcgtg agtgatgtgc 60
 catttccttt ctctgccag tctggggctg gggtgccagg ctggggcacc gcgctgctgg 120
 tgctggtctg tgttctgggt gcgctggcca ttgtctatct cattgccttg gctgtctgtc 180
 agtgccgccg aaagaactac gggcagctgg acatctttcc ag cccgggat acctaccacc 240
 ctatgagcga gtacccacc taccacaccc atggggcgct atgtgcccc taggcagtac 300
 cgatcgtagc ccctatgaga aggtttttng caggtaatng gttggcagca gcttttttta 360
 caaaaaaccc aggcagtngg cagccatttt tgtccaattt ttag 404

<210> 58

<211> 1721

<212> DNA/RNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(1721)

<223> mucin 1, transmembrane (MUC1) gene.

<400> 58

gaattccctg gctgcttgaa tctgttctgc cccctcccca cccatttcac caccaccat g 60
 acaccgggca cccagtctcc tttcttctg ctgctgctcc tcacagtgt tacagttgtt 120
 acaggttctg gtcattgaag ctctacccca ggtggagaaa aggagacttc ggctaccacg 180
 agaagttcag tgcccagctc tactgagaag aatgctgtga gtatgaccag cagcgtactc 240
 tccagccaca gcccgggttc aggtctctcc accactca gg gacaggatgt cactctggcc 300
 ccggccacgg aaccagcttc aggttcagct gccacctggg gacaggatgt cacctcggtc 360
 ccagtaccca ggccagccct gggctccacc accccggcag cccacgatgt cacctcagcc 420
 ccggacaaca agccagcccc gggctccacc gccccccag cccacggtgt cacctcggcc 480
 ccggacacca ggccgc cccc gggctccacc gccccccag cccacggtgt cacctcggcc 540
 ccggacacca ggccgcccc gggctccacc gcgcccgcag cccacggtgt cacctcggcc 600
 ccggacacca ggccgcccc gggctccacc gccccccag cccatggtgt cacctcggcc 660
 ccggacaaca ggccgcctt ggcgtccacc gccccccag tccacaatgt cacctcgg cc 720
 tcaggctctg catcaggctc agcttctact ctggtgcaca acggcacctc tgccagggt 780
 accacaaccc cagccagcaa gagcactcca ttctcaattc ccagccacca ctctgatact 840
 cctaccaccc ttgccagcca tagcaccaag actgatgcca gtagcactca ccatagcacg 900
 gtacctctc tcacctctc caatcacagc acttct cccc agttgtctac tgggggtctct 960
 ttctttttcc tgtcttttca catttcaaac ctccagtta attctctct ggaagatccc 1020

43/292

```

agcaccgact actaccaaga gctgcagaga gacatttctg aaatgttttt gcagatttat 1080
aaacaagggg gttttctggg cctctccaat attaagttca ggccaggatc tgtggtggta 1140
caattgactc tggccttccg agaaggtacc atcaatgtcc acgacgtgga gacacagttc 1200
aatcagtata aaacggaagc agcctctcga tataacctga cgatctcaga cgtcagcgtg 1260
agtgatgtgc catttccttt ctctgccag tctggggctg gggtgccagg ctggggcatc 1320
gcgctgctgg tgctggtctg tgttctggtt gcgctggcca ttgtctatct cattgccttg 1380
gctgtctgtc agtgccgccc aaagaactac gggcagctgg acatctttcc agcccgggat 1440
acctaccatc ctatgagcga gtacccacc taccacacc atgggcgcta tgtgccccct 1500
agcagtaccg atcgtagccc ctatgagaag gtttctgcag gtaatggtg cagcagcctc 1560
tcttacacaa acccagcagt ggcag cact tctgccaaact tgtaggggca cgtcgccctc 1620
tgagctgagt ggccagccag tgccattcca ctccactcag ggctctctgg gccagtcctc 1680
ctgggagccc ccaccacaac acttcccagg catggaattc c 1721

```

<210> 59

<211> 359

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(359)

<223> 3' terminal sequence. insulin-like growth factor 2 (somatomedin a) (IGF2) gene.

<400> 59

```

ttagccaatt gatttttttg gtggttgttt tttttaagc caatttctga gcttttgtgg 6 0
ggtgtttcta aaaagccaat tagttttaag aggggtgttg tggggggggg ggaagggggg 120
tagtttaatg ttttgatttt ttatgtgttg ggataatttg ggataatttg gggggagggt 180
atgtgaaggg tgtttaagc caatcgattt tgtacatgtt tgaagatgct gctgtgcttc 240
ctcagcccga tggagggggc cgaggagagt agcctgtttc ggggaggcng ggcacgggga 300
ctgggtcang agaagcccca gggggaccgt ngacccaga gattttcggg atggaacc 359

```

<210> 60

<211> 410

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(410)

<223> 5' terminal sequence. insulin-like growth factor 2 (somatomedin a) (IGF2) gene.

<400> 60

```

gtcgacccct ccgaccgtgc ttccggacaa cttcccaga taccocgtgg gcaagttctt 60
ccaatatgac acctgggaag cagtccacc agcgcctgca ggggcnctgc ctgccctcct 120
gcgtgccgc cggggtc acg tgctcgccaa ggagctcgag gcgttcaggg aggccaaacg 180
tcaccgtccc ctgattgtc taccaccca agaccccgcc cacggggcgc nccccccaga 240
gatgggccag caatcggaag tgagcaaaat tgccgcaagt ntttcagccc ggcgncacca 300
ttccttgca gcttntntnt gaaccacgga gttttcttn aggtttccat tccngaaaa t 360
ttttnggtt ttncaagttt cccttggggg gttttttttt tttgaaacca 410

```

<210> 61
<211> 1356
<212> DNA/RNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<220>
<221> misc_feature
<222> (1)..(1356)
<223> insulin-like growth factor 2 (somatomedin a)
(IGF2) gene.

<400> 61
ttctcccgca accttccctt cgtccctcc cgtcccccc agctcctagc ctccgactcc 60
ctccccccct cagcgccgcc ctctcgctt cgcggaacca aagtggatta attacacgct 120
ttctgtttct ctccgtgctg ttctctcccg ctgtgcgcct gcccgctct cgtgtcctc 180
tctccccctc gccctctctt cggccccccc ctttcacgtt cactctgtct ctcccactat 240
ctctgcccc ctctatcctt gatacaacag ctgacctcat ttcccgatac cttttcccc 300
ccgaaaagta caacatctgg ccgccccag ccggaagaca gcccgctctc cctggacaat 360
cagacgaatt ctcccccccc ccccaaaa aa aaaagccatc ccccgctct gcccgctgc 420
acattcggcc cccgcgactc ggccagagcg gcgctggcag aggagtgtcc ggcaggaggg 480
ccaacgccc ctgttcggtt tgcgacacgc agcaggagg tggcgcgag cgtcgccggc 540
ttccagacac caatgggaat cccaatggg aagtcgatgc tgggtgctt cacttcttg 600
gccttcgct cgtgtgcat tgtgtcttac cgccccagt agaccctgt cggcggggag 660
ctggatggca ccttcagatt cgtctgtgg gaccgcgct tctacttcag caggcccgca 720
agccgtgtga gccgtcgag ccgtggcatc gttgaggagt gctgtttccg cagctgtgac 780
ctggccctcc tggagacgta ctgtgtacc ccgcgaagt ccgagagg ga cgtgtcgacc 840
cctccgaccg tgcctccgga caacttcccc agatacccc tgggcaagtt cttccaatat 900
gacacctgga agcagtcac ccagcgctg cgcaggggcc tgcctgccct cctgcgtgcc 960
cgccggggtc acgtgctgc caaggagctc gaggcgttca gggaggccaa acgtcacctg 1020
ccctgattg ctctaccac ccaag accc gccacgggg gcgcccccc agagatggcc 1080
agcaatcgga agtgagcaaa actgcgcaa gtctgcagcc cggcgccacc atcctgcagc 1140
ctctctctga ccacggacgt ttccatcagg ttccatccc aaaatctctc ggttccacgt 1200
ccccctggg cttctctga cccagtcccc gtgccccgc tccccgaaac aggctactct 1260
cctcgcccc ctccatcgg ctgaggaagc acagcagcat cttcaaacat gtacaaaatc 1320
gattggcttt aaacaccct cacataccct ccccc 1356

<210> 62
<211> 474
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<220>
<221> misc_feature
<222> (1)..(474)
<223> 3' terminal sequence. egf-like module
containing, mucin-like, hormone receptor-like
sequence 1 (EMR1) gene.

<400> 62
tttaggagna aatcagtcag acaggcgaca aatcatttat tgagaggttc tctgtgtcag 60
gcgtatgata ggcgctggag gggcacgctt agaaccatgc accaacaagg gcaggagaaa 120
acaaaatggt agccagggtg tcttggtcat gccattgaat ttgggtctgt tctcagaaac 180
tctggaattg aagaagttgc aganaccgaa gataaatgg tcgtttggag cagaaacacc 240
tgattttctc tcaagtgcata caaccacagg aagacggccc ccaacatt ct tccccagagg 300

45/292

gtttctggggc tgggtgggga tccctcattt cccatgttaa gcttgaggaa gagatttcag 360
 ggtaggctcc ctgcaggga actacttgtc cctcaacttt nggcctccca tagcatattt 420
 tnaaagccag naagggtttt ttaacccctt ntttggaag cccgattggc att 474

<210> 63
 <211> 457
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:primer

<220>
 <221> misc_feature
 <222> (1)..(457)
 <223> 5' terminal sequence. egf-like module
 containing, mucin-like, hormone receptor-like
 sequence 1 (EMR1) gene.

<400> 63
 tctgtcaac ggccaggtac gagaagaata caagaggtgg atcactggga agacgaagcc 60
 cagctccag tcccagacct caaggatott gctgtcctcc atgcatccg cttccaagac 120
 gggtaaaagt cttttcttgc tttcaaata gctatggagc cacagttgag gacagtagtt 180
 tcctgcagga gcctaccctg aaatctcttc tcag cttaac atgggaaatg aggatccac 240
 cagccccagg aaccctctgg gggaaggaat gttggggggc cgtcttcctg tgggttgat 300
 tgcantgatg gaggaatatca ggtgtttttt gntccaaacg gaccatttta ntctttcgtg 360
 gntttgcaan ttttttcaan ttccagagtt ttttgaggna caggaccaa nttcantggg 420
 catgnaccag gaacatcggg gttaaccntt tttgttt 457

<210> 64
 <211> 3149
 <212> DNA/RNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:primer

<220>
 <221> misc_feature
 <222> (1)..(3149)
 <223> egf-like module containing, mucin-like,
 hormone receptor-like sequence 1 (EMR1) gene.

<400> 64
 ctaaagtttt tttctttgaa tgacagaact acagcataat gcgtggcttc aacctgctcc 60
 tcttctgggg atgttgtgtt atgcacagct gggaaggga cataagacc acacggaaac 120
 caaacacaaa ggtaataaac ttagagaca gtaccttggt c ccagcttat gccacctgca 180
 ccaatacggg ggacagttac tattgcactt gcaaacaagg cttcctgtcc agcaatgggc 240
 aaaatcactt caaggatcca ggagtgcgat gcaaagatat tgatgaatgt tctcaaagcc 300
 cccagccctg tggctctaac tcactctgca aaaacctgtc agggaggtag aagtgcagct 360
 gtttagatgg tttctcttct cccactggaa atgactgggt cccaggaaaag ccgggcaatt 420
 tctcctgtac tgatatcaat gactgcctca ccagcagggt ctgcctgag cattctgact 480
 gtgtcaactc catgggaagc tacagttgca gctgtcaagt tggattcatc tctagaaact 540
 ccacctgtga agacgtgaat gaatgtgcag atccaagagc ttgccagag catgcaactt 600
 gtaataacac tgttggaac tactcttggt tctgcaacc aggatttgaa tccagcagtg 660
 gccacttgag ttgccagggt ctcaaagcat cgtgtgaaga tattgatgaa tgcactgaaa 720
 tgtgccccat caattcaaca tgcaccaaca ctctgggag ctacttttgc acctgccacc 780
 ctggctttgc accaagcagt ggacagttga atttcacaga ccaaggagtg gaatgtagag 840
 atattgatga gtgcccga gatccatcaa cctgtggtcc taattctatc tgcaccaatg 900

46/292

```

ccctgggctc ctacagctgt ggctgcattg taggctttca tcccaatcca gaaggtccc 960
agaaagatgg caacttcagc tgccaaaggg ttctcttcaa atgtaaggaa gatgtgatac 1020
ccgataataa gcagatc cag caatgccaaag agggaaaccgc agtgaacct gcataatgtct 1080
ccttttgtgc acaaataaat aacatcttca gcgttctgga caaagtgtgt gaaaaataaaa 1140
cgaccgtagt ttctctgaag aatacaactg agagctttgt ccctgtgctt aaacaaatat 1200
ccatgtggac taaattcacc aaggaagaga cgtcctccct ggccacagtc ttcctg gaga 1260
gtgtggaag catgacactg gcctcttttt ggaaaccctc agcaaatgtc actccggctg 1320
ttcgggcgga ataccttagac attgagagca aagttatcaa caaagaatgc agtgaagaga 1380
atgtgacgtt ggacttggtg gccaaagggg ataagatgaa gatcgggtgt tccacaattg 1440
aggaatctga atccacagag accactgggtg tggcttttgt ctcttttgtg ggcattggaat 1500
cggttttaaa tgagcgtctc ttccaagacc accaggctcc ctgaccacc tctgagatca 1560
agctgaagat gaattctcga gtctgtgggg gcataatgac tggagagaag aaagacggct 1620
tctcagatcc aatcatctac actctggaga acgttcagcc aaagcagaag ttgagaggc 1680
ccatctgtgt ttccctggagc actgatgtga aggttggaag atggacatcc ttggctgtg 1740
tgatcctgga agcttctgag acatatacca tctgcagctg taatcagatg gcaaatcttg 1800
ccgttatcat ggctctgtgg gagctcacga tggacttttc cttgtacatc attagccatg 1860
taggcattat catctccttg gtgtgcctcg tcttgccat cgcc accttt ctgctgtgtc 1920
gtcccatccg aaatcacaaac acctacctcc acctgcacct ctgcgtgtgt ctctcttg 1980
cgaagactct ctctctgcc ggtatacaca agactgacaa caagacgggc tgcgccatca 2040
tcgcgggctt cctgcactac ctttctcttg cctgcttctt ctggatgctg gtggaggctg 2100
tgatactgtt cttgatggc agaaacctga aggtgggtgaa ttacttcagc tctcgcaaca 2160
tcaagatgct gcacatctgt gcctttggtt atgggctgcc gatgctggtg gtggtgatct 2220
ctgccagtgt gcagccacag ggctatggaa tgcataatcg ctgctggctg aatacagaga 2280
caggggtcat ctggagtctc ttggggccag ttgacagat tatagtatc aactccct tc 2340
tctgacctg gaccttgtgg atcctgaggc agaggctttc cagtgttaat gccgaagtct 2400
caacgctaaa agacaccagg ttactgacct tcaaggcctt tgcccagctc ttcatcctg 2460
gctgctcctg ggtctgggc attttcaga ttggacctgt ggcagggtgc atggcttacc 2520
tgttcacat catcaacagc ctgcaggggg cc ttcactct cctcatccac tgtctgctca 2580
acggccaggt acgagaagaa tacaagaggt ggatcactgg gaagacgaag cccagctccc 2640
agtcccagac ctcaaggatc ttgctgtcct ccattgccatc cgcttccaag acgggttaaa 2700
gcctttcttg ctttcaataa tgctatggag ccacagttaga ggacagtatg ttctgcagg 2760
agcctacctt gaaatctctt ctacagctaa catggaaatg aggatccac cagccccaga 2820
acctctggg gaagaatgtt gggggccgtc ttctgtggt tgtatgact gatgagaaat 2880
cagacgtttc tgctccaaac gaccatttta tcttctgtct ctgcaacttc ttcaattcca 2940
gagtttctga gaacagaccc aaattcaatg gcatgaccaa gaacac ctgg ctaccatttt 3000
gttttctcct gccctgttg gtgcatggt ctaagcgtgc ccctccagcg cctatcatac 3060
gcctgacaca gagaacctct caataaatga tttgtgcct gtctgactga tttaccctaa 3120
aaaaaaaaa aaaaaaaaaa aaaaaaaaaa 3149

```

<210> 65

<211> 412

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: primer

<220>

<221> misc_feature

<222> (1)..(412)

<223> 3' terminal sequence. k1aa0427 gene product
(K1AA0427) gene.

<400> 65

```

ttaatatcga ctggccaac atttacattt acatg gatgg acaggacgat ccccaaacag 60
tgaaggttta cagactggtc aaggaaggac gaacagagag aatggggtct gaggggtcac 120
atcccgtgga ggggtggcgg gctcctggcc tcgtctgggt gaggttggga gcctcgctgg 180
ggctgcggtc ccagagcttc ggcaaaagca ccaggccttg gggagcaggg ctttggcaag 240
caggccgcct cgga gaaaaa caatgactaa ctatcctga cagggcagtt ggggagactt 300
taggacaggn ttcaacattc agatgggctt ggaccncctt tttccattnc ggccaaggaa 360

```

ccccggggcn agggngngaaa gcaattncaa agccttttagg aaatttcaat tt

412

<210> 66

<211> 442

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(442)

<223> 5' terminal sequence. kiaa0427 gene product
(KIAA0427) gene.

<400> 66

atctgaacaa caacacttta agctgttttt ctaaatgcag gttgctgctc ctttttcaga 60
tatggaagga aaacgttaag actatttttt ttttaaagaa acaacagtca agcctaaaat 120
ttgagacccc gaggcagctt cccgaggag actgctcaga caggaaactgc aggacagaag 180
tgatgcccc acagaccctg ggccccctcc ccaagtccat cccctctctg tgggcatgag 240
gaaggccgcg tccgagttga cctctgaatg tatgtgatga gaggcagagc tgggatattg 300
catttcttaa gggttgcatt gcttttcccc ttccgcccgcg ttctttggcg catggaagga 360
ggcggttcca gccatcttga tgtttgatcc ngttttcagt nttccccant tgcctnttca 420
gggatngagt tagttcattt tt 442

<210> 67

<211> 5737

<212> DNA/RNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(5737)

<223> kiaa0427 gene product (KIAA0427) gene.

<400> 67

gtcagatcag ggatcatttt ttttccttcc tctactccct cccccctacc cgccccctccc 60
tccctgtttc ctttccctcc ctccctcccc tctctgtctg gtctgtgctc tggggcgccc 120
gatccccctc gcagctggga cgctccgaac tcgaggcagg agtcggctct ccggagcctc 180
gtccctccct tccccttccc tgcccccttc ccccacccc gactcgggct tggcgcgggc 240
gccagaggaa ccccgagtcc cggcccaggc ccctgagctg ga gggatgga aaactcctct 300
gcagcatcag cctcctcgga ggcagggagc agccgctccc aggagatcga ggagctggag 360
cgcttcatcg acagctacgt gctggagtac cagggtgcagg ggctgctggc tgacaagacg 420
gagggtgatg gcgagagcga gaggaccacg tcccacatct ccagtgagc agcggactgc 480
agcgaaccgc tggacagcag ctgttccttc tcccaggggc gagccccccc acagcagaat 540
ggcagcaaag acaactctct ggacatgctg ggcacggaca tctgggcggc caacaccttc 600
gattccttca gtggtgccac ctgggacctg cagccggaaa agctggactt caccagttc 660
caccgcaaag tccgacacac gcccaagcag cccctgccac acatcgaccg cgaagggtgt 72 0
ggcaaaggga agctggaaga tggggatggc atcaacctga atgacatcga gaaggtcctt 780
ccagcctggc agggctacca cccgatgcc catgaagtgg agatcgaca caccaagaag 840
ctgttcgca ggaggagaaa tgatcgaagg cggcagcaga gacctccggg gggcaacaag 900
ccccacagc atggtgacca ccagccaggc agtgccaaac acaacaggga ccaccagaaa 960
tctaccagg ggggtcagc accccacccc tcaggagggc ccactcacca tggctacagc 1020
cagaaccggc gctggcacca tggaacatg aagcaccac caggcgacaa gggggaggca 1080
ggcgcacacc gcaatgccaa agagaccatg accatcgaga acccaaaact ggaggacact 1140

gcaggggaca ccgggc acag cagcctcgag gcccccgca gccctgacac cctggccccg 1200
 gtggcttctg agcggtgcc cccacagcag tcaggggggc cagaggttga gacaaaacgt 1260
 aaagacagta ttcttccga gcgcacggg gagcgccca aaattaccct gctccagtct 1320
 tccaaagaca gactgcgcg aaggctaaag gaaaaggatg aagtggccgt ggaga cgacc 1380
 actccccagc agaacaagat ggacaagctg atcgagatcc tgaacagcat gcggaacaac 1440
 agcagcgagc tggacaccaa gctcaccacc ttcatggagg aggccagaa ctccaccaac 1500
 tccgaggaga tgctggcgga gatcgtgcgc acaatctacc agaaggctgt gtccgaccgc 1560
 agcttcgctc tcaccgctgc caagctctgc gacaagatgg cgctctttat ggtggagggg 1620
 accaagttcc ggagcctgct cctcaacatg ctgcagaagg acttcacggt gcgcgaggag 1680
 ctgcagcagc aggacgtgga gcgctggctg ggcttcatca ccttctctgt tgaggtcttc 1740
 ggcaccatgc gcagcagcac aggcgagccc ttccgtgtgc tcgtgtgccc catctacacc 1800
 tgctcaggg agctcttgca atctcaggat gtgaaggaag atgctgtcct ttgctgctct 1860
 atggagctgc agagtacagg ccggtgctg gaggaacagc tgccctgagat gatgacagag 1920
 ctctggcca gcgcagggga caagatgctg tgccctcgg agtccatgct gaccggctcg 1980
 ctgctcctag aggtcatcga gctccacgct aacagctgga acc ctctgac gcccccatc 2040
 acgcagtact acaacagaa catccagaaa ctgacagcct gacagccagg gggcctggca 2100
 ggcggccac ggcagctgg ggcctggtg cacagggcca gatggacagg cgggaggaca 2160
 ggggtggccc tggcgggaga aagaaatggg gaggagggca ggcagagtcg gtggccagtc 2220
 tggagccaga cggggaag gg agcaaatccc tgagaggagt gccccgcac aagcccccca 2280
 gcccgagcat gcaagctcac accaataagg gaagcatgtt tcttttctc ggtggccctg 2340
 gccctccct tcctcactcc cgcctctccc caaaccatca gacctatccc ccacggagct 2400
 ttgtgtgagg gatctcatcg ctgtgactcc tcggagacct tggcagcctc gcacgcc ggg 2460
 gcaccgcttg ggtcagaaag gacctcggaa ggctgaaaaa gtgggtcgga gacgggctcg 2520
 cattgttccc gcatgctgtc agccgcagtc gccactggc agcaggcgac gtgtagcaga 2580
 tgtccgggag gacaaaggca ggcacggctc ccaccagccg ccgtaattg acggcctttg 2640
 tcagccatgg cagagctgac gctccacctc c cacctcaa gtctctctca ctgcagcccc 2700
 cacagcctca ggctagggg gtcaggcgca gcgggggaga tggagtttg agttccactt 2760
 gcaactcttt gtttattgtg ttttattttt caaaagtcgg ttgctttgaa gtctctttgg 2820
 ccaatgaaaa tgcccgtag gtgatcacac agtcagcact gttgaggacc cccgattag 2880
 tgggagatca aaccagctc cctctagaa gaaggattcg agccacagac agcttgccag 2940
 tagccaatta ggtaattgg aaacttctgc ccggcgggg ggtccccgt ggaatcctgt 3000
 gttcctcgcc actggtctcc agcgcctctg ttttctcaaa gggctgatac tgtcaccact 3060
 gggaccaagt taaacctgg cctggcccca ggggccttgt ggcaa acagg gcacagaacg 3120
 agactggcaa attaaaacca aaattctaga tgggtcttg cgctccacac gcaggtctta 3180
 ctggggaaaa ggatgggagt gggggctccc caggactcga ttttagctaa tgcgctgtgt 3240
 cactgcccc gctcggacgt agaagcccag ccctcctgta gctcttgga aaggggtgaa 3300
 ttcactgggt catggaagg acagtcagg gaccagcggg gtcgccagat gaagcttccc 3360
 agccgggaaa caagacggg tttcttgga ggcctggtc ctggggagca ggcctgttg 3420
 ttggctggag aggaagggtg ggggtggaac aggtgtccac atagctccat ctctggggg 3480
 tggagcacac accttagtc gcccccgg ggcagggcc tgggtcact tggaggcccc tcttggtcca 3600
 tttgctcttt tattgaggc gatgggggg gaaggttctc gtgattgatt gattctgagt 3660
 cactggactg gccgggagg ctgagagtgg cgagtgggga gaggttccc cagttctctc cagcttccc tgcagctgca 3720
 acctgcctc tggctccagg tgtggagcct ttg cctgtct ctaaaaagag cctgttggcg 3780
 acaagggtga gggggcacaa gtttacctga aacaggtcag tggctctctc caagaagcgc 3840
 acgccacctc tggctccctg ccctgaacc tcctctctc ctccctccac ggttctctc 3900
 cagactttct caagctctc ctactgccc ttctcccca gccagcctg ggaacacaga 3960
 tgcccccg gtagggaggc tcgaggagg agccgggctg atgcggggt gctcagggca 4020
 ggcgccagg cgagcttgcc atcgtggcca ggcagcctc acctgtgctt cagtggccc 4080
 tgccccctg aagcatgtg ggtttgtcc ctaggaggag gcaaggcccc cgaagagagg 4140
 agagacctg gagtgggagc tcaggtcagg gaggaggcag gggagtg ggg tctccagac 4200
 ccaacggtga gctcagagca agcttcacgc aggacgctc gaaacactgt gtggagggg 4260
 ctgtgttg ggcacctg ggcctgattc tccttctcc gaacgggctc cttgatggcc 4320
 tggccacag ggcagctccc cattggctgt gtagaccaga gtgtgaagaa gaagtgaat 4380
 ataaatatgt atacatat a aatatatt ttaattacat gtcgtgtcac ggtggctcca 4440
 gacatactgt ttgctagt ttttccactg cttgaaagc cttcctagcc aatctgaaca 4500
 acaacacttt aagctgtttt tctaaatgca ggttgctgct cctttttcag atatggaagg 4560
 aaaacgttaa gactattttt tttttaaaga aacaacagtc aagcctaaa tttgagacc 4620
 cgaggcagct tcccaggga gactgctcag acaggaactg caggacagaa gtggatgccc 4680
 cacagacct ggccccctc ccaagtccat cccctctctg tggcatgagg aaggccgct 4740
 ccgagttgac ctctgaatgt atgtgatgag aggcagagct ggatattgca tttctaaggc 4800

49/292

```
ttgcattgct ttcccctcgc ccgcggttct tggcg catgg aagaggcggg ccagccatct 4860
gatgttgatc ctgtctcagt ctccccactg cctgtcagga tgagttagtc attgtttttc 4920
tccgaggcgg cctgcttgcc acagccctgc tccccaaggc ctggtggctt tgccgaagct 4980
ctgggaccgc agccccagcg agggcccca cctcaccag acgaggccag gagccccgcc 5040
accctccacg ggatgtgcac cctcagacc cattctctct gttcgtcctt ccttgaccag 5100
tctgtaaacc ttcactgttt ggggatcgtc ctgtccatcc atgtaaatgt aaatgttggc 5160
cgagtcggta tttattctga ttgattttta tttatttota ttattttctc cgagggatga 5220
gggtgggggg tgtgggaagg gtaccacaga tcaggccggg gcagctgta g gggcgggggc 5280
ccagacagcc aggcgcgcac cagagcagcc ccatgggggtg cccagacgc gggcctccaa 5340
gaagccaagt ccagctctgt tttctggcat cagacaccg cccgtgttcc ttgtcagaca 5400
gacagactct caggcctgcc tggggagtgc tgtccctcag ctgcagggca ctgtgttggg 5460
aaaccattgg ctgggccttt gag gacacag atcagaagaa agaaagacaa ctttccctctg 5520
cgcggaacac tcacacggaa gggctggccg cctccctgag ccggctggga gtggacgaca 5580
ggacctacct cccagagca agggcctggg gcttcccgcc aaagctgccg cggaaccccg 5640
ctagtgcgac caccctccct ccgtcgggat gtcctgcttt ccagctgaac ccaaactaca 57 00
agtgggttta aaaaaataa acaccaccac caaaac 5737
```

<210> 68

<211> 377

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(377)

<223> 3' terminal sequence. spleen tyrosine kinase
(SYK) gene.

<400> 68

```
tctttctttc tttccttaac tggtacatg cttagaaact gcactggtca aacttgattt 60
tctttttaaa gcctcaaaac atttttattg tcaggaaagc ttttcagtgg ccagggatca 120
gtctcatggc cgtagaagca gccaaattcc tctgcctttg ccttcccttc aggagtca ca 180
tgctaaggca tccttggggc atttgggaaa agngccgctt gggggtgaga gtgctctagg 240
gccactctgc aatgtccctg gggnccgatg aggtaacaaa tgcaccccg ggaccagag 300
gagtggggaa agacatgaag gggatttggg aacagatccg taaaaataa cctgttntgg 360
aaattcacca caggcca 377
```

<210> 69

<211> 323

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(323)

<223> 5' terminal sequence. spleen tyrosine kinase
(SYK) gene.

<400> 69

```
ttaattttgg aggcctcca caacttccag gttcccatcc tgcgacttgg tcagcgggtg 60
gaataatctc aagaatcaaa tcatactcct tcccaaagcc tggccacaga aagtcctccc 120
ctgcccagg ggaccgncaa gagagtactg tgtcattcaa tccgtatgag gccaggaact 180
tgcacccggg gcttgcagga caaagggcc cca gaggagg aagccctacc cntgggacac 240
```

50/292

agaggtgtta cggaggagcc cntacggcgg gaccccgagg gagnttcagg gcccaagggn 300
gtttttactt gggggaccga aag 323

<210> 70

<211> 2541

<212> DNA/RNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(2541)

<223> spleen tyrosine kinase (SYK) gene.

<400> 70

gaggaagagc cgcgggcccg gcggtgagg ccaccccggc ggcggtgga gagcgaggag 60
gagcggtggtg ccccgcgctg cgcgcgcct cgctcacct ggcgaggtg g acacctgcg 120
caggtgtgtg cccctcgggc cctgaagcat ggccagcagc ggcatggctg acagcgccaa 180
ccacctgccc ttctttttcg gcaacatcac ccgggaggag gcagaagatt acctggtcca 240
ggggggcatg agtgatgggc tttatttgct gcgccagagc cgcaactacc tgggtggctt 300
cgccctgtcc gtggcccacg ggaggaaggc acaccactac accatcgagc gggagctgaa 360
tggcacctac gccatcgccg gtggcaggac ccatgccagc ccgcccagacc tctgccacta 420
ccactcccag gagtctgatg gcctggtctg cctcctcaag aagcccttca accggcccca 480
aggggtgcag cccaagactg ggccctttga ggatttgaag gaaaacctca tcagggaata 540
tgtgaagcag acatggaacc tgcaggggtca ggctctggag caggccatca tcagtcagaa 600
gcctcagctg gagaagctga tcgctaccac agcccatgaa aaaatgcctt ggttccatgg 660
aaaaatctct cgggaagaat ctgagcaaat tgcctgata ggatcaaaga caaatggaaa 720
gttcctgatc cgagccagag acaacaacgg ctctacgcc ctgtgcctgc tgcacgaagg 780
gaaggtgctg cactatcgca tcgacaaaga caagacaggg aagctctcca tccccgaggg 840
aaagaagttc gacacgctct ggagctagt cgagcattat tcttataaag cagatggttt 900
gttaagagtt cttactgtcc catgtcaaaa aatcggcaca cagggaatg ttaattttgg 960
aggcctccca caacttccag gttcccat cc tgcgtcctcc cctgcccagg ggaaccggca 1020
agagagtact gtgtcattca atccgtatga gccagaactt gcaccctggg ctgcagacaa 1080
aggcccccag agagaagccc taccatgga cacagaggtg tacgagagcc cctacgcgga 1140
ccccgaggag atcaggccca aggagggtta cctggaccga aagctgctga cgctggaaga 1200
caaagaactg ggctctggtg attttggaac tgtgaaaaag ggctactacc aaatgaaaaa 1260
agttgtgaaa accgtggctg tgaaaatact gaaaaacgag gccaatgacc ccgctcttaa 1320
agatagagtt ttgacagaag caaatgtcat gcagcagctg gacaacccgt acatcgtgag 1380
gatgatcggg atatgcgagg ccgagtcctg gatgctggtt a tggagatgg cagaacttgg 1440
tcccctcaat aagtatttgc agcagaacag acatgtcaag gataagaaca tcatagaact 1500
ggttcacag gtttccatgg gcatgaagta cttggaggag agcaattttg tgcacagaga 1560
tctggctgca agaaatgtgt tgctagttag ccaacattac gccaaagatca gtgatttcgg 1620
actttccaaa gcactg cgtg ctgatgaaaa ctactacaag gccagacccc atggaaagtg 1680
gcctgtcaag tggtagctc cggaatgcat caactactac aagttctcca gcaaaagcga 1740
tgtctggagc tttgagtggt tgatgtggga agcattctcc tatgggcaga agccatatcg 1800
agggatgaaa ggaagtgaag tcaccgctat gttagagaaa ggagagcgga tgggg tgccc 1860
tgcagggtgt ccaagagaga tgtacgatct catgaatctg tgctggacat acgatgtgga 1920
aaacaggccc ggattcgag cagtggaaact gcggctgctg aattactact atgacgtggt 1980
gaactaaccg ctcccgacc tgctgggtggc tgcctttgat cacaggagca atcacaggaa 2040
aatgtatcca gaggaattga ttgtcagcca cctccctctg ccagtcggga gagccaggct 2100
tggatggaac atgtccacaa cttgtcacc aaagcctgtc ccaggactca cctccacaa 2160
agcaaaagca gtcccgggag aaaagacgga tggcaggatc caaggggcta gctggatttg 2220
tttgttttct tgtctgtgtg attttcatac aggttatttt tacgatctgt ttccaaatcc 2280
ctttcatgtc tttccacttc tctgggtccc ggggtgcatt tgttactcat cgggcccagg 2340
gacattgcag agtggcctag agcactctca cccaagcgg ccttttccaa atgccaagg 2400
atgccttagc atgtgactcc tgaagggaa gcaaaggcag aggaatttgg ctgcttctac 2460
ggccatgaga ctgatccctg gccactgaaa agctttctctg aca ataaaaa tgttttgagg 2520
ctttaaaaaa aaaaaaaaaa a 2541

<210> 71
<211> 312
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<220>
<221> misc_feature
<222> (1)..(312)
<223> 5' terminal sequence. interleukin 7 receptor
(IL7R) gene.

<400> 71
taacatcttt gtaagaaacc aagaaaaaat ttaaatgtga gtttcaatcc tgaaagtttc 60
ctggactgcc agattcatag ggtggatgac attcaagcta gagatgaagt ggaaggtttt 120
ctgcaagata cgtttcctca gcaactagaa gaatctga ga agcagaggct tngaggggat 180
gtgcagagcc ccaactgccc atctgaggat gtagtcatca ctccaggaaa gctttgggaa 240
ggagattcat ccctcacatg cctgggctng ggaatgttca gtgcatgtga cgccctatt 300
tttctccttt t 312

<210> 72
<211> 1658
<212> DNA/RNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<220>
<221> misc_feature
<222> (1)..(1658)
<223> interleukin 7 receptor (IL7R) gene.

<400> 72
ctctctctct atctctctca gaatgacaat tctagggtaca acttttggca tggt tttttc 60
tttacttcaa gtcgtttctg gagaaagtgg ctatgctcaa aatggagact tggaagatgc 120
agaactggat gactactcat tctcatgcta tagccagttg gaagtgaatg gatcgagca 180
ttcactgacc tgtgcttttg aggaccaga tgtaacacc accaatctgg aatttgaaat 240
atgtggggcc ctggtggagg taaagtgcct gaa tttcagg aaactacaag agatatattt 300
catcgagaca aagaaattct tactgattgg aaagagcaat atatgtgtga aggttgagga 360
aaagagtcta acctgcaaaa aaatagacct aaccactata gttaaacctg aggctccttt 420
tgacctgagt gtcattctatc gggaaggagc caatgacttt gtggtgacat ttaatacatc 480
acacttgcaa aagaagtatg taaaagtttt aatgcatgat gtagcttacc gccaggaaaa 540
ggatgaaaac aaatggacgc atgtgaattt atccagcaca aagctgacac tctgcagag 600
aaagctcaa ccggcagcaa tgtatgagat taaagttcga tccatccctg atcactattt 660
taaaggcttc tggagtgaat ggagtccaag ttattacttc agaactccag aga tcaataa 720
tagtcaggg gagatggatc ctatcttact aaccatcagc attttgagtt ttttctctgt 780
cgctctgttg gtcattcttg cctgtgtgtt atggaaaaaa aggattaagc ctatcgtatg 840
gcccagtctc cccgatcata agaagactct ggaacatctt tgtaagaaac caagaaaaaa 900
tttaaatgtg agtttcaatc ctgaaagttt c ctggactgc cagattcata gggtgatga 960
cattcaagct agagatgaag tggaagggtt tctgcaagat acgtttctc agcaactaga 1020
agaatctgag aagcagaggc ttggagggga tgtgcagagc cccaactgcc catctgagga 1080
tgtagtcgtc actccagaaa gctttggaag agattcatcc ctccatgccc tggctgggaa 1140
tgtcagtga tgtgacgccc ctattctctc ctcttcagg tccctagact gcaggagag 1200
tggcaagaat gggcctcatg tgtaccagga cctctgctt agccttgga ctacaaacag 1260
cacgctgccc cctccatttt ctctocaatc tggaatcctg acattgaacc cagttgctca 1320

52/292

gggtcagccc attcttactt ccctgggac aaatcaagaa gaagca tatg tcaccatgtc 1380
cagcttctac caaaaccagt gaagtgtgaa aaaccagac tgaacttacc gtgagcgaca 1440
aagatgattt aaaagggaag tctagagttc ctagtctccc tcacagcaca gagaagacaa 1500
aattagcaaa accccactac acagtctgca agattctgaa acattgcttt gaccactctt 1560
cctgagttca gtggcactca acatgagtca agagcatcct gcttctacca tgtggatttg 1620
gtcacaaggt ttaagggtgac ccaatgattc agctattt 1658

<210> 73

<211> 236

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(236)

<223> 3' terminal sequence. v-myc avian
myelocytomatosis viral oncogene homolog (MYC)
gene.

<400> 73

taaaaacaat agaaaaaat caactttaaa aagcaaatg tacttaata aaaaaatta 60
gggtttatag tacctataat actaggnact atatactagg attgaaa ttc tgtgtaactg 120
ctataaacgt ttatttaaag ttatttacat ttaatgggca atatttacag aggaaacatt 180
gtgtaaactt taaaattttt taaaanccaa ttcttaata ccaaatctgt taaggg 236

<210> 74

<211> 413

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial S equence:primer

<220>

<221> misc_feature

<222> (1)..(413)

<223> 5' terminal sequence. v-myc avian
myelocytomatosis viral oncogene homolog (MYC)
gene.

<400> 74

acgtctccac acatcagcac aactacgcag cgctccctc cactcggaag gactatcctg 60
ctgccaagag ggtcaagttg gacagtgtca gagtctgag acagatcagc aacaaccgaa 120
aatgcaccag cccaggtcc tcggacaccg aggagaatgt caagaggcga acacacaacg 180
tcttgggagc gccagaggag gaacgagcta aaacggagct tttttgccct gcgtgaccag 240
atcccgaggt tgggaaaaca atgaaaaggc cccaaggta gttattcctt taa aaaagcc 300
acagcntaca tcctgttccg ttccaaggca ggaggagacc aaaagttcat tttnttgaag 360
gagggnnttt ttttcgggn aacgacgag aaccatttn aaacacaant ttt 413

<210> 75

<211> 2121

<212> DNA/RNA

<213> Artificial Sequence

<220>

53/292

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(2121)

<223> v-myc avian myelocytomatosis viral oncogene
homolog (MYC) gene.

<400> 75

```
ctgctcgcg cgcaccgc cgggccccg ccgtccctg ctccccctc gcctcgagaa 60
gggcagggt tctcagagg ttggcggga aaaagaacg g agggaggat cgcgctgagt 120
ataaaagccg gttttcggg ctttatctaa ctcgctgtag taattccagc gagaggcaga 180
gggagcgagc gggcggccg ctaggggtga agagccggc gagcagagc gcgctgcggg 240
cgctctggga agggagatcc ggagcgaata gggggcttcg cctctggccc agccctccc 300
cttgatcccc caggcca gcg gtccgcaacc cttgccgat ccacgaaact ttgcccatag 360
cagcggcgcg gcacttttga ctggaactta caacaccga gcaaggacgc gactctccc 420
acgcggggag gctattctgc ccatttggg acaattcccc gccgctgcca ggaccgctt 480
ctctgaaagg ctctccttgc agctgcttag acgtggatt tttttcggg agtggaana c 540
cagcagctc ccgcagcat gccctcaac gttagcttca ccaacaggaa ctatgacctc 600
gactacgact cgggtgcagc gtatttctac tgcgacgag aggagaactt ctaccagcag 660
cagcagcaga gcgagctgca gcccccgcg cccagcgagg atatctggaa gaaattcgag 720
ctgctgcccc ccccgccct gtcccctagc cgccgct ccg ggctctgctc gccctcctac 780
gttgcggtca cacccttctc ctttcggga gacaacgac gcggtggcg gagcttctcc 840
acggccgacc agctggagat ggtgaccgag ctgctgggag gagacatggt gaaccagagt 900
ttcatctgag acccgagca cgagacctt atcaaaaaca tcatcatcca ggactgtatg 960
tggagcggt tctcg gccgc cgcgaagctc gtctcagaga agctggcctc ctaccaggct 1020
gcgcgcaaa acagcgcgag cccgaacccc gcccgcgcc acagcgtctg ctccacctcc 1080
agcttgtacc tgcaggatct gagcgcggc gcctcagagt gcatcgacct ctcggtggtc 1140
ttcccctacc ctctcaacga cagcagctcg cccaagtcct gcgcctcgca agac tccagc 1200
gccttctctc cgctcctcga ttctctgctc tctcgacgg agtccctccc gcagggcagc 1260
cccagcccc tgggtgctca tgaggagaca ccgccacca ccagcagcga ctctgaggag 1320
gaacaagaag atgaggaaga aatcgatgtt gtttctgttg aaaagaggca ggctcctggc 1380
aaaaggtcag agtctggatc accttctgc t ggaggccaca gcaaacctcc tcacagccca 1440
ctggtcctca agaggtgcca cgtctccaca catcagcaca actacgcagc gcctccctcc 1500
actcggaagg actatcctgc tgccaagagg gtcaagttgg acagtgtcag agtccctgaga 1560
cagatcagca acaaccgaaa atgcaccagc ccaggtcct cggacaccga ggagaatgtc 1620
aagaggcgaa cacacaacgt cttggagcgc cagaggagga acgagctaaa acggagcttt 1680
tttgcctgct gtgaccagat cccggagttg gaaaacaatg aaaaggcccc caaggtagtt 1740
atccttaaaa aagccacagc atacatcctg tccgtccaag cagaggagca aaagtcatt 1800
tctgaagagg acttgttgcg gaaacgacga gaacagttga aa cacaaact tgaacagcta 1860
cggaactctt gtgcgtaagg aaaagtaagg aaaacgattc cttctaacag aaatgtcctg 1920
agcaatcacc tatgaacttg ttcaaagtgc atgatcaaat gcaacctcac aaccttgggt 1980
gagtcttgag actgaaagat ttagccataa tgtaaaactgc ctcaaattgg actttgggca 2040
taaaagaact tttttat gct taccatcttt ttttttctt taacagattt gtatttaaga 2100
attgttttta aaaaatttta a 2121
```

<210> 76

<211> 260

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(260)

<223> 3' terminal sequence. gata-binding protein 3
(GATA3) gene.

54/292

<400> 76

tcacagcact agagaccctg ttaaataggg gatatgagtc agaatggctt attcacagat 60
ggggtccaga ttcagtgggt ggaacacaga caccacagtg agtcctttg caaagtggca 120
aacataatth tgctttctgc cttcaaaaac atatatccat cgcgtttagg cttcatgata 180
ctgctcctgc aaaaatgcaa gtcgaaaggg actgcaggga ctctcgctgg ggggccctgt 240
gagcatcgag cagggtcttt 260

<210> 77

<211> 409

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(409)

<223> 5' terminal sequence. gata -binding protein 3
(GATA3) gene.

<400> 77

cattctgggt catagatggc atcttttcac tgtgttctca cattgttga aaggaagaac 60
tctggtttct tcacttctt ataagggcac caatcttatt cagagggtc tcacctcga 120
aataatcacg tcctcaaaac cccaccttc taatattcta ataccatcac gtgagggtt 180
aggtttcaac ataagaattc ggtggtggtt ggggttnggg gagaggaaa caaacatcca 240
gaccagaaac cgaaaaatgt ctagcaaatc caaaaagtgc aaaaaagt gc atgactcact 300
ggaggacttc cccaagganc agctncgttt taaccggggc cgcccttttc caggacacat 360
gttccttccc tggnggccac atnttgncc, ttnaggccan tccagggca 409

<210> 78

<211> 2365

<212> DNA/RNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(2365)

<223> gata-binding protein 3 (GATA3) gene.

<400> 78

tcccagcctt cccatccccc caccgaaagc aaatcattca acgacccccg accctccgac 60
ggcaggagcc ccccgacctc ccaggcggac cgcccttccc tccccgcgag ggttccgggc 120
ccggcgagag ggcgcgacga cagccgaggc catggagggt acggcggacc agccgcgctg 180
ggtgagccac caccaccccc cggtgctcaa cgggcagcac ccggacacgc accaccggg 240
cctcagccac tcctacatgg acgcggcgca gtaccgctg ccggaggagg tggatgtgct 300
ttttaacatc gacgggtcaag gcaaccacgt cccgcctac ta cgaaact cggtcagggc 360
cacggtgacg aggtacccct cgaccacca cgggagccag gtgtgccgcc cgctctgct 420
tcatggatcc ctaccctggc tggacggcgg caaagccctg ggcagccacc acaccgctc 480
ccccgggaat ctacgcccct tctccaagac gtccatccac cacggctccc cggggccct 540
ctccgtctac ccccggcct cgtcctctc cttgtcgggg ggccacgcca gcccgcacct 600
cttcaccttc ccgcccaccc cgccgaagga cgtctccccg gacccatcgc tgtccacccc 660
aggctcggcc ggctcggccc ggaggagca gaaagagtgc ctcaagtacc aggtgcccct 720
gcccagaccg atgaagctgg agtcgtccca ctcccgtggc agcatgaccg ccctgggtgg 78 0
agcctcctcg tcgaccacc acccatcac cacctaccg ccctacgtgc ccgagtacag 840
ctccggactc ttcccccca gcagcctgct gggcggctcc cccaccggct tcggatgcaa 900

```
gtccaggccc aaggcccggg ccagcacagg cagggagtgt gtgaactgtg gggcaacctc 960
gacccccactg tggcggcgag atggcacggg acactacctg tgcaacgcct gcgggctcta 1020
tcacaaaatg aacggacaga accggccctt cattaagccc aagcgaaggc tgtctgcagc 1080
caggagagca gggacgtcct gtgcgaactg tcagaccacc acaaccacac tctggaggag 1140
gaatggcaat ggggaccctg tctgcaatgc ctgtgggctc tactacaagc ttcacaatat 1200
taacagaccc ctgac tatga agaaggaagg catccagacc agaaaccgaa aaatgtctag 1260
caaatccaaa aagtgcacaaa aagtgcacat ctactggag gacttcccca agaacagctc 1320
gtttaacccg gccgcctctt ccagacacat gtctctccctg agccacatct cgccttcag 1380
ccactccagc cacatgctga ccacgcccac gccgatgcac ccgccatcca gcct gtcctt 1440
tggaccacac caccctctca gcatggtcac cgccatgggt tagagccctg ctgatgctc 1500
acagggcccc cagcgagagt ccctgcagtc cctttcgact tgcatTTTTg caggagcagt 1560
atcatgaaag ctaaacgcga tggatatatg ttttgaagg cagaaagcaa aattatgttt 1620
gccactttgc aaaggagctc actgtgtgt t ctgtgttcca accactgaat ctggaccca 1680
tctgtgaata agccattctg actcataatc cctatttaac aggttctcta gtgtgtgaa 1740
aaaaaaaaat cctgaacatt gcatataact tatattgtaa gaaatactgt acaatgactt 1800
tattgcatct gggtagctgt aaggcatgaa ggatgccaag aagttaaagg aatatgggag 1860
aaatagtgtg gaaattaaga agaaactagg tctgatattc aaatggacaa actgccagtt 1920
ttgtttcctt tcactggcca cagttgtttg atgcattaaa agaaaataaa aaaaagaaaa 1980
aagagaaaag aaaaaaaaag aaaaaagttg taggcgaatc atttgttcaa agctgttggc 2040
cctctgcaaa ggaaatacca gttctgggca atcagtgtta cc gttcacca gttgccattg 2100
agggtttcag agagcctttt tctaggccta catgctttgt gaacaagtcc ctgtaattgt 2160
tgtttgtatg tataattcaa agcaccacaaa taagaaaaga ttagatttta tttcatcata 2220
ttatacagac cgaactgttg tataaattta tttactgcta gtcttaagaa ctgctttctt 2280
tcgtttgttt gtttcaa tat tttccttctc tctcaatttt cggttgaata aactagatta 2340
cattcagttg gcaaaaaaaaa aaaaa 2365
```

<210> 79

<211> 328

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(328)

<223> 3' terminal sequence. growth factor
receptor-bound protein 7 (GRB7) gene.

<400> 79

```
ttgtatnttt naaataatct ttattgtcac tagtataaaa cagagcagat caactggcct 60
ctcggctctgt acaaagtgtg gggcgtgaaa ccgctgggct gccccactt ctcccataat 120
tccctgccct agagcagcag ctccagagct aggagaagga gagggggcca cccaaggcct 180
tcccttgagg agaggggtca ggagtggact ggagtgggg ctgttttcta tctgaggag 240
gcaaagaagc agaggagaaa actggagtgg cggaaccctc ccgntcctca tcccgcccc 300
tgtggccgat cccanagtcc actnggat 328
```

<210> 80

<211> 428

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(428)

<223> 5' terminal sequence. growth factor
receptor-bound protein 7 (GRB7) gene.

<400> 80

```
ggctcccccac ccttgagaag tgcctcagat aataccctgg tggccatgga cttctctggc 60
catgtctgggc gtgtcattga gaacccccgg gaggctctga gtgtggccct ggaggaggcc 120
caggcctgga ggaagaagac aaaccaccgc ctcagcctgc ccatgccagc ctccggacga 180
gcctcagtgc agccatccac cgcacccaac tctggttcca cgggcgcatt tcccgtgagg 240
agagccagcg tttattggga cagcagggct tngtagacgg cctgttcctg ggtccgggag 300
agtcagcggg aacccccagg ggtttttcct ctttttnttg ccaccttgca gaaagtgaag 360
cnttattttc attccttgcc gagcgaagga ggaagggccg cttttatatt aagcattggt 42 0
tgattggc 428
```

<210> 81

<211> 2205

<212> DNA/RNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(2205)

<223> growth factor receptor-bound protein 7
(GRB7) gene.

<400> 81

```
cacagggtc cccccgcct ctgacttctc tgtccgaagt cgggacaccc tcctaccacc 60
tgtagagaag cgggagtgga tctgaaataa aatccaggaa tctgggggtt cctagacgga 120
gccagacttc ggaacgggtg tcctgctact cctgctgggg ctctccagg acaaggga c 180
acaactggtt cgttaagcc cctctctcgc tcagacgcca tggagctgga tctgtctcca 240
cctcatctta gcagctctcc ggaagacctt tggccagccc ctgggacccc tcctgggact 300
ccccggcccc ctgatacccc tctgcctgag gaggtaaaga ggtcccagcc tctcctcatc 360
ccaaccaccg gcaggaaact tcgagaggag gagaggc gtg ccacctcct cccctctatc 420
cccaaccctc tcctgagct ctgcagtcct cctcacaga gcccaattct cgggggcccc 480
tccagtcaa gggggtgct ccccgcgat gccagccgcc cccatgtagt aaaggtgtac 540
agtgaggatg gggcctgcag gtctgtggag gtggcagcag gtgccacagc tcgccacgtg 600
tgtgaaatgc ttgtg cagcg agctcacgcc ttgagcagc agacctgggg gctggtggag 660
tgccaccccc acctagcact ggagcggggt ttggaggacc acgagtccgt ggtggaagtg 720
caggctgcct ggcccgtggg cggagatagc cgcttcgtct tcggaaaaa cttcgccaag 780
tacgaactgt tcaagagctc cccacactcc ctgttcccag aaaaaatggt ctccagc tgt 840
ctcgatgcac aactgggtat atcccatgaa gacctatcc agaacttct gaatgctggc 900
agctttcctg agatccaggg ctttctgcag ctgcggggtt caggacggaa gctttggaaa 960
cgctttttct gtttcttgcg ccgatctggc ctctattact ccaccaaggg cacctctaag 1020
gatccgaggc acctgcagta cgtggcagat gtga acgagt ccaacgtgta cgtggtgacg 1080
caggccgca agctctacgg gatgccact gacttcggtt tctgtgtcaa gcccaacaag 1140
cttcgaaatg gacacaaggg gcttcggatc ttctgcagtg aagatgagca gagccgcacc 1200
tgctggtctg ctgccttccg cctcttcaag taoggggtgc agctgtacaa gaattaccag 1260
caggcacagt ctgcctatct gcacctatct tgtttgggct cccaccctt gagaagtgcc 1320
tcagataata ccctggtggc catggacttc tctggccatg ctgggcgtgt cattgagaac 1380
ccccgggag ctctgagtgt ggccctggag gaggcccagg cctggaggaa gaagacaaac 1440
caccgcctca cgtgccccat gccagcctcc ggcacgagcc tcagtga gc catccaccgc 1500
acccaaactct ggttccacgg gcgcatttcc cgtgaggaga gccagcggct tattggacag 1560
cagggcttgg tagacggcct gtctctggtc cgggagagtc agcggaaacc ccagggcttt 1620
gtcctctctt tgtgccacct gcagaaagtg aagcattatc tcatcctgcc gagcaggag 1680
gagggtcgcc tgtacttcag ca tggatgat ggccagacc gcttcaactga cctgctgcag 1740
ctcgtggagt tccaccagct gaaccgcggc atcctgccgt gcttgcctgc ccattgctgc 1800
acgcgggtgg ccctctgacc aggcctgga ctggctcatg cctcagccc ccttcaggct 1860
gcccgcgcgc cctccaccca tccagtggac tctggggcgc ggccacaggg gacgggatga 1 920
```

57/292

ggagcgggag ggttcgccca ctccagtttt ctccctctgct tctttgcctc cctcagatag 1980
aaaacagecc ccaactccagt ccaactcctga cccctctcct caagggaagg ccttgggtgg 2040
ccccctctcc ttctcctagc tctggagggtg ctgctctagg gcagggaatt atgggagaag 2100
tgggggcagc ccaggcggtt tcacgccccca cacttt gtac agaccgagag gccagttgat 2160
ctgctctggt ttatactagt gacaataaag attatttttt gatac 2205

<210> 82

<211> 313

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(313)

<223> 5' terminal sequence. topoisomerase (dna) ii
beta (180kd) (TOP2B) gene.

<400> 82

gaaatttgac agtaatgaag aagattctgc ttctgttttt tcaccatcat ttggtctgaa 60
acagacagat aaagttccaa gtaaaacggt agctgctaaa aagggtatgt acttatattt 120
gattgagtta agcattggat agagatagtt aatgtaaaag gaaatgtaat ttaatttgaa 180
actatttgca tttttttatc ataaaacaat taaggaaagta taagtgttta taaggaggac 240
ctctcgtttt ctagccatct gagggcggtta ataaatttct gtaggactta nttaaagct 300
gttgantttt taa 313

<210> 83

<211> 4866

<212> DNA/RNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(4866)

<223> topoisomerase (dna) ii beta (180kd) (TOP2B)
gene.

<400> 83

atggccaagt cgggtggtg cggcgcggtg gccggcgtgg gcggcggtgaa cggggcactg 60
acctgggtga acaatgctgc aaaaaaagaa gagtcagaaa ctgccaaaca aaatgattct 120
tcaaagaagt tgtctgttga gagagtgtat cagaagaaga cacaacttga acacattctt 180
cttcgtctcg atacatatat tgggtcagtg gagccattga cgcagttcat gtgggtgt at 240
gatgaagatg taggaatgaa ttgcaggag gttacctttg tgccaggttt atacaagatc 300
tttgatgaaa ttttggttaa tgctgctgac aataaacaga gggataagaa catgacttgt 360
attaaagttt ctattgatcc tgaatctaac attataagca tttggaataa tgggaaaggc 420
attccagtag tagaacacaa gtagagaaa gtttat gttc ctgctttaat tttggacag 480
cttttaacat ccagtaacta tgatgatgat gagaaaaaag ttacaggtgg tcgtaatggt 540
tatggtgcaa aactttgtaa tattttcagt acaaagttta cagtagaaac agcttgcaaa 600
gaatacaaac acagttttaa gcagacatgg atgaataata tgatgaagac ttctgaagcc 660
aaaattaaac attttgatgg tgaagattac acatgcataa cattccaacc agatctgtcc 720
aaatttaaga tggaaaaact tgacaaggat attgtggccc tcatgactag aagggcata 780
gatttggctg gttcgtgtag aggggtcaag gtcattgtta atggaaagaa attgcctgta 840
aatggatttc gcagtttatgt agatctttat gtgaaagaca aattggatga aactgg ggtg 900
gccctgaaag ttattcatga gcttgcaaat gaaagatggg atgtttgtct cacattgagt 960

58/292

gaaaaaggat tccagcaaat cagcttttga aatagtattg caactacaaa aggtggacgg 1020
 cacgtggatt atgtggtaga tcaagttggt ggtaaaactga ttgaagtagt taagaaaaag 1080
 aacaaagctg gtgtatcagt gaaaccattt ca agtaaaaa accatatatg ggtttttatt 1140
 aattgcctta ttgaaaatcc aacttttgat tctcagacta aggaaaaacat gactctgcag 1200
 cccaaaagtt ttgggtctaa atgccagctg tcagaaaaat tttttaaaagc agcctctaata 1260
 tgtggcattg tagaaagtat cctgaactgg gtgaaattta aggctcagac tcagctgaat 1320
 aagaagtgtt catcagtaaa atacagtaaa atcaaaggta ttcccaaact ggatgatgct 1380
 aatgatgctg gtggtaaaca ttccctggag tgtacactga tattaacaga gggagactct 1440
 gccaaatcac tggctgtgtc tggattaggt gtgattggac gagacagata cggagttttt 1500
 ccactcaggg gcaaaattct taatgtacgg gaagcttctc ataaac agat catggaaaaat 1560
 gctgaaataa ataataattt taaaatagtt ggtctacaat ataagaaaag ttacgatgat 1620
 gcagaatctc tgaaaacctt acgctatgga aagattatga ttatgaccga tcaggatcaa 1680
 gatggttctc acataaaagg cctgcttatt aatttcattc atcacaattg gccatcactt 1740
 ttgaagcatg gttttcttga agagttcatt actcctattg taaaggcaag caaaaaaag 1800
 caggaaactt ccttctacag ttttctgaa tttgacgaat ggaaaaaaca tatagaaaac 1860
 cagaaagcct ggaaaaataa gtactataaa ggattgggta ctagtacagc taaagaagca 1920
 aaggaatatt ttgctgatat ggaaaggcat cgcattctgt ttagatatgc tggctctgaa 1980
 gatgatgctg ccattacott ggcathtagt aagaagaaga ttgatgacag aaaagaatgg 2040
 ttaacaaatt ttatgggaag ccggagacag cgtaggctac atggcttacc agagcaattt 2100
 ttatgtgta ctgcaacaaa gcatttgact tataatgatt tcatcaacaa ggaattgatt 2160
 ctcttctcaa actcagacaa tgaagatctc atac catctc ttgttgatgg ctttaaacct 2220
 ggccagcggg aagttttatt tacctgtttc aagaggaatg ataaacgtga agtaaaagt 2280
 gccagttgg ctggctctgt tgcgtgatag tgcgcttacc atcatggaga acaagcattg 2340
 atgatgacta ttgtgaattt ggctcagaac tttgtgggaa gtaacaacat taacttgctt 2400
 cagcctattg gtcagtttgg aactcggctt catgggtggc aagatgctgc aagccctcgt 2460
 tatattttca caatgttaag cacttttagc aggtactttt ttctgtctgt ggatgacaac 2520
 ctcttaagt tcctttatga tgataatcaa cgtgtagagc ctgagtggta ttttctata 2580
 attcccatgg ttttaataaa tgggtgctgag ggcattggta ctggatgg gc ttgtaaacta 2640
 cccaactatg atgctaggga aattgtgaac aatgtcagac gaatgctaga tggcctggat 2700
 cctcatcca tgcttccaaa ctacaaaaac tttaaaggca cgattcaaga acttggtcaa 2760
 aaccagtagt cagtcagtg tgaatatatt gtatgggaca gaaacacagt agaaattaca 2820
 gagcttccag ttagaacttg ga cacaggtg tataaagaac aggtttttaga acctatgcta 2880
 aatggaacag ataaaacacc agcatttaatt tctgattata aagaatatca tactgacaca 2940
 actgtgaaat ttgtggtgaa aatgactgaa gagaaactag cacaagcaga agctgctgga 3000
 ctgcataaag tttttaaaact tcaaactact cttacttgta attccatggg actttttgat 3 060
 catatgggat gtctgaagaa atatgaaact gtgcaagaca ttctgaaaga attctttgat 3120
 ttacgattaa gttattacgg tttacgtaag gagtggcttg tgggaatgtt gggagcagaa 3180
 totacaaagc ttaacaatca agcccgtttc atttttagaga agatacaagg gaaaattact 3240
 atagagaata ggtcaaagaa agatttgatt caaatg ttag tccagagagg ttatgaatct 3300
 gaccagtgaa aagcctggaa agaagcacaa gaaaaggcag cagaagagga tgaaacacaa 3360
 aaccagcatg atgatagttc ctccgattca ggaactcctt caggcccaga ttttaattat 3420
 attttaaata tgtctctgtg gtctcttact aaagaaaaag ttgaagaact gattaacag 3480
 agagatgcaa aagggcgaga ggtcaatgat cttaaaagaa aatctccttc agatctttg 3540
 aaagaggatt tagcggcatt tgttgaagaa ctggataaag tggaaatctca agaacgagaa 3600
 gatgttctgg ctggaatgtc tggaaaagca attaaaggta aagttggcaa acctaagggtg 3660
 aagaactcc agttggaaga gacaatgcc tcaccttatg gcagaagaat aattcctgaa 3720
 attacagcta tgaaggcaga tgccagcaaa aagttgctga agaagaagaa ggggtgatctt 3780
 gatactgcag cagtaaaagt ggaatttgat gaagaattca gtggagcacc agtagaagg 3840
 gcaggagaag aggcattgac tccatcagtt cctataaata aaggtcccaa acctaagagg 3900
 gagaagaagg agcctggtac caga gtgaga aaaacaccta catcatctgg taaacctagt 3960
 gcaaagaaag tgaagaaacg gaatccttgg tcagatgatg aatccaagtc agaaagtgat 4020
 ttggaagaaa cagaacctgt ggttattcca agagattctt tgcttaggag agcagcagcc 4080
 gaaagaccta aatacacatt tgatttctca gaagaagag atgatgatgc tgatgatgat 414 0
 gatgatgaca ataagtatt agaggaattg aaagttaaag catctcccat acaaatgat 4200
 ggggaagatg aatttgttcc ttcatagggg ttagataaag atgaatatac attttacca 4260
 ggcaaatcaa aagccactcc agaaaaatct ttgcatgaca aaaaaagtca ggattttgga 4320
 aatctctctc catttcttcc atattctcag aagtcaga ag atgattcagc taaatttgac 4380
 agtaatgaag aagattctgc ttctgtttt taccatcat ttggtctgaa acagacagat 4440
 aaagttccaa gtaaaacggg agctgctaaa aagggaaaac cgtcttcaga tacagtccct 4500
 aagcccaaga gagcccaaaa acagaagaaa gtagtagagg ctgtaaaactc tgactcggat 4560
 tcagaatttg gcattccaaa gaagactaca acacaaaaag gtaaaaggccg aggggcaaa 4620

59/292

aaaaggaaag catctggctc tgaaaatgaa ggcgattata accctggcag gaaaacatcc 4680
aaaacaacaa gcaagaaacc gaagaagaca tcttttgatc aggattcaga tgtggacatc 4740
ttcccctcag acttccttac tgagccacct tctctgccac gaaccggtcg g gctaggaaa 4800
gaagtaaaat attttacaga gtctgatgaa gaagaagatg atgttgattt tgcaatgttt 4860
aattaa 4866

<210> 84
<211> 311
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<220>
<221> misc_feature
<222> (1)..(311)
<223> 3' terminal sequence. caspase 4,
apoptosis-related cysteine protease (CASP4) gene.

<400> 84
cacttttatt gaaatacaaa atgttaaata tgcaagctgt actaatgaag gtgctccttg 60
aagttgatta aggagggtcg ggctgcttgg ggcttccatt ttcaattgcc aggaaagagg 120
tagaaatatac ttgtcatgga cagtcgttct atgggtgggca tttgagcttt ggcccttgga 180
gtttcaaatg attgctgtac ctccgaaat acttctctta ggtggcagca ccaagaatat 240
ttctgggaag catgtgatga gttgtgtgat gaagatagag cccattgtg ctgtctctcc 300
cagggcacgt t 311

<210> 85
<211> 1291
<212> DNA/RNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<220>
<221> misc_feature
<222> (1)..(1291)
<223> caspase 4, apoptosis-related cysteine
protease (CASP4) gene.

<400> 85
gctctttcca acgctgtaaa aaaggacaga ggctgttccc tatggcagaa ggcaaccaca 60
gaaaaaagcc acttaagggtg ttggaatccc tgggcaaaga ttctctcact ggtgttttgg 120
ataacttggg ggaacaaaat gtactgaact ggaaggaaga ggaaaaaag aa atattacg 180
atgctaaaac tgaagacaaa gtccgggtca tggcagactc tatgcaagag aagcaacgta 240
tggcaggaca aatgcttctt caaacctttt ttaacataga ccaaatatcc cccaataaaa 300
aagctcatcc gaatatggag gctggaccac ctgagtcagg agaatctaca gatgccctca 360
agctttgtcc tcatgaagaa ttcctgagac tatgtaaaga aagagctgaa gagatctatc 420
caataaagga gagaacaacac cgacacgcc ttgctctcat catatgcaat acagagtttg 480
accatctgcc tccgaggaat ggagctgact ttgacatcac agggatgaag gagctacttg 540
agggctctga ctatagtgtg gatgtagaag agaacttgac agccagggat atggagtcag 600
cgctgagggc atttgtacc agaccagagc acaagtcctc tgacagcaca ttcttggtac 660
tcatgtctca tggcatcctg gaggaatct gcggaactgt gcatgatgag aaaaaccag 720
atgtgctgct ttatgacacc atcttccaga tattcaacaa ccgcaactgc ctcagtctga 780
aggacaaacc caaggtcatc attgtccagg cctgcagagg tgcaaacctg ggggaactgt 840
gggtcagaga ctctccagca tccttggaag tggcctctc acagtcactc gagaacctgg 900
aggaagatgc tgtttacaag acccacgtgg agaaggactt cattgctttc tgctcttcaa 960

60/292

cgccacacaa cgtgtcctgg agagacagca caatgggctc tatcttcac acacaactca 1020
 tcacatgctt ccagaaatat tcttggtg ct gccacctaga ggaagtattt cggaaggtag 1080
 agcaatcatt tgaaactcca agggccaaag ctcaaagcc caccatagaa cgactgtcca 1140
 tgacaagata tttctacctc tttcctggca attgaaaatg gaagccacaa gcagcccagc 1200
 cctccttaat caacttcaag gagcaccttc attagtacag cttgcatatt taacattttg 1260
 tatttcaata aaagtgaaga caaaaaaaaa a 1291

<210> 86

<211> 319

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(319)

<223> 5' terminal sequence. tissue inhibitor of metalloproteinase 2 (TIMP2) gene.

<400> 86

tggacccatg ggatgagtgt tttattcatg ctgtttccag gaagggatgt cagagctgga 60
 ccagtcgaaa cccttgaggg ctttttttgc agttggccac aggggcgttg gaggcctgct 120
 tatgggtcct cgatgtcgag aaactcctgc ttggnggaen ccgcg ccgcg tnnccacgca 180
 caggagccnt cacttctott gatgcaggcg aagaacttgg cctggnnccc gttnatgttc 240
 ttctctgtga ccagtcocat ccagaggcac tcgtccgggg agganatgta gcacgggatc 300
 atngggcanc gcgtgatct 319

<210> 87

<211> 1075

<212> DNA/RNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(1075)

<223> tissue inhibitor of metalloproteinase 2 (TIMP2) gene.

<400> 87

cgcagcaaac acatccgtag aaggcagcgc ggccgcga g agccgcagcg ccgctcgcgc 60
 gccgcccccc accccgcgcg cccgcccgcg gaattgcgc ccgcgccct cccctcgcgc 120
 ccccagagaca aagaggagag aaagtittgc cggccgagcg gggcaggtga ggagggtgag 180
 ccgcgcggga ggggcccgcg tcggcccgcg ctacgcccc gccgcgcgc ccagcccgcg 240
 gccgcgagca gcgcccgc ac ccccagcgc cggccccgc cgcgccagcc ccccgcccg 300
 ccatgggcgc cgcggcccgc accctgcgcg tggcgtcgc cctcctgctg ctggcgacgc 360
 tgcttcgccc ggccgacgc tgacgtgct cccgggtgca ccgcgaacag gcgttttgca 420
 atgcagatgt agtgatcagg gccaaagcgc tcagtgaaga ggaagtggac tctggaaacg 480
 acatttatgg caacctatc aagaggatcc agtatgagat caagcagata aagatgttca 540
 aagggcctga gaaggatata gagtttatc acacggcccc ctctcggca gtgtgtgggg 600
 tctcgttga cgttgaggga aagaaggaat atctcattgc aggaaggcc gagggggacg 660
 gcaagatgca catcacctc tgtgacttca tcgtgcc tg ggaacacctg agcaccaccc 720
 agaagaagag cctgaaccac aggtaccaga tgggctgcga gtgcaagatc acgcgctgcc 780
 ccatgatccc gtgctacatc tctccccg acgagtgcc ctggatggac tgggtcacag 840
 agaagaacat caacgggcac caggccaagt tcttcgcctg catcaagaga agtgacggct 900

61/292

cctgtgcgtg gtaccg cggc gggcgcccc ccaagcagga gtttctcgac atcgaggacc 960
cataagcagg cctccaacgc ccctgtggcc aactgcaaaa aaagcctcca agggtttcga 1020
ctggtccagc tctgacatcc cttcctggaa acagcatgaa taaaacactc atccc 1075

<210> 88
<211> 225
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<220>
<221> misc_feature
<222> (1)..(225)
<223> 3' terminal sequence. d -dopachrome
tautomerase (DDT) gene.

<400> 88
ttttttgaat gaggaagctc ttttcattta tttcanatga ggatgaagaa gaggattatg 60
tgancacagg aatnttgcat ggggataat ccaaagctgg ttatctccag gncctcantn 120
tgccaagaga tctctctgga agaagcagcc agttcacaga tgccctggat cctccgtgc 180
ccaatcataa aaaagtcatg accgtcccta tnttgccaat ntgcc 225

<210> 89
<211> 312
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<220>
<221> misc_feature
<222> (1)..(312)
<223> 5' terminal sequence. d -dopachrome
tautomerase (DDT) gene.

<400> 89
cgttcctgga gctggacacg aatttgcccg ccaaccgagt gcccgcggn tngagaaac 60
gactctgcgc cgccgctgcc tccatcctgg gcaaacctgc ggaccgctg aacgtgacg 120
tacggccggg cctggccatg gcgctgagcg ggtccaccga gccctgcgcg cagtgttcca 180
tctctccat cggcgtagtg gggcaccgcy agggacaacc gcagccacag cgccatttc 240
ttttgagttt tttcaccaag gagctaagcc cctgccaggg acccgat ant tattccnttt 300
ttttcccttt gg 312

<210> 90
<211> 666
<212> DNA/RNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<220>
<221> misc_feature
<222> (1)..(666)
<223> d-dopachrome tautomerase (DDT) gene.

<400> 90
gatccccgtg ccagggaccc tgcccagttc caggcgctgc ctaaccaga aacgactggg 60
cgccgcgtcc tggaaaggcc ccagcgacag gacatctgag gagctgtttc cgttcctctg 120
cccgccatgc cgttcctgga gctggacacg aatttgccc ccaaccgagt gcccgcgggg 180
ctggagaaac gactctgcgc cgccgctgcc tccatctgg gcaaacctgc ggaccgctg 240
aacgtgacgg tacggccggg cctggccatg gcgctgagcg ggtccaccga gccctgcgcg 300
cagctgtcca tctcctccat cggcgtagtg ggcaccgagg aggacaaccg cagccacagc 360
gccacttct ttgagtttct caccaaggag ctagccctgg gcc aggaccg gatacttacc 420
cgctttttcc ccttgagtc ctggcagatt ggcaagatag ggacggtcac gactttttta 480
tgattgggca cggagggatc cagggcattc gtgaactggc tgcttcttcc agagagatct 540
cttggcacag tgagggcctg gagataacca gctttggatt atcccgcacg caacattcct 600
gtgatcacat aatcctcttc ttcctctca tatgaaataa atgaagagag ctctctcatt 660
caaaaa

<210> 91
<211> 443
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<220>
<221> misc_feature
<222> (1)..(443)
<223> 3' terminal sequence. prolactin (PRL) gene.

<400> 91
gantttgatg tctctaagga gtcagttttt attttttaag aggagacctg ttacacccaa 60
gcatggattc aaaagagata caactaaaag aagcttgcaa tggaaaggat cattaaggac 120
cttctcagaa atagatgaaa tggatgtggg cttagca gtt gttgttgagg atgattcggg 180
cacttcaggg agcttgagga taattgtcga ttttatgtga atccctgcgt aggcaatggg 240
agagggtata ataaggcagg aaaggcgag actcttcacg agccatctgc aggggatggg 300
aagtccccga ccagacagg gtagatctca tttcttttgg gttttcaggg atgaacctgg 360
gcttgactat ccagcttcca tgnccctctt ggaagccctt ttggttttgc tccctcaatc 420
ttctacagct tttgggttag ggt 443

<210> 92
<211> 243
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<220>
<221> misc_feature
<222> (1)..(243)
<223> 5' terminal sequence. prolactin (PRL) gene.

<400> 92
gaagaatcgg aacatacagg ctttgatata aaaggtttat aaagccaata tctgggaaag 60
agaaaacgt gagacttcca gatcttctct ggtgaagtgt gtttcctgca acgatcacga 120
acatgaacat caaaggatcg ccatgggaaa gggccctcc tgctgtgct ggggtgttcaa 180
acctgtcct gtgccagagc gtgggcccc ttggcccatc tgtcccgnc gggcttgccc 240
gat 243

<210> 93
<211> 833
<212> DNA/RNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<220>
<221> misc_feature
<222> (1)..(833)
<223> prolactin (PRL) gene.

<400> 93
aaacatgaac atcaaaggat cgccatggaa agggtccttc ctgctgctgc tgggtgtcaaa 60
cctgctgctg tgccagagcg tggccccctt gcccatctgt cccggcgggg ctgcccgatg 12 0
ccagggtgacc cttcgagacc tgtttgaccg cgccgtogtc ctgtcccaact acatccataa 180
cctctcctca gaaatgttca gcgaattcga taaacgggat acccatggcc ggggggttcat 240
taccaaggcc atcaacagct gccacacttc ttcccttgcc acccccgaag acaaggagca 300
agcccaacag atgaatcaaa aagactttct gagcctgata gtcagcatat tgcgatcctg 360
gaatgagcct ctgtatcatc tggtcacgga agtacgtggt atgcaagaag ccccgaggcg 420
tattctatcc aaagctgtag agattgagga gcaaaccaaa cggtttctag agggcatgga 480
gctgatagtc agccaggttc atcctgaaac caaagaaaat gagatctacc ctgtctggtc 540
gggacttcca tccctgcag a tggctgatga agagtctcgc ctttctgctt attataacct 600
gctccactgc ctacgcaggg attcacataa aatcgacaat tatctcaagc tcctgaagtg 660
cogaatcatc cacaacaaca actgctaagc ccacatccat ttcatctatt tctgagaagg 720
tccttaatga tccgttccat tgcaagcttc ttttagttgt atctcttttg aatccatgct 780
tgggtgtaac aggtctcctc ttaaaaaata aaaactgact cgtagagac atc 833

<210> 94
<211> 304
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<220>
<221> misc_feature
<222> (1)..(304)
<223> 3' terminal sequence. prolactin receptor
(PRLR) gene.

<400> 94
actaagcagt gtgcttttat ttcatagaac acatagtttt ataactaaca gcaaaaagta 60
aatctacaaa tcacagtttag gaaacataat gatttgttct ggaatcagct gctggagaaa 120
gaggcaagtg gttaaaaatg gagcatgaaa ggagctggga gctttagtag tgtcagtctg 180
actacattct tgaggcattt cacgtactct gtagtggtac ctgaagaaaa atcacatttt 240
aaccaatcat tccattagtc aagctatcag tgaaaggagt gtgtaaaaca tgcgggatcc 300
cggg 304

<210> 95
<211> 366
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<220>
 <221> misc_feature
 <222> (1)..(366)
 <223> 5' terminal sequence. prolactin receptor
 (PRLR) gene.

<400> 95
 gaggtcattg agaagccaga gaatcctgaa acanccacaca cctggaaccc ccantgcata 60
 agcatggaag gcaaaatccc ctatttncat gctggtggat ccaaagtgtc aacatggccc 120
 ttaccacagc ccagccagca caacccagaga tcctcttacc acaatattac tgatgtgtgt 180
 gagctggctg tgggccctgc aggtgcaccg gccactctgt tgaatgaagc aggtaaagat 240
 gctttaaaat cctctcaaac cattaagtct agagangag g gnaaggcaac ccaggcagag 300
 ggaggtagga aagcttccat tcttgagnac tgaccagggg tacgncctgg gttgcttgcc 360
 ccaggg

<210> 96
 <211> 2723
 <212> DNA/RNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:primer

<220>
 <221> misc_feature
 <222> (1)..(2723)
 <223> prolactin receptor (PRLR) gene.

<400> 96
 ggaggtctgaa atcccagac gccggttttc tgggctgggc tttctgctta ctcaactcctt 60
 ctccctcttt ctggatttta ccgaccgttc gcgaaacagc tttccacaca atggagcttc 120
 atgtctcgt gcaggaagta ctcatcgact gatgtggcag actttgctcc ctgacaaaac 180
 taaagaactc tcctattcat ggaggcgaac actgaggatg ctttccacat gaaccctgaa 240
 gtgaacttct gatacatttc ctgcagcaag agaaggcagc caacatgaag gaaaatgtgg 300
 catctgcaac cgttttcaact ctgctacttt ttctcaac ac ctgccttctg aatggacagt 360
 tacctcctgg aaaacctgag atctttaaat gtctgtctcc caataaggaa acattcacct 420
 gctggtggag gcctgggaca gatggaggac ttctaccaa ttattcactg acttaccaca 480
 ggggaaggaga gacactcatg catgaatgtc cagactacat aaccgggtgg cccaactcct 540
 gccactttgg caagcagtc acctccatgt ggaggacata catcatgatg gtcaatgcca 600
 ctaaccagat ggggaagcag ttctcggatg aactttatgt ggacgtgact tacatagttc 660
 agccagaccc tcctttggag ctggctgtgg aagtaaaaca gccagaagac agaaaaccct 720
 acctgtggat taaatggtct ccacctacc tgattgactt aaaaactggt tggttcac gc 780
 toctgtatga aattcgatta aaaccogaga aagcagctga gtgggagatc cattttgctg 840
 ggcagcaaac agagtttaag attctcagcc tacatccagg acagaaatac cttgtccagg 900
 ttcgctgcaa accagaccat ggatactgga gtgcatggag tccagcgacc ttcattcaga 960
 tacctagtga cttcaccatg aatgatacaa ccgtgt ggat ctctgtggct gtcctttctg 1020
 ctgtcatctg tttgattatt gtctgggcag tggctttgaa gggctatagc atggtgacct 1080
 gcatctttcc gccagttcct gggccaaaaa taaaaggatt tgatgctcat ctggttgaga 1140
 agggcaagtc tgaagaacta ctgagtgcct tgggatgcca agactttcct ccacttctg 1200
 actatgagga cttgctggtg gagtatttag aagtagatga tagtgaggac cagcatctaa 1260
 tgtcagtcga ttcaaaagaa caccgaagtc aaggtatgaa acccacatac ctggatcctg 1320
 acactgactc aggcggggg agctgtgaca gcccttccct tttgtctgaa aagtgtgagg 1380
 aacccagc caatccctoc acattctatg atctcgaggt cattgagaag ccagagaatc 1440
 ctgaaacaac ccacacctgg gacccccagt gcataagcat ggaaggcaaa atcccctatt 1500
 ttcatgctgg tggatccaaa tgttcaacat ggcccttacc acagcccagc cagcacaacc 1560
 ccagatctc ttaccacaat attactgatg tgtgtgagct ggctgtgggc cctgcaggtg 1620
 caccggccac tctgttgaat gaag caggta aagatgctt aaaatcctct caaaccatta 1680
 agtctagaga agagggaaag gcaaccagc agaggagggt agaaagcttc cattctgaga 1740
 ctgaccagga tacgacctgg ctgctgcccc aggagaaaac cccctttggc tccgctaaac 1800
 ccttgatta tgtggagatt cacaaggtca acaaagatgg tgcattatca ttgctacca 186 0

65/292

```
aacagagaga gaacagcggc aagcccaaga agccccgggac tcctgagaac aataaggagt 1920
atgccaaagt gtccgggggc atggataaca acatcctggt gttggtgccca gatccacatg 1980
ctaaaaacgt ggcttgcttt gaagaatcag ccaaagaggc cccaccatca cttgaacaga 2040
atcaagctga gaaagccctg gccaaactca ctgcaaca tc aagcaagtgc aggctccagc 2100
tgggtggttt ggattacctg gatcccgcat gttttacaca ctcctttcac tgatagcttg 2160
actaatggaa tgattggtta aaatgtgatt tttcttcagg taacactaca gagtacgtga 2220
aatgctcaag aatgtagtca gactgacact actaaagctc ccagctcctt tcatgctcca 2280
tttttaacca cttgcctctt tctccagcag ctgattccag aacaaatcat tatgtttcct 2340
aactgtgatt tgtagattta ctttttgctg ttagttataa aactatgtgt tcaatgaaat 2400
aaaagcacac tgcttagtat tcttgaggga caatgccaat aggtatatcc tctggaaaag 2460
gctttcatga tttggcatgg gacagacgga aatgaaattg tcaaaattgt t taccataga 2520
aagatgacaa aagaaaattt tccacatagg aaaatgccat gaaaattgct tttgaaaaac 2580
aactgcataa cctttacact cctcgtccat tttattagga ttacccaaat ataaccattt 2640
aaagaaaaga tgcatccag aacaaattgt ttacataagt tcctatacct tactgacaca 2700
ttgctgatat gcaagtaaga aat                                     2723
```

<210> 97

<211> 365

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(365)

<223> 3' terminal sequence. interleukin 2
receptor, beta (IL2RB) gene.

<400> 97

```
gtacagttac cttttattta tagcgaaaat gggttttttc atttacagag taacaaagat 60
ttttctttaa ataatgtat ttcaacgaaa atgaactgac ttaaagaaaa aatattaagg 120
aaataatcac aaagatggta cacacggatc attaaaagat acggatgtat aggatacata 180
tgtcacaaat gattaaggac ttaaaaaatg taaccctccc aagaagtggg gagcctccca 240
aagtggggga agggcaaata caatttcnt ttgggggggg atagggngac cccctttgca 300
gagagggggt aggtgggggt tccccccggn acacacaggc aagggttttg gngccccttg 360
tgggg                                     365
```

<210> 98

<211> 366

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(366)

<223> 5' terminal sequence. interleukin 2
receptor, beta (IL2RB) gene.

<400> 98

```
nattcggcac tagggggcac ctgaccacac gccccacag gctctgacca gcagcctatg 60
aggggggttt gcaccaagct ctgtccaatc aggtaggctg ggctgaacta gccaatcaga 120
tcaactctgt cttgggcgtt tgaactcagg gagggaggcc cttgggagca ggtgcttggt 180
gacaaggctc cacaagcgtt gagccttgga aaggtagaca agcgttg agc cactaagcag 240
aggaccttgg gttcccaata caaaaatacc tactgctgag aggggntgct gaccattttg 300
```

gtcaaggatt tcngtttgcc ttatatccca aataaantcc ctttttttn aggtttntt 360
agtntt 366

<210> 99

<211> 4034

<212> DNA/RNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(4034)

<223> interleukin 2 receptor, beta (IL2RB) gene.

<400> 99

gcagccagag ctcagcaggg ccctggagag atggccacgg tcccagcacc ggggagg act 60
ggagagcgcg cgctgccacc gcccacatgtc tcagccaggg ctcccttccct cggctccacc 120
ctgtggatgt aatggcggcc cctgctctgt cctggcgtct gccctcctc atcctcctcc 180
tgccctggc tacctcttgg gcatctgcag cgggtgaatgg cacttcccag ttcacatgct 240
tctacaactc gagagccaac atctcctgtg tctgga gcc aagatggggct ctgcaggaca 300
cttctgcca agtccatgcc tggccggaca gacggcgggt gaaccaaacc tgtgagctgc 360
tcccctgtgag tcaagcatcc tgggcctgca acctgatect cggagcccca gattctcaga 420
aactgaccac agttgacatc gtcaccctga ggggtgctgt cctgagggg gtgcgatgga 480
gggtgatggc catcaggac ttcaagccct ttgagaacct tcgctgatg gcccctatct 540
ccctccaagt ttccacgtg gagaccaca gatgaacat aagctgggaa atctccaag 600
cctccacta ctttgaaga cacctggagt tcgaggcccg gacgctgtcc ccaggccaca 660
cctgggagga ggccccctg ctgactctca agcagaagca ggaatggatc tgcctg gaga 720
cgctcacccc agacaccag tatgagtttc aggtgcgggt caagcctctg caaggcgagt 780
tcacgacctg gagccccctg agccagcccc tggccttcag gacaaagcct gcagcccttg 840
ggaaggacac cattccgtgg ctgggccacc tctcgtggg cctcagcggg gcttttggct 900
tcctcatctt agtgacttg ctgatcaact gcag gaacac cgggccatgg ctgaagaagg 960
tctgaagtg taacacccca gaccctcga agttcttttc ccagctgagc tcagagcatg 1020
gaggagacgt ccagaagtgg ctctcttcgc ccttcccctc atcgtccttc agccctggcg 1080
gcctggcacc tgagatctcg ccactagaag tgcctggagag ggacaagggt acgcagctgc 1140
tctgcagca ggacaagggt cctgagcccc catccttaag cagcaaccac tcgctgacca 1200
gctgcttca caaccagggt tactttctt tccacctccc ggatgccttg gagatagagg 1260
cctggcagggt gtactttact tacgaccct actcagagga agaccctgat gagggtgtgg 1320
ccggggcacc cacaggttct tcccccaac cctgcagcc tctgtcagg gaggacgacg 1380
cctactgcac ctccccctcc agggatgacc tgcctgctct cccccagct cctcctgggtg 1440
gccccagccc ccaagcact gcccctgggg gcagtggggc cgggtgaagag aggatgcccc 1500
cttctttgca agaaagagtc ccagagact gggaccccca gcccctgggg cctccacccc 1560
caggagtccc agacctggtg gat tttcagc caccacctga gctgggtgctg cgagaggctg 1620
gggaggagggt cctgacgct ggccccaggg agggagtacg tttccctgg tccaggcctc 1680
ctgggcaggg ggagttcagg gcccttaatg ctgcctgcc cctgaacact gatgcctact 1740
tgtccctcca agaactocag ggtcaggacc caactcactt ggtgtagaca gatggccagg 18 00
gtgggaggca ggcagctgcc tgcctgctgc cgagcctcag aaggacctg ttgagggtcc 1860
tcagtcact gctgaggaca ctacgtgtcc agttgcagct ggacttctcc acccgatgg 1920
ccccaccca gtctgcaca cttgggtccat ccatttccaa acctccactg ctgctcccg 1980
gtcctgctgc ccgagccagg aactgtgtgt gttgcag ggg ggcagtaact ccccaactcc 2040
ctcgttaatc acagatccc acgaatttag gctcagaagc atcgtcctc tccagccctg 2100
cagctattca ccaatatcag tcttcgggc tctccaggc tccctgccct gacctcttc 2160
ctgggttttc tgccccagcc tctccttcc ctccccctcc cgtccacagg gcagcctgag 2220
cgtgctttcc aaaaacccaa tatggccacg ctccccctcg gttcaaaacc ttgcacaggt 2280
cccactgccc tcagccccac ttctcagcct ggtacttgta cctccggtgt cgtgtgggga 2340
catcccttcc tgcaatctc cctaccgtcc tccogagcca ctacagctc cctcacccc 2400
cctctgttgc acatgctatt ccctggggct gctgtgcgt cccctcatc taggtgacaa 2460
acttcctga ctctcaagt gccggtttt cttctcctg agggaagcac tgccctcctt 2520
aatctgccag aaacttctag cgtcagtgtc ggaggagaa gctgtcagg acccaggcg 2580

67/292

```

cctggagaaa gaggcctgt tactattcct ttgggatctc tgaggcctca gagtgccttg 2640
ctgctgtatc ttaaatgctg gggcc caagt aagggcacag atccccccac aaagtggatg 2700
cctgctgcat cttcccacag tggtttcaca gaccacacag agaagctgat ggggagtaaa 2760
ccctggagtc cgaggcccag gcagcagccc cgcctagtgg tgggccctga tgctgccagg 2820
cctgggacct cccactgccc cctccactgg aggggtctcc tctgcagctc agggactggc 2880
acactggcct ccagaagggc agctccacag ggcagggcct cattattttt cactgcccc 2940
gacacagtgc ccaacacccc gtctataacc ctggatgaac gaattaatta cctggcacca 3000
cctcgtctgg gctccctgcg cctgacattc acacagagag gcagagtccc gtgcccatta 3060
ggtctggcat gccccctcct gcaaggggct caacccct a ccccgacccc tccacgtatc 3120
tttcctagga agatcacgtt gcaatggctc aaacaacatt ccaccccagc aggacagtga 3180
ccccagtccc agctaactct gacctgggag ccctcaggca cctgcactta caggccttg 3240
tcacagtga ttgggcacct gaccacacgc cccacacagg cctgaccagc agcctatgag 3300
ggggttttggc accaagctct gtccaatcag gtaggctggg cctgaactag ccaatcagat 3360
caactctgtc ttgggcgttt gaactcaggg agggaggccc ttgggagcag gtgcttggg 3420
acaaggctcc acaagcgttg agccttggaa aggtagacaa gcgttgagcc actaagcaga 3480
ggaccttggg ttccaatac aaaaatacct actgctgaga gggctgctga cc atttggtc 3540
aggattcctg ttgcctttat atccaaaata aactccctt tcttgaggtt gtctgagtct 3600
tgggtctatg ccttgaaaaa agctgaatta ttggacagtc tcacctcctg ccatagggtc 3660
ctgaatgttt cagaccacaa ggggtctccac acctttgctg tgtgttctgg ggcaacctac 3720
taatcctctc tccaagtcgg tctcct atc ccccacaaatg gaaattgtat ttgccttctc 3780
cactttggga ggctccact tcttgggagg gttacatttt ttaagtctta atcatttgtg 3840
acatatgtat ctatacatcc gtatctttta atgatccgtg tgtaccatct ttgtgattat 3900
ttcttaata ttttttcttt aagtcagttc attttcgttg aaatacattt ataaagaaa 3960
atctttgtta ctctgtaa at gaaaaaaccc attttcgcta taaataaaag gtaactgtac 4020
aaaataagta caat 4034

```

<210> 100

<211> 444

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(444)

<223> 3' terminal sequence. gata -binding protein 3
(GATA3) gene.

<400> 100

```

tttctatttt tttattttct ttaaatgcat caaacaactg tggccagtga aaggaaacaa 60
aactggcagt ttgtccattt gaatatcaga cctagtttct tcttaatttc cacacta ttt 120
ctcccatatt ccttaaactt cttggcatcc ttcattgcctt acagctaccc agatgcaata 180
aagtcattgt acagtatttc ttacaatata agttatatgg caatgttcag gcattttttt 240
ttttcacagg cactaggagg accctgttta aatgggggat atgaggtcag gaatgggctt 300
attcacagga tgggggggtcc cggattcagg tgggt tgggg ancacaggac accacagggt 360
aggctccctt tgccaaaggt gggggccaaac ataattttgg cttttctggc cttcaaaaa 420
catatttccn tcgcgttttg gggg 444

```

<210> 101

<211> 396

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature
<222> (1)..(396)
<223> 5' terminal sequence. gata-binding protein 3
(GATA3) gene.

<400> 101
gcaatgggga cctgtctgc aatgcctgtg gntctactac aagcttcaca atattaacag 60
acccttgact atgaagaagg aaggcatcc a gaccagaaac cgaaaaatgt ctacaaatc 120
caaaaagtgc aaaaagtgc tgactcactg gaggacttcc ccaagaacag ctggtttaac 180
ccggccgccc tctccagaca catgtcctcc ctgagccaca tctcgccctt cagccactcc 240
agccacatgc tgaccacggc ccacgccgat ggcacccgcc atccagcctg tcctttggga 300
ccacaccacc cctccagctg ggtcaccgcc ntgggtttag agccttgtn gatggttcac 360
agggggcccc cagcgagagt tncctgnagt tccttt 396

<210> 102
<211> 416
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<220>
<221> misc_feature
<222> (1)..(416)
<223> 5' terminal sequence. placental growth
factor, vascular endothelial growth factor -related
protein (PGF) gene.

<400> 102
attcgccact aggggagacc caagggcagg gggaagagga ggagagagaa gcagagaccc 60
acagactgcc acctgtgcgg cgatgctgtt ccccgagta acccaaccct tggaggagag 120
agaccccgca cccggctcgt gtatttatta ccgtcacact cttcagtgcac tcctgctggt 180
acctgccctc tatttattag ccaactgttt ccctgctgaa tgccctcgtc ccttcaagac 240
gaggggcagg gaaggacagg accctcagga attcagtgcc ttcaacaacg tga gagaaag 300
agagaagcca gccacagacc cctggggagc ttccgcttt tgaaagaagc aagacaagtt 360
ggccttggtt aggggcaagg ttaggggcca ggaggccctn gggaagtttt tcaggg 416

<210> 103
<211> 1645
<212> DNA/RNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<220>
<221> misc_feature
<222> (1)..(1645)
<223> placental growth factor, vascular
endothelial growth factor -related protein (PGF)
gene.

<400> 103
gggattcggg ccgcccagct acgggaggac ctggagtggc actgggcgcc cgacggacca 60
tccccgggac ccgctgccc ctgcgcgcc cgcccgcgg ggccgctccc cgtcgggttc 120
cccagccaca gccttaccta cgggctcctg actccgcaag gcttccagaa gatgctcgaa 180
ccaccggccg gggcctcggg gcagcagtga gggaggcgtc cagccccca ctcagctctt 240
ctctcctgt gccaggggct cccgggggga tgagcatggt ggttttcct cggagcccc 300

```
tggctcggga cgtctgagaa gatgccggtc atgaggctgt tcccttgctt cctgcagctc 360
ctggccgggc tggcgctgcc tgctgtgcc ccccagcagt gggccttgtc tgctgggaac 420
ggctcgtcag aggtggaagt ggtacccttc caggaagtgt ggggcccag ctactgcccg 480
gcgctggaga ggctgggtga cgtcgtgtc c gagtacccca gcgaggtgga gcacatgttc 540
agcccatcct gtgtctccct gctgcgtgc accggtgct gcgcgatga gaatctgcac 600
tgtgtgcccg tggagacggc caatgtcacc atgcagctcc taaagatccg ttctggggac 660
cggccctcct acgtggagct gacgttctct cagcacgttc gctgcgaatg ccggcctctg 720
cgggagaaga tgaagccgga aaggtgcggc gatgctgttc cccggaggta acccaccct 780
tggaggagag agaccccga cccggctcgt gtatttatta ccgtcacact cttcagtgc 840
tcctgctggt acctgccctc tatttattag ccaactgttt ccctgctgaa tgccctcgtc 900
ccttcaagac gaggggacag gaaggacagg accctcagga attcagtgc c ttcaacaacg 960
tgagagaag agagaagcca gccacagacc cctgggagct tccgctttga aagaagcaag 1020
acacgtggcc tcgtgagggg caagctaggg cccagaggcc ctggaggctt ccaggggcct 1080
gcagaaggaa agaagggggc cctgctacct gttcttgggc ctcaggctct gcacagacaa 1140
gcagcccttg ctttcggagc tcct gtccaa agtagggatg cggattctgc tggggccggc 1200
acggcctggt ggtgggaagg ccggcagcgg gcggagggga ttcagccact tccccctctt 1260
cttctgaaga tcagaacatt cagctctgga gaacagtggg tgccctgggg cttttgccac 1320
tccttgctcc ccgtgatctc ccctcacact ttgccatttg cttgtactgg gacattgttc 138 0
tttcggccg aggtgccacc accctgcccc cactaagaga cacatacaga gtgggccccg 1440
ggctggagaa agagctgcct ggatgagaaa cagctcagcc agtggggatg aggtcaccag 1500
gggaggagcc tgtgcgtccc agctgaaggc agtggcaggg gagcagggtc cccaagggcc 1560
ctggcaccac cacaagctgt ccctgcaggg ccactctga ct gccaaagccag attctcttga 1620
ataaagtatt ctagtgtgga aacgc 1645
```

<210> 104

<211> 309

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(309)

<223> 5' terminal sequence. ubiquitin protein

ligase e3a (human papilloma virus e6 -associated
protein, angelman syndrome) (UBE3A) gene.

<400> 104

```
ttcggcanag gggaaatgaa gcctgcacga atgagttttg tgcttcctgt ccaacttttc 60
ttcgtatgga taataatgca gc agctatta aagccctcga gctttataag antagggcaa 120
aactctgtga tcctcatccc tccaagaaag gagcaagctc agcttacctt gagaactcga 180
aaggtgcccc caacaactcc tgctctgaga taaaaatgaa caaggaaagg gcgctaggaa 240
ttggatttta aagatgtgac ttactttaac aggaaggagg aagggtatta tggaaaattt 300
tctttggac 309
```

<210> 105

<211> 2628

<212> DNA/RNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(2628)

<223> ubiquitin protein ligase e3a (human

70/292

papilloma virus e6-associated protein, angelman
syndrome) (UBE3A) gene.

<400> 105

```
atggagaagc tgcaccagtg ttattggaaa tcaggagaac ctcagtctga cgacattgaa 60
gctagccgaa tgaagcgagc agctgcaaag catctaatag aacgctacta ccaccagtta 120
actgagggct gtggaaatga agcctgcacg aatgagtttt gtgcttcctg tccaactttt 180
cttcgtatgg ataataatgc agcagctatt aaagccctcg agctttataa gattaatgca 240
aaactctgtg atcctcatcc ctccaagaaa ggagcaagct cagcttacct tgagaactcg 300
aaaggtgccc ccaacaactc ctgctctgag ataaaaatga aca agaaagg cgctagaatt 360
gatttttaag atgtgactta cttaacagaa gagaagggtat atgaaattct tgaattatgt 420
agagaaagag aggattatcc ccctttaatc cgtgttattg gaagagtttt ttctagtgtc 480
gaggcattgg tacagagctt ccggaaggtt aaacaacaca ccaaggaaga actgaaatct 540
cttcaagcaa aagaagactc agaagcatct tcctcaagga taggtgatag ctcacaggga 600
gctgtctatgg aagaagactc agaagcatct tcctcaagga taggtgatag ctcacaggga 660
gacaacaatt tgcaaaaatt aggccctgat gatgtgtctg tggatattga tgccattaga 720
aggggtctaca ccagattgct ctctaataaa aaaattgaaa ctgcctttct caatgcactt 780
gtatatttgt cacctaactg ggaatgtgac ttgacgtatc acaatgtata ctctcgagat 840
cctaattatc tgaatttgtt cattatcgga atggagaata gaaatctcca cagtcctgaa 900
tatctggaaa tggctttgct attattttgc aaagcgatga gcaagctacc ccttgacgcc 960
caaggaaaac tgatcagact gtggtctaaa tacaatgcag a ccagattcg gagaatgatg 1020
gagacatttc agcaacttat tacttataaa gtcataagca atgaatttaa cagtcgaaat 1080
ctagtgaatg atgatgatgc cattgttgct gcttcgaagt gcttgaaaat ggtttactat 1140
gcaaatgtag tgggagggga agtgagacaca aatcacatg aagaagatga tgaagagccc 1200
atccctgagt ccagcg agct gacacttcag gaacttttgg gagaagaaaag aagaaacaag 1260
aaaggtcctc gagtggaccc cctggaaact gaacttggtg ttaaaaccct ggattgtcga 1320
aaaccactta tcctttttga agagtttatt aatgaaccac tgaatgaggt tctagaaatg 1380
gataaagatt atactttttt caaagtagaa acagagaaca aattctcttt tatga catgt 1440
ccctttatat tgaatgctgt cacaaagaat ttgggattat attatgacaa tagaattcgc 1500
atgtacagtg aacgaagaat cactgttctc tacagcttag ttcaaggaca gcagtgaat 1560
ccatatttga gactcaaagt tagacgtgac catatcatag atgatgcact tgtccggcta 1620
gagatgatcg ctatggaaaa tcctgcagac ttgaagaagc agttgtatgt ggaatttgaa 1680
ggagaacaag gattgatga gggaggtgtt tccaaagaat tttttcagct ggttgtggag 1740
gaaatcttca atccagatat tggatgttcc acatacgatg aatctacaaa attgttttgg 1800
tttaatccat cttcttttga aactgagggt cagtttactc tgattggcat agtactgggt 1860
ctggctattt acaataactg tatactggat gtacattttc ccatggttgt ctacaggaa 1920
ctaattggga aaaaagggaac tttctgtgac ttgggagact ctcaccagct tctatatcag 1980
agtttaaaag atttatttga gtatgaaggg aatgtggaag atgacatgat gatcactttc 2040
cagatatcac agacagatct ttttggtaac ccaatgatgt atg atctaaa ggaaaatggt 2100
gataaaaatt caattacaaa tgaaaacagg aaggaatttg tcaatcttta ttctgactac 2160
attctcaata aatcagtaga aaaacagttc aaggcttttc ggagaggttt tcatatggtg 2220
accaatgaat ctcccttaaa gtacttatcc agaccagaag aaattgaatt gcttatatgt 2280
ggaagccgga atctagat tt ccaagcacta gaagaaacta cagaatatga cggtggctat 2340
accagggact ctgttctgat tagggagttc tgggaaatcg ttcatcatt tacagatgaa 2400
cagaaaagac tcttcttgca gtttacaacg ggcacagaca gagcacctgt gggaggacta 2460
ggaaaattaa agatgattat agccaaaaat ggcccagaca cagaaagggt acctaca tct 2520
catacttgc ttaatgtgct ttacttccg gaatactcaa gcaaagaaaa acttaaaagag 2580
agattgttga aggccatcac gtatgcaaaa ggatttggca tgctgtaa 2628
```

<210> 106

<211> 363

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence :primer

<220>

<221> misc_feature

<222> (1)..(363)

71/292

<223> 3' terminal sequence. oncogene tc21 (TC21)
gene.

<400> 106
aattttaatt ctagcacctg aagctataca agggatgct ctataaactt catgggactg 60
tcgtacacac ttgataaagt gacaactgtg caataccact tagcatctca aaatcag gaa 120
catactattg aattgcttaa acacaatcca caganttaaa aacaaaatca ggatgccatc 180
cacagttata ctaattatcc attaaaaggc ttacacttaa tacttgaant aacaatcaat 240
atctagnccg ggnatactgg aaagtggatt tcagnngtct catcctgttg gtactctatt 300
ggggnggggt ttcttgaggt aggttatggg ggact gggnc caagngtggg ggggtaccacc 360
cag 363

<210> 107

<211> 408

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(408)

<223> 5' terminal sequence. oncogene tc21 (TC21)
gene.

<400> 107
gaattgaatc tacaaaagtg aaccatctca gacctttact gatactacaa cttttgtttt 60
ctgatggcca aaataccaaa tgcctgttgt atttatggat taaaaactgc ttataaaacc 120
ctgtgttact actcctactc ttggagatga taatatct ta tgtgggtcaaa ttttggact 180
catttaggac ttagatattt cagtgtactt gattttttta tttaactctt tttcacagcc 240
acgctaaggg taaaaggaa taatttcctt ctgtcttcct tttcaagtat ttctgggtaa 300
gggattcaaa aaactaaaac tgtttttgtt tgtaataata aatatgggat tgatctttcc 360
ggggtcagag atgattaatg tttttgctat atacttttat acatgntt 408

<210> 108

<211> 612

<212> DNA/RNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(612)

<223> oncogene tc21 (TC21) gene.

<400> 108
atggccgcgg cggtggcgg acggctccgg caggagaagt accggctcgt ggtggtcggc 60
gggggcggcg tgggcaagtc ggcgctcacc atccagttca tccagtccta ttttgaacg 120
gattatgatc caaccattga agattcttac acaaagcagt gtgtgataga tgacagagca 180
gcccggtctag atatttttga tacagcagga caagaagagt t tggagccat gagagaacag 240
tatatgagga ctggcgaagg ctctctgttg gtcttttcag tcacagatag aggcagtttt 300
gaagaaatct ataagtttca aagacagatt ctacagagtaa aggatcgtga tgagttccca 360
atgattttaa ttgtaataa agcagatctg gatcatcaaa gacaggtaac acaggaagaa 420
ggacaacagt tagcacggca gcttaaggta acatacatgg aggcacagc aaagattagg 480
atgaatgtag atcaagcttt ccatgaactt gtccgggtta tcaggaaatt tcaagagcag 540
gaatgtcctc cttcaccaga accaacacgg aaagaaaaag acaagaaagg ctgccattgt 600

gtcattttct ag

6 12

<210> 109
<211> 592
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<220>
<221> misc_feature
<222> (1)..(592)
<223> 5' terminal sequence. tyrosine kinase with
immunoglobulin and epidermal growth facto r
homology domains (TIE) gene.

<400> 109
ngtcggagag aacctagcct ccaagattgc agacttcggc ctttctcggg gagaggaggt 60
ttatgtgaag aagacgatgg ggcgtctccc tgtgcgctgg atggccattg agtccctgaa 120
ctacagtgtc tataccacca agagtgtgt ctggtccttt ggagtccttc ttggggagat 1 80
agtgagcctt ggaggtacac cctactgtgg catgacctgt gccgagctct atgaaaagct 240
gccccagggc taccgcatgg agcagcctcg aaactgtgac gatgaagtgt acgagctgat 300
gcgttcagtg ctggcgggac cgtccctatg agcgaccccc ctttgcccag attgcgctaa 360
cagctaggcc gcatgctggg aagccaggga aggcctatgt gaacatgttc gctgtttgag 420
aacttcaatt aacgcgggca ttgatgccac agctgaggag gnetgagctg ccatccagcc 480
agaactnggt ctgttgccg gagcaaat tttgtctaaa ctgtgaccag ttnaacctta 540
aagctttgat ttaagttgct taaggatttt ttaattaag ggagaaaaat tt 592

<210> 110
<211> 3845
<212> DNA/RNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<220>
<221> misc_feature
<222> (1)..(3845)
<223> tyrosine kinase with immunoglobulin and
epidermal growth factor homology domains (TIE)
gene.

<400> 110
cgctcgtcct ggctggcctg ggtcggcctc tggagtatgg tctggcgggt gccccctttc 60
ttgctcccca tcctcttctt ggcttctcat gtgggcgcgg cgggtggacct gacgctgctg 120
gccaacctgc ggctcacgga cccccagcgc ttcttcctga cttgcgtgtc tggggaggcc 180
ggggcgggga ggggctcgga cgcctggggc cc gccctgc tgcaggagaa ggacgaccgt 240
atcgtgcgca ccccgcccg gccaacctg cgcctggcgc gcaacgggtc gcaccaggtc 300
acgcttcgcg gcttctccaa gccctcggac ctgctgggcg tcttctcctg cgtgggcggg 360
gctggggcgc ggcgcacgcg cgtcatctac gtgcacaaca gccctggagc ccacctgctt 420
ccagacaagg tcacacacac tgtgaacaaa ggtgacaccg ctgtactttc tgcacgtgtg 480
cacaaggaga agcagacaga cgtgatctgg aagagcaacg gatcctactt ctacacctg 540
gactggcatg aagcccagga tggcgggttc ctgctgcagc tcccaaatgt gcagccacca 600
tcgagcggca tctacagtgc cacttacctg gaagccagcc cctggggcag cg ccttcttt 660
cggctcatcg tgcggggttg tgggctggg cgctgggggc caggctgtac caaggagtgc 720
ccaggttgcc tacatggagg tgtctgccac gaccatgacg gcgaatgtgt atgccccct 780
ggcttcactg gcaccgcgtg tgaacaggcc tgcagagagg gccgttttgg gcagagctgc 840

```

caggagcagt gccagggcat atcaggctgc cggggcctca ccttctgcct ccagacccc 900
tatggctgct cttgtggatc tggctggaga ggaagccagt gccaagaagc ttgtgcccct 960
ggtcattttg gggctgattg ccgactccag tgccagtgtc agaattggtg cacttgtgac 1020
cggttcagtg gttgtgtctg cccctctggg tggcatggag tgcactgtga gaagtcagac 1080
cggatccccc agatcctcaa catggcctca gaactggagt tcaacttaga gacgatgcc 1140
cggatcaact gtgcagctgc aggaaccccc ttccccgtgc ggggcagcat agagctacgc 1200
aagccagacg gcactgtgct cctgtccacc aaggccattg tggagccaga gaagaccaca 1260
gctgagttcg aggtgccccg cttgtttctt gctgacagtg ggttct ggga gtgccgtgtg 1320
tccacatctg gcggccaaga cagccggcgc ttcaagggtca atgtgaaagt gcccccgctg 1380
cccttggtcg cactcggct cctgaccaag cagagccgcc agcttgtggt ctccccgctg 1440
gtctcgttct ctggggatgg acccatctcc actgtccgcc tgcactaccg gcccaggac 1500
agtaccatgg actggtcgac cattgtggtg gacccagtg agaactgtac gttaatgaac 1560
ctgaggccaa agacaggata cagtgttcgt gtgcagctga gccggccagg ggaaggagga 1620
gagggggcct gggggcctcc caccctcatg accacagact gtccctgagcc tttgttgacg 1680
ccgtggttgg aggtctggca tgtggaaggc actgacggcg tgcagtgag ctggtccttg 1740
cccttggtgc ccgggccact ggtgggcgac ggtttcctgc tgcgcctgtg ggacgggaca 1800
cgggggcagg agcggcgga gaacgtctca tccccccagg ccgcactgc cctcctgacg 1860
ggactcacgc ctggcaccca ctaccagctg gatgtgcagc tctaccactg caccctcctg 1920
ggcccggcct cgccccctgc acacgtgctt ctgc ccccca gtgggcctcc agcccccca 1980
cactctcacg ccaggccct ctccagactcc gagatccagc tgacatgaa gcacccggag 2040
gctctgcctg ggccaatata caagtacgtt gtggagggtc aggtggctgg gggtcagga 2100
gacccactgt ggatgacgt gaacaggcct gatgagacaa gcaccatcat ccgtggcctc 2160
aacgccagca cgcgtacct cttccgcatg cgggccagca ttcaggggct cggggactgg 2220
agcaacacag tagaagagtc caccctgggc aacgggctgc aggtgaggg ccagtcaca 2280
gagagccggg cagctgaaga gggcctggat cagcagctga tcttgccgtt ggtgggctcc 2340
gtgtctgcca cctgcctcac catcctggcc gcccttttaa ccctggtg tg catccgcaga 2400
agctgcctgc atcggagacg cactctcacc taccagtcag gctcgggcga ggagaccatc 2460
ctgcacttca gctcaggac cttgacactt acccgccgc caaaactgca gcccgagccc 2520
ctgagctacc cagtgtaga gtggaggac atcaccttg aggacctcat cggggagggg 2580
aacttcggcc aggtcatccg gg ccatgatc aagaaggacg ggctgaagat gaacgcagcc 2640
atcaaatgca tgaaagagta tgctctgaa aatgaccatc gtgactttgc gggagaactg 2700
gaagttctgt gcaaattggg gcatcaccac aacatcatca acctcctggg ggctgtaag 2760
aaccgaggtt acttgatat cgtattgaa tatgccccct acgggaacct gctagatatt 2 820
ctgcggaaaa gccgggtcct agagactgac ccagcttttg ctcgagagca tgggacagcc 2880
tctaccctta gctcccgga gctgctgcgt ttgcagagt atgcggccaa tggcatgcag 2940
tacctgagtg agaagcagtt catccacagg gacctggctg ccggaatgt gctggtcgga 3000
gagaacctag cctccaagat tgcagacttc ggcctt tctc ggggagagga ggtttatgtg 3060
aagaagacga tggggcgtct ccctgtgcgc tggatggcca ttgagtcct gaactacagt 3120
gtctatacca ccaagagtga tgtctggtcc tttggagtcc ttctttggga gatagtgagc 3180
cttgagggtta caccctactg tggcatgacc tgtgccgagc tctatgaaaa gctgccccag 3240
ggctaccgca tggagcagcc tcgaaactgt gacgatgaag tgtacgagct gatgcgtcag 3300
tgctggcgga accgtcccta tgagcgaccc ccctttgccc agattgcgt acagctaggc 3360
cgcatgctgg aagccaggaa ggcctatgtg aacatgtcgc tgtttgagaa cttcacttac 3420
gcgggcattg atgccacagc tgaggaggcc tgagctgcca tccagccaga acgtggctct 3480
gctggcgga gcaaactctg ctgtctaacc tgtgaccagt ctgacctta cagcctctga 3540
cttaagctgc ctcaaggaat ttttttaact taaggagaaa aaaaaggat ctggggatgg 3600
ggtgggctta ggggaactgg gtcccatgc tttgtagtg tctcatagct atcctgggca 3660
tccttcttcc tagttcagct gcc cacagg tgtgtttccc atccactgc tcccccaaca 3720
caaaccccca ctccagctcc ttcgcttaag ccagcactca caccactaac atgcccgtt 3780
cagctactcc cactcccggc ctgtcattca gaaaaaata aatgttctaa taagctcaa 3840
aaaaa

```

384 5

<210> 111

<211> 202

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>
<221> misc_feature
<222> (1)..(202)
<223> 3' terminal sequence. autocrine motility
factor receptor (AMFR) gene.

<400> 111
aaagcccttc aaggtttact cncccanctt gcaaggccca cancttggtc aaggaccaa 60
cccacaggct ttagcactgc ctaatttact tcaccaatga atgaaaacca taaaccaaag 120
cttgctgcct aaccactccc cagggccaga cgggacaagg aaatgctgag aggggagggg 180
acccatgggg canantnatg ag 202

<210> 112
<211> 450
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<220>
<221> misc_feature
<222> (1)..(450)
<223> 5' terminal sequence. autocrine motility
factor receptor (AMFR) gene.

<400> 112
attcaagtac cttttoctac acagcgggtca gatagcatca gacctgcatt gaacagtcct 60
gtggaaaggc caagcagtga ccaggaagag ggagaaactt ctgctcagac cgagcgtgtg 120
ccactggacc tcagtcctcg cctggaggag acgctggact tcggcgaggt ggaagtggag 180
cccagtgagg tgaagactt cgaggctcgt gggagcgctt tctccaagtc tgctgatgag 240
agacagcgca tgtggtngca gcgtaaggac gaactcctcc agcaagctcg caaacgtttt 300
cttgaacaaa agttctgaag atgatgccgg ccttcagaga gctttcctnc ctttcggaaa 360
ggtgccgttc cttttgaacc ccgtgaaccc ctgncgttcg aaaggattgc ttggcttgcc 420
cgccgcggga aacggaggct ttcagaagca 450

<210> 113
<211> 1810
<212> DNA/RNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<220>
<221> misc_feature
<222> (1)..(1810)
<223> autocrine motility factor receptor (AMFR)
gene.

<400> 113
ggggggaagg ccaagcagtg accaggaaga gggagaaact tctgctcaga ccgagcgtgt 60
gccactggac ctcagtcctc gcctggagga gacgtggac ttcggcgagg tggaagtgga 120
gcccaagtga gtggaagact tcgaggctcg tgggagccgc ttctccaagt ctgctgatga 180
gagacagcgc atgctggctg cagcgtaagg acgaactcct ccagcaagct cgcaaactgt 240
tcttgaacaa aagttctgaa gatgatgcgg cctcagagag cttcctcccc tcggaagggtg 300
cgtcctctga ccccgtagac ctgctgagaa ggatgctggc tgccgcgcgg aacggaggct 360
tcagaagcag cagacctcct agcgctccct tgccttctc agctgcct cc tgcgccctgt 420
gcccgaactga ctggaggagg cctgtcccaa ttctgccgct ccatggaaaa ggggcttga 480

```

ctgcattgcc gctgtataaa gcatgtggtc ttatagtgtt tggacagctg ataaatttaa 540
tccttccttg taatactttc tatgtgacat ttctcttccc cttagaaaca ctgcaaattt 600
taactgtagg tatgatctct tctggg gttg actggactgc ttgggggtggg ggacgatcag 660
gaggaagtga gccagtcgcc tgcctgcagc aggcagcttc tactcctgcc tcatgcatac 720
gtcccacaaa tgcaggtgtc ctgagcacca caccagctgg gaagagtgtg ggggaggcgc 780
acagtgtgag cccgccccca cgtcgtgggg taacatctgt tatcaaactg ctgtcgttgt 840
tgtggaagca tgtagactgt gccagagcca gaccacggg ctcatgcacc cctgagcagc 900
aggcatctt ggaaaaggaa ctcttggttc gatacctgga gcagaggagg ggaaagtcca 960
gggctatagg gtgtgatgaa gtcacccctt tctgtccac tacatctggg actgactttc 1020
cgagcctcca gtccaaagcc ggcttgattt ccgtgaactc tgggtg ctctt gcatctcatg 1080
agtgtgcccc atgggtcccc tcccctctca gcatttcctt gtcccgtctg gacctgggga 1140
gtggttaggc agcaagcttt ggtttatggt ttctattcat tgggtgaagta aattaggcag 1200
tgctaaagcc tgtgggtttg gtccttgaa aagatgtggg ccttgcaaga tgggagagta 1260
aaccttgaag ggctttatta aagaaataaa aaagaacttt tgtatctttt atcctgggag 1320
cactgcgttt tcctagctgt gttattcctg gtttaattca gcagagaagg taagggtgtga 1380
acctacctgc cttggagagg ccaggtccc aaatctcttc aaattcttca catgtttaac 1440
tttaaggatt tgaacatga agtcataggt tacagacctc agttttatgc cccattgga t 1500
tacttttttt tttttttttt tttttttact ctttgaaagc tttgttttgt ggtagtcgct 1560
tttgggaaga atccagtatt atctacaatt attggcaaag tttaaatgta ttttacataa 1620
cggaaagtgt ttagaatgtt gaaaagtaat tgaaaaaggt gataggtaaa tttttaggca 1680
aagataattt atttcaataa atctttcaaa agc cttacct tgaaatgctg ttagtaaat 1740
tctgtgcatt tttttttttt aatttgttt gctgagagca tagctatttg tttttattgt 1800
aaaccgccc 1810

```

<210> 114

<211> 248

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(248)

<223> 3' terminal sequence. homo sapiens mrna;
 cdna dkfzp434c136 (from clone dkfzp434c136) (EST
 R81127) gene.

<400> 114

```

gaaattccaa aatcactcta gtttattcac ataatatagn atttgattcc attcttttgn 60
actgtncccn acttttacia tgtgtacaat gtttcacat gtnccaatta atggttgagc 120
tttaaatgaa aatattctgg ancttccatt tatnggnatc aaccacaata gcaagacccc 180
cangaaatac ttgatctaaa ctgggagggt ccaacacaat tttttttttt aatgggnctt 240
gccacctt 248

```

<210> 115

<211> 415

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(415)

<223> 3' terminal sequence. b-cell cll/lymphoma 2
 (BCL2) gene.

<400> 115
ttttttaag cagctttoga aatatcaacc acagcattaa acattgaaca ggtacattc 60
caaagttaat acagataaat ggtatataat gcaataatgc cacagagtta ttccatcaat 120
gtttcanggc tgattctaaa ctggangaaa aaaaaaattn cctagtttat ttgctganga 180
tgtcacttct tttgttactt ctttatagtt cccaccatt gattttnttt ttaatgcccc 240
ggggtgtaca ggataacccc catattccac accggggnac ttttttttg tcagggtttt 300
caaataaanc caaactacag tgacaggata atgttttaca ggtaattccn tgggcccggg 360
ggtcaattat nccctggacac ctcaattcaa ggcntcctt gggggtttgg gggcc 415

<210> 116
<211> 468
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<220>
<221> misc_feature
<222> (1)..(468)
<223> 5' terminal sequence. b-cell cl1/lymphoma 2
(BCL2) gene.

<400> 116
aattgtgcca gaaaagcatt ttagcaatth atacaatatc atccagtacc ttaagccctg 60
attgtgtata ttcataatatt ttggatacgc acccccacac tcccataact ggctctgtct 120
gagtaagaaa cagaatcctc tggaaactga ggaagtgaac atttcggtga cttccgcac 180
aggaaggcta gagttaccca gagcatcagg ccgccacaag tgccctgctt t aggagaccg 240
aagtccgcag aacctgcctn tgtcccagct tggaggcctg gtccctgggaa ctgagccggg 300
gccctcactn gcctcctcca gggatgatca acaggngcag tgtggtntcc gaatgtctgg 360
aagcttgatg ggagctcaga atttccactg ttcaagaaag agncagtaga ggggtgtngc 420
tgggncctgtt cacctggggg ccctncagggt agngcccntt tttcacgt 468

<210> 117
<211> 6030
<212> DNA/RNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<220>
<221> misc_feature
<222> (1)..(6030)
<223> b-cell cl1/lymphoma 2 (BCL2) gene.

<400> 117
gttggcccc gttacttttc ctctgggaaa tatggcgcac gctgggagaa cagggtacga 60
taaccgggag atagtgatga agtacatcca ttataagctg tcgcagaggg gctacgagt 120
ggatgcggga gatgtgggag ccgcgcccc gggggccgccc ccgcgcccgg gcatcttctc 180
ctcgcagccc gggcacacgc cccatacagc cgcacccgg gaccg gtcg ccaggacctc 240
gccgtgcag accccggctg ccccgggcgc cgcgcgggg cctgcgtca gcccggtgcc 300
acctgtggtc cacctgacct tccgccaggc cggcgacgac ttctcccgc gctaccgcg 360
cgacttcgcc gagatgtcca ggcagctgca cctgacgccc ttaccgcgc ggggacgctt 420
tgccacggtg gtggaggagc tctt caggga cggggtgaac tgggggagga ttgtggcctt 480
ctttgagttc ggtggggtca tgtgtgtgga gagcgtcaac cgggagatgt cggccctggt 540
ggacaacatc gccctgtgga tgactgagta cctgaaccgg cacctgcaca cctggatcca 600
ggataacgga ggctgggatg cctttgtgga actgtacggc cccagcatgc ggcctctgtt 660

tgattttctcc tggctgtctc tgaagactct gctcagtttg gccctggtgg gagcttgcac 720
 caccctgggt gcctatctgg gccacaagtg aagtcaacat gcctgcccc aacaaatatg 780
 caaaagggtc actaaagcag tagaataaat atgcattgtc agtgatgttc catgaaacaa 840
 agctgcaggc tgtttaagaa aaaataaacac acatataaac atca cacaca cagacagaca 900
 cacacacaca caacaattaa cagtcttcag gcaaaacgtc gaatcagcta tttactgcca 960
 aagggaaata tcattttatt tttacattat taagaaaaaa agattttattt atttaagaca 1020
 gtcccatcaa aactcctgtc tttgaaatc cgaccactaa ttgccaagca ccgcttcctg 1080
 tggctccacc tggatgttct gtgcctgtaa acatagattc gctttccatg ttgttggccg 1140
 gatcaccatc tgaagagcag acggatggaa aaaggacctg atcattgggg aagctggctt 1200
 tctggctgct ggaggctggg gagaaggtgt tcattcactt gcattttctt gccctggggg 1260
 ctgtgatatt aacagaggga gggttcctgt ggggggaagt ccatgcctcc ctggcctgaa 1320
 gaagagactc tttgcataat actcacatga tgcatacctg gtgggaggaa aagagttggg 1380
 aacttcagat ggacatagta cccactgaga ttccacgcc gaaggacagc gatgggaaaa 1440
 atgcccttaa atcataggaa agtatttttt taagctacca attgtgccga gaaaagcatt 1500
 ttagcaattt atacaatatc atccagtacc ttaa gccctg attgtgtata ttcataatatt 1560
 ttggatacgc accccccaac tcccaatact ggctctgtct gagtaagaaa cagaatcctc 1620
 tggaaactga ggaagtgaac atttcgggtga cttccgcacac aggaaggcta gagttacca 1680
 gagcatcagg ccgccacaag tgcttgcctt taggagaccg aagtcgcag aacctgcctg 1740
 tgtcccagct tggaggcctg gtcttggaaac tgagccgggg ccctcactgg cctcctccag 1800
 ggatgatcaa cagggcagtg tggctccga gctgtggaa gctgatggag ctgagaattc 1860
 cactgtcaag aaagagcagt agaggggtgt ggtggggcct gtcaccctgg ggccctccag 1920
 gtagggccct tttcacgtgg agcatgggag ccacgaccct tcttaaga ca tgtatcactg 1980
 tagagggaag gaacagaggc cctggggcct tccatcaga aggacatggt gaaggctggg 2040
 aacgtgagga gaggcaatgg ccacggccca ttttggctgt agcacatggc acgttggctg 2100
 tgtggccttg gccacctgt gagtttaaag caaggcttta aatgactttg gagagggtca 2160
 caaatcctaa aagaagcatt ga agtgaggt gtcattggatt aattgacccc tgtctatgga 2220
 attacatgta aaacattatc ttgtcactgt agtttggttt tatttgaaaa cctgacaaaa 2280
 aaaaagttcc aggtgtggaa tatgggggtt atctgtacat cctggggcat taaaaaaaaa 2340
 atcaatggtg gggaactata aagaagtaac aaaagaagtg acatcttcag caaataaact 2 400
 aggaaatttt tttttctcc agtttagaat cagccttgaa acattgatgg aataactctg 2460
 tggcattatt gcattatata ccatttatct gtattaaact tggaaatgtac tctgttcaat 2520
 gtttaatgct gtggttgata tttcgaaagc tgctttaaaa aaatacatgc atctcagcgt 2580
 ttttttggtt ttaattgtat ttagtattgg cctata cact atttgtgagc aaaggtgatc 2640
 gttttctgtt tgagattttt atctcttgat tcttcaaaag cattctgaga aggtgagata 2700
 agccttgagt ctcagctacc taagaaaaac ctggatgtca ctggccactg aggagctttg 2760
 tttcaaccaa gtcattgtca tttccacgtc aacagaattg tttattgtga cagttatata 2820
 tgttgtccct ttgacctgtt ttcttgaagg tttcctcgtc cctgggcaat tccgattta 2880
 attcatggtt ttcaggatta catgcatggt tggttaaacc catgagattc attcagttaa 2940
 aaatccagat ggcaaatgac cagcagattc aaatctatgg tggtttgacc tttagagagt 3000
 tgctttacgt ggccgtgttc aacacagacc caccagagc cctcctgccc tccctccgag 3060
 ggggctttct catggtgtgc cttcagggtc ttcctgaaat gcagtgtgtc ttacgctcca 3120
 ccaagaaagc aggaacctg tggatgaag ccagacctcc ccggcgggccc tcagggaaca 3180
 gaatgatcag accttgaat gattctaatt ttaagcaaa atattatttt atgaaagggt 3240
 tacattgtca aagtgatgaa tatg gaatat ccaatcctgt gctgctatcc tgccaaaatc 3300
 attttaatgg agtcagtttg cagtatgtc cacgtggtaa gatcctccaa gctgctttag 3360
 aagtaacaaat gaagaacgtg gacgttttta atataaagcc tgttttgtct tctgttgtt 3420
 ttcaaacggg attcacagag tatttgaaaa atgtatatat attaagaggt cacgggggct 348 0
 aattgtctgc tggctgcctt ttgctgtggg gttttgttac ctggttttta taacagtaaa 3540
 tgtgccagc ctcttggccc cagaactgta cagtattgtg gctgcacttg ctctaagagt 3600
 agttgatgtt gcattttcct tattgttaaa aacatgttag aagcaatgaa tgtatataaa 3660
 agcctcaact agtcattttt ttctcctctt cttttttt tc attatatcta attattttgc 3720
 agttgggcaa cagagaacca tccctatttt gtattgaaga gggattcaca tctgcatctt 3780
 aactgcctct tatgaatgaa aaaacagtc ctctgtatga ctccctttta cactggccag 3840
 ggtcagagtt aaatagagta tatgcacttt ccaaattggg gacaagggt ctaaaaaaag 3900
 ccccaaaagg agaagaacat ctgagaacct cctcgccct ccagtcctc cgctgcacaa 3960
 atactccgca agagaggcca gaatgacagc tgacagggtc tatggccatc gggctgtctc 4020
 cgaagatttg gcaggggagc aaaactctgg caggcttaag atttggaata aagtcacaga 4080
 atcaagggaag cactcaatt tagttcaaac aagacgcaa cattctctcc a cagctcact 4140
 tacctctctg tgttcagatg tggccttcca tttatatgtg atctttgtt tattagtaaa 4200
 tgcttatcat ctaaagatgt agctctggcc cagtgggaaa aattaggaag tgattataaa 4260
 tcgagaggag ttataataat caagattaaa tgtaaataat cagggaatc ccaacacatg 4320

```

tctagctttc acctccagga tctatt gagt gaacagaatt gcaaatagtc tctatttgta 4380
attgaactta tcctaaaaca aatagtttat aaatgtgaac ttaaactcta attaattcca 4440
actgtacttt taaggcagtg gctgttttta gactttctta tcacttatag ttagtaatgt 4500
acacctactc tatcagagaa aaacaggaaa ggctcgaaat acaagccatt ctaaggaaat 4560
tagggagtcg gttgaaattc tattctgata ttattctgtg gtgtcttttg cagcccagac 4620
aaatgtggtt acacactttt taagaaatac aattctacat tgtcaagctt atgaaggttc 4680
caatcagatc tttattgtta ttcaatttggt atctttcagg gatttttttt tttaaattatt 4740
atgggacaaa ggacatttgt tggaggggtg ggagggagga acaattttta aatataaaac 4800
attcccaagt ttggatcagg gaggttggaag ttttcagaat aaccagaact aagggtatga 4860
aggacctgta ttggggtcga tgtgatgcct ctgcgaagaa ccttggtgta caaatgagaa 4920
acattttgaa gtttgtggta cgacctttag attccagaga catcagcatg gctcaaagtg 4980
cagctccggt tggcagtgca atggtataaa ttccaagctg gatatgtcta atgggtattt 5040
aaacaataaa tgtgcagttt taactaacag gatatttaat gacaaccttc tgggttgtag 5100
ggacatctgt ttctaaatgt ttattatgta caatacagaa aaaaatttta taaaattaag 5160
caatgtgaaa ctgaattgga gagtataat acaagtcctt tagtcttacc cag tgaatca 5220
ttctgttcca tgtctttgga caaccatgac cttggacaat catgaaatat gcatctcact 5280
ggatgcaaag aaaatcagat ggagcatgaa tggtagctga ccggttcac tggactgcc 5340
cagaaaaata acttcaagca aacatcctat caacaacaag gttgttctgc ataccaagct 5400
gagcacagaa gatgggaaca ctggtgga gg atggaaaggc tcgctcaatc aagaaaattc 5460
tgagactatt aataaataag actgtagtgt agatactgag taaatccatg cacctaaacc 5520
ttttggaaaa tctgccgtgg gccctccaga tagctcattt cattaagtgt ttccctccaa 5580
ggtagaattt gcaagagtga cagtggattg catttctttt ggggaagctt tcttttggtg 5640
gttttgttta ttataaccttc ttaagttttc aaccaagggt tgcctttgtt ttgagttact 5700
gggtttattt ttgttttaaa taaaaataag tgtacaataa gtgtttttgt attgaaagct 5760
tttgttatca agattttcat acttttacct tccatggctc tttttaagat tgatactttt 5820
aagagggtgc tgatattctg caacactgta cacataaaaa a tacggttaag gatactttac 5880
atggttaagg taaagtaagt ctccagttgg ccaccattag ctataatggc actttgtttg 5940
tgttgttga aaaagtcaca ttgccattaa actttccttg tctgtctagt taatattgtg 6000
aagaaaaata agttacagtg tgagatactg 6030

```

<210> 118

<211> 343

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(343)

<223> 5' terminal sequence. v-erb-b2 avian
erythroblastic leukemia viral oncogene homolog 2
(neuro/glioblastoma derived oncogene homolog)
(ERBB2) gene.

<400> 118

```

caaggggctg caaactnncc cacacatgac cccagccctc tacagcggtg cagtgaggac 60
cccacagtac cctgcccctc tgagactgat ggctacgttg cccccctgac ctgcagcccc 120
cagcctgaat atgtgaacca gccagatgtt cgccccagc cccct tcgcc ccgagaggcc 180
ctctgcctgc tgcccgacct gctggtgcc ctctggaaag gcccaagact ctctccccag 240
ggaagaatgg ggtcgtcaaa gattttttgc ctttgggggt gccgtgggag aacccccagt 300
attgacaccc caggggaggg agcttgccct tcagcccccac ctt 343

```

<210> 119

<211> 4530

<212> DNA/RNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(4530)

<223> v-erb-b2 avian erythroblastic leukemia viral
oncogene homolog 2 (neuro/glioblastoma derived
oncogene homolog) (ERBB2) gene.

<400> 119

```
aattctcgag ctcgtcgacc ggtcgacgag ctcgaggggtc gacgagctcg agggcgcgcg 60
cccgcccccc acccctcgca gcaccccgcg ccccgcgccc tcccagcccg gtccagcccg 120
agccatgggg cgggagccgc agtgagcacc atggagctgg cggccttgtg ccgctggggg 180
ctcctcctcg cctctttgcc cccggagcc gcgagcacc aagtgtgcac cggcacagac 240
atgaagctgc ggctccctgc cagtcccag acccactgg acatgctccg ccacctctac 300
cagggctgcc aggtgtgtgca gggaaacctg gaactcacct acctgcccac caatgccagc 360
ctgtccttcc tgcaggatat ccaggaggtg cagggtacg tgctcatcgc t cacaaccaa 420
gtgaggcagg tcccactgca gaggctgcgg attgtgcgag gcacccagct ctttgaggac 480
aactatgccc tggccgtgct agacaatgga gaccgctga acaataccac ccctgtcaca 540
ggggcgctcc caggagcct gcgggagctg cagcttcgaa gcctcacaga gatcttgaaa 600
ggaggggtct tgatccagcg gaaccccgag ctctgtctacc aggcacgat tttgtggaag 660
gacatcttcc acaagaacaa ccagctgggt ctcacactga tagacaccaa ccgctctcgg 720
gcctgccacc cctgttctcc gatgtgtaag ggctcccgct gctggggaga gagttctgag 780
gattgtcaga gcctgacgcg cactgtctgt gccggtggct gtgcccgctg caaggggcca 840
ctgcccactg actgctgcca tgagcagtg gctgccggct gcacggggcc caagcactct 900
gactgctgg cctgcctcca cttcaaccac agtggcatct gtgagctgca ctgcccagcc 960
ctggtcacct acaacacaga cacgtttgag tccatgccc atcccaggcg ccggtatata 1020
ttcgggcgca gctgtgtgac tgcctgtccc tacaactacc tttctacgg a cgtgggatcc 1080
tgcacctcg tctgccccct gcacaaccaa gaggtgacag cagaggatgg aacacagcgg 1140
tgtgagaagt gcagcaagcc ctgtgccoga gtgtgctatg gtctgggcat ggagcacttg 1200
cgagaggtga gggcagttac cagtgcgaat atccaggagt ttgctggctg caagaagatc 1260
tttgggagcc tggcatttct gcc ggagagc tttgatgggg acccagcctc caacactgcc 1320
ccgctccagc cagagcagct ccaagtgtt gagactctgg aagagatcac aggttaccta 1380
tacatctcag catggccgga cagcctgcct gacctcagcg tcttccagaa cctgcaagta 1440
atccggggac gaattctgca caatggcgcc tactcgtga ccctgcaagg gctgggcata 15 00
agctggctgg ggctgcgctc actgagggaa ctgggcagt gactggccct catccacat 1560
aacaccacc tctgtcttgt gcacacggtg ccctgggacc agctctttcg gaacccgcac 1620
caagctctgc tccacactgc caaccggcca gaggacgagt gtgtgggcca gggcctggcc 1680
tgccaccagc tgtgcgcccg agggcactgc tgggggtc cag ggccccacca gtgtgtcaac 1740
tgcagccagt tcctcgggg ccaggagtgc tggaggaat gccagtgact gcaggggctc 1800
cccaggaggt atgtgaatgc caggcactgt ttgccgtgcc accctgagt tccagcccag 1860
aatggctcag tgacctgtt tggaccggag gctgaccagt gtgtggcctg tgccactat 1920
aaggaccctc ctttctcggt ggcccgtgc cccagcgtg tgaaacctga cctctcctac 1980
atgccatct ggaagtttcc agatgaggag ggcgcatgcc agccttgccc catcaactgc 2040
accactcct gtgtggacct ggatgacaag ggctgcccc cggagcagag agccagccct 2100
ctgacgtcca tcgtctctgc ggtggttggc attctgtgtg tcgtgttctt gggggtggtc 2160
tttgggatcc tcatcaagcg acggcagcag aagatccgga agtacacgat gcggagactg 2220
ctgcaggaaa cggagctggg ggagccgctg acacctagcg gagcgatgcc caaccaggcg 2280
cagatgcgga tcctgaaaga gacggagctg aggaaggtga aggtgcttgg atctggcgct 2340
tttggcacag tctacaagg catct ggatc cctgatgggg agaagtgtga aattccagtg 2400
gccatcaaag tgttgaggga aaacacatcc cccaaagcca acaaagaaat cttagacgaa 2460
gcatacgtga tggtgtgtg gggctcccca tatgtctccc gccttctggg catctgcctg 2520
acatccacgg tgacgttgt gacacagctt atgccctatg gctgcctctt agaccatgtc 2580
cgggaaaacc cgggagcct gggctcccag gacctgcta actggtgtat gcagattgcc 2640
aaggggatga gctacctgga gcatgtgcgg ctcgtaacaa gggacttggc cgtcgggaac 2700
gtgtgtgtca agagtcccaa ccatgtcaaa attacagact tcgggctggc tcggctgctg 2760
gacattgacg agacagagta ccatgcagat gggggcaag g tgcccatcaa gtggatggcg 2820
ctggagtcca ttctcgcgg gcggttcacc caccagagt atgtgtggag ttatggtgtg 2880
actgtgtgg agctgatgac ttttggggcc aaaccttac atgggatccc agccgggag 2940
atccctgacc tgctggaanaa gggggagcgg ctgccccagc ccccatctg caccattgat 3000
```



```
gtctacatga tca tgggtcaa atgttgatg attgactctg aatgtcggcc aagattccgg 3060
gagttgggtg ctgaattctc ccgcatggcc agggaccccc agcgctttgt ggtcatccag 3120
aatgaggact tgggcccagc cagtcccttg gacagcacct tctaccgctc actgctggag 3180
gacgatgaca tgggggacct ggtggatgct gaggagtatc tggtagccca gc agggcttc 3240
ttctgtccag accctgcccc gggcgctggg ggcattgtcc accacaggca ccgcagctca 3300
tctaccagga gtggcggttg ggacctgaca ctagggttg agccctctga agaggaggcc 3360
cccaggtctc cactggcacc ctccgaagg gctggctccg atgtatttga tggtagcctg 3420
ggaatggggg gacccaagg gctgcaa agc ctccccacac atgaccccag cctctacag 3480
cggtacagtg aggaccccac agtacccttg ccctctgaga ctgatggcta cgttgcccc 3540
ctgacctgca gccccagcc tgaatatgtg aaccagccag atgttcggcc ccagcccct 3600
tcgccccgag agggccctct gctgtctgcc cgacctgtg gtgccactct ggaaagggcc 3660
aagactctct cccagggaa gaatggggtc gtcaaagacg tttttgcctt tgggggtgcc 3720
gtggagaacc ccgagtactt gacaccccag ggaggagtgt cccctcagcc ccaccctct 3780
cctgccttca gccagcctt cgacaacctc tattactggg accaggaccc accagagcgg 3840
ggggctccac ccagcacctt caaagggaca ctacggcag agaaccaga gtacctgggt 3900
ctggacgtgc cagtgtgaac cagaaggcca agtccgcaga agccctgatg tgtcctcagg 3960
gagcagggaa ggctgactt ctgctggcat caagaggttg gagggccctc cgaccacttc 4020
caggggaacc tgccatgcca ggaacctgtc ctaaggaacc ttccttcctg cttgagttcc 4080
cagatggctg gaagggttc agcctcgttg gaagaggaac agcactggg agtctttgtg 4140
gattctgagg cctgcccaca tgagactcta ggtccagtgt gatgccacag cccagcttgg 4200
ccctttcctt ccagatcctg ggtactgaaa gccttagga agctggcctg agaggggaag 4260
cgcccttaag ggagtgtcta agaacaaaag cgaccattc agagactgtc cctg aaacct 4320
agtactgccc cccatgagga aggaacagca atgggtgtcag tatccaggct ttgtacagag 4380
tgcttttctg tttagttttt actttttttt ttttgtttt ttaaagacga aataaagacc 4440
caggggagaa tgggtgttgt atggggaggc aagtgtggg ggtccttctc cacaccact 4500
ttgtccattt gcaaatatat ttggaaaa c 4530
```

<210> 120

<211> 319

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(319)

<223> 5' terminal sequence. mouse double minute 2,
human homolog of; p53-binding protein (MDM2) gene.

<400> 120

```
nacttatttc ccctagttga cctgtctata agagaattat atatttctaa ctatataacc 60
ctaggaattt agacaacctg aaatttattc acatatatca aagttagaaa atgcctcaat 120
tcacatagat ttcttctctt tagtataatt gacctacttt ggtagtggga a tagtgaata 180
cttactataa tttgacttga atatgtaggc tcaccttcta caccaactcc taatttttaa 240
taattttctac tctgtcttaa atgaggaggc acttgggntt tttttttct taaatatggt 300
atatggacat ttaaagtgt 319
```

<210> 121

<211> 2372

<212> DNA/RNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(2372)

<223> mouse double minute 2, human homolog of;
p53-binding protein (MDM2) gene.

<400> 121

```
gcaccgcgcg agcttggctg cttct ggggc ctgtgtggcc ctgtgtgtcg gaaagatgga 60
gcaagaagcc gagcccgagg ggccggccgcg acccctctga ccgagatcct gctgctttcg 120
cagccaggag caccgtccct ccccgatta gtgcgtacga gcgccagtg ccctggcccg 180
gagagtggaa tgatccccga ggccagggc gtcgtgcttc cgcagtagtc agtccccgtg 240
aaggaaactg gggagtcttg agggaccccc gactccaagc gcgaaaacc cggatggtga 300
ggagcaggca aatgtgcaat accaacaatgt ctgtacctac tgatggtgct gtaaccacct 360
cacagattcc agcttcggaa caagagacct tggtagacc aaagccattg cttttgaagt 420
tattaaagtc tgttggtgca caaaaagaca cttatactat gaaaga gggt cttttttatc 480
ttggccagta tattatgact aaacgattat atgatgagaa gcaacaacat attgtatatt 540
gttcaaatga tcttctagga gatttgtttg gcgtgccaag cttctctgtg aaagagcaca 600
ggaaaatata taccatgac tacaggaact tggtagtagt caatcagcag gaatcatcgg 660
actcaggtac atctgtgagt gaga acaggt gtcaccttga aggtgggagt gatcaaaagg 720
accttgtaca agagcttcag gaagagaaac cttcatcttc acatttgggt tctagacct 780
ctacctatc tagaaggaga gcaattagtg agacagaaga aaattcagat gaattatctg 840
gtgaacgaca aagaaaacgc cacaatatctg atagtatttc cctttccttt gatgaaagcc 900
tggtctctgtg tgtaataagg gagatatgtt gtgaaagaag cagtagcagt gaatctacag 960
ggacgccatc gaatccgat cttgatgctg gtgtaagtga acattcaggt gattggttgg 1020
atcaggattc agtttcagat cagtttagtg tagaatttga agttgaatct ctgcactcag 1080
aagattatag ccttagtgaa gaaggacaag aactctcaga tg aagatgat gaggtatata 1140
aagttactgt gtatcaggca ggggagagtg atacagattc atttgaagaa gatcctgaaa 1200
tttccttagc tgactattgg aaatgcactt catgcaatga aatgaatccc ccccttccat 1260
cacattgcaa cagatgttgg gcccttctgtg agaattggct tcctgaagat aaagggaaaag 1320
ataaagggga aatctct gag aaagccaaac tggaaaactc aacacaagct gaagaggggt 1380
ttgatgttcc tgattgtaaa aaaactatag tgaatgattc cagagagtca tgtgttgagg 1440
aaaatgata taaaattaca caagcttcac aatcacaaga aagtgaagac tattctcagc 1500
catcaacttc tagtagcatt atttatagca gccaaagaaga tgtgaaagag tttgaa aggg 1560
aagaaaccca agacaaagaa gagagtgtgg aatctagttt gccccttaat gccattgaac 1620
cttgtgtgat ttgtcaaggc cgacctaaaa atggttgcac tgtccatggc aaaacaggac 1680
atcttatggc ctgctttaca tgtgcaaaga agctaaagaa aaggaataag ccctgcccag 1740
tatgtagaca accaattcaa atgattgtgc taacttattt cccctagtgt accgtgtctat 1800
aagagaatta tatatttcta actatataac cctaggaatt tagacaacct gaaatttatt 1860
cacatatatc aaagtgagaa aatgcctcaa ttcacataga tttcttctct ttagtataat 1920
tgacctactt tggtagtgga atagtgaata cttactataa tttgacttga atatgtagct 1980
catcctttac accaactcct aattttaaat aatttctact ctgtcttaaa tgagaagtac 2040
ttggtttttt ttttcttaaa tatgtatatg acatttaaat gtaacttatt attttttttg 2100
agaccgagtc ttgctctgtt acccaggctg gagtgacgtg ggtgatcttg gctcactgca 2160
agctctgccc tccccgggtt cgcaccattc tcctgcctca gcct cccaat tagcttgccc 2220
tacagtcac tgccaccaca cctggctaata tttttgtact tttagtagag acagggtttc 2280
accgtgttag ccaggatggt ctgactctcc tgacctctg atccgccac ctgcgcctcc 2340
caaagtgcgtg ggattacagg catgagccac cg 2372
```

<210> 122

<211> 343

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(343)

<223> 3' terminal sequence. gata-binding protein 3
(GATA3) gene.

<400> 122
atgcttataa tattattcca acagactgta tta aaggcag tgatcactaa cacagancac 60
gacagggcga ngaggcagcc nggcccataa ncaggacgtg gccnntcggc cagggttcgc 120
tgacatgcac gctggtagct catacactgc taccctcagc acaggctgca ggaataggga 180
caagacagat gccgccggac tcttaggaag ctatttaata aatatcatcc aaanacaaaa 240
tgggaaaaag aaacaaggaa accctccggg gcacaaccac cttagggggc aactggaatg 300
gtaattctag gttttatttc caacccaaaa nttgaggaga gga 343

<210> 123
<211> 258
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<220>
<221> misc_feature
<222> (1)..(258)
<223> 3' terminal sequence. src homology 3
domain-containing protein hip-55 (HIP-55) gene.

<400> 123
cgagttagnt atgttgagg aacatgttgt gtctgccgtt tttgaatacc cagggtggga 60
gcttgccat ctgcatcccc acttoccata gcccaggcag agggac agag aaatggagtn 120
gggagcacag agcaggctcc aacaagacaa attccctgct gccaaaccac catgatccac 180
tctgactttg gncacaaact ctgctaataa caattctcta cgttcactgt tccaagggg 240
canttttaaa cagtgggtg 258

<210> 124
<211> 443
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<220>
<221> misc_feature
<222> (1)..(443)
<223> 5' terminal sequence. src homology 3
domain-containing protein hip-55 (HIP-55) gene.

<400> 124
gccagggctc agtgggcaag ggctctgtgc cgtngnccgtg tacgactacc atgcagccga 60
cgacacagag atctcctttg accccgagaa cctcatcacg ggcacgagg tgatcgacga 120
aggctgggtg cgtggctatg ggccggatca tntgttngca tgttccctgc caactacgtg 180
gagctcattg agtgaggtg agggcacatc ttgcccttcc cctctcagac atggcttc ct 240
tattgctgga agaggaggcc tggggagttg acattcagca ctcttcagg gaatagggac 300
ccccagttga ggattgaggc ntcagggttc cctccggnnt gggcagattc agccttttca 360
ccccaaatgg cagcaattgg cntgggtgat tccccaaaa tcnttcctg cattcccccg 420
acctttccca gacagtttg ttt 443

<210> 125
<211> 1331
<212> DNA/RNA
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(1331)

<223> src homology 3 domain-containing protein
hip-55 (HIP-55) gene.

<400> 125

```
atggcggcga acctgagccg gaacgggcca gcgctgcaag aggcctacgt gcgggtggtc 60
accgagaagt ccccgaccga ctgggctctc ttacctatg aaggcaacag caatgacatc 120
cgcggtggctg gcacagggga ggggtggcctg gaggagatgg tggaggagct caacagcggg 180
aaggtgatgt acgccttctg cagagtgaag gacccaact ctggactgcc caaatattgtc 240
ctcatcaact ggacaggcga gggcggtgaac gatgtgcga agggagcctg tgccagccac 300
gtcagcacca tggccagctt cctgaagggg gcccatgtga ccatcaacgc acgggcccag 360
gaggatgtgg agcctgagtg catcatggag aaggtggcca aggccttcagg tgccaactac 42 0
agctttcaca aggagagtgg ccgcttcag gacgtgggac cccaggcccc agtgggctct 480
gtgtaccaga agaccaatgc cgtgtctgag attaaaaggg ttggtaaaga cagcttctgg 540
gccaaagcag agaaggagga ggagaaccgt cgctggagg aaaagcggcg ggccgaggag 600
gcacagcggc agctggagca ggagcgccgg gagcgtgagc tgctgaggc tgcacgccgg 660
gagcagcgct atcaggagca ggggtggcga gccagcccc agaggacgtg ggagcagcag 720
caagaagtgg tttcaaggaa ccgaaatgag caggagtctg ccgtgcaccc gagggagatt 780
ttcaagcaga aggagagggc catgtccacc acctccatct ccagtccctca gcctggcaag 840
ctgaggagcc ccttctctgc a gaagcagctc acccaaccag agaccactt tggcagagag 900
ccagctgtg ccatctcaag gccagggga gatctccctg ctgaggagcc ggcgcccagc 960
actcctccat gtctggtgca ggcagaagag gaggtgtgt atgaggaacc tccagagcag 1020
gagactttct acgagcagcc ccactggtg cagcagcaag gtgccggctc tgagcacatt 1080
gaccaccaca ttcagggccca ggggtcagtg gggcaaggcg tctgtgcccg tgccctgtac 1140
gactaccagg cagccgacga cacagagatc tcctttgacc ccgagaacct catcacgggc 1200
atcgaggtga tcgacgaagg ctggtggcgt ggctatgggc cggatggcca ttttggcatg 1260
ttccctgcc actacgtgga gtcattgag tgag gctgag ggcggccgct agactagtct 1320
agagaaaaaa c 1331
```

<210> 126

<211> 430

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(430)

<223> 3' terminal sequence. cathepsin d (lysosomal
aspartyl protease) (CTSD) gene.

<400> 126

```
gtatttccat gtcagctggg gctctcagcc gcccaagggg aggacaacag aggtcagctg 60
cagaggaagg ctggcaccag ccccaatccc aacccacact ccaggccaat acatgccctc 120
gggactggct cagtccacgc accaccctgc aggcctcaac aaggtgggtt ttgtcccctc 180
tactccttc cagctcatcc tcaggcctct agcggcctca tcctcaacgg gcccgggaca 240
ctgaacaggt aggggtggga gagccagctg ggncccaagc tnggcaagag gggccctcag 300
gcagggcagg ttttncaagg gagggneccg gagacggcc ttgggtnttg g ggtaagggc 360
ttaanccagt cngggctttg gtaagggcc ggnaagggat tccntgggna aattaaagg 420
aanccccagg 430
```

<210> 127

<211> 339
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<220>
<221> misc_feature
<222> (1)..(339)
<223> 5' terminal sequence. cathepsin d (lysosomal
aspartyl protease) (CTSD) gene.

<400> 127
gtggatgagg tgcgcgactg cagaaggcca tcggggcgtn gccgctgatt cagggcgagt 60
acatgatccc ctgtgagaag gtgtccacc c tgcccgcgat cacactgaag ctgggaggca 120
aaggctacaa gctgtcccca gaggactaca cgtcgaagg gtgcgaggcc gggaagaccc 180
tctgctgag cgcttcatg ggcattgaca tcccgcacc cagcggncac tctggatcct 240
ggggcgacgt cttcattcgg ccgttantac attgtgtttt gaccgtgaca acaacagggt 300
tgggtttcgc gaggttgcc cgcttttagt ttcccaagg 339

<210> 128
<211> 1988
<212> DNA/RNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<220>
<221> misc_feature
<222> (1)..(1988)
<223> cathepsin d (lysosomal aspartyl protease)
(CTSD) gene.

<400> 128
ccatgcagcc ctccagcctt ctgccgctcg cctctgcct gctggctgca cccgcctccg 60
cgctcgtcag gatcccgctg cacaagttca cgtccatccg cgggaccatg tcggaggttg 120
ggggctctgt ggaggacctg attgccaaag gcccgcgtctc aaagtactcc caggcggtgc 180
cagccgtgac cgaggggccc attcccaggg tgctcaagaa ctacatggac gccagttact 240
acggggagat tggcatcggg acgccccccc agtgcctcac agtcgtcttc gacacgggct 300
cctccaacct gtgggtcccc tccatccact gcaaaactgct ggacatcgct tgctggatcc 360
accacaagta caacagcgac aagtccagca cctacgttaa gaatggtacc tcgtttgaca 420
tccactatgg ctcgggcagc ctctccgggt acctgagcca ggacactgtg tcggtgccct 480
gccagttagc gtcgtcagcc tctgcccttg gcggtgtcaa agtggagagg caggtctttg 540
gggaggccac caagcagcca ggcattacct tcatcgagc caagttcgat ggcattcctg 600
gcatggccta cccccgcac tccgtcaaca acgtgctgcc cgtcttcgac aacctgatgc 660
agcagaagct ggtggaccag aacatcttct ccttctacct gacgaggac ccagatgcgc 720
agcctggggg tgagctgatg ctgggtggca cagactccaa gtattacaag ggttctctgt 780
cctacctgaa tgtcaccgcg aaggcctact ggcaggtcca cctggaccag gtggaggtgg 840
ccagcgggct gacctgtgc aaggagggt gtgaggccat tgtggacaca ggcacttccc 900
tcatggtggg cccggtgatg gaggtgcgcg agctgcagaa ggccatcggg gccgtgccgc 960
tgattcaggg cgagtacatg atccctgtg agaaggtgtc caccctgccc gcatcacac 1020
tgaagctggg aggcaaaggc tacaagctgt ccccagag ga ctacacgctc aaggtgtcgc 1080
aggccgggaa gacctctgc ctgagcggct tcatgggcat ggacatccc ccaccagcg 1140
ggcctactct gatcctggc gacgtcttca tcggccgcta ctacactgtg tttgaccgtg 1200
acaacaacag ggtgggcttc gccgaggtg cccgcctcta gttcccaagg cgtccgcgcg 1260
ccagcacaga aacagaggag agtcccagag caggaggccc ctggcccagc ggcccctccc 1320
acacacaccc acactctgc ccgcccactg tcttgggag cctggaagcc ggcggcccaa 1380
gcccgaactg ctgttttgtt ctgtggtttt cccctccctg ggttcagaaa tgctgcctgc 1440

ctgtctgtct ctccatctgt ttggtggggg tagagctgat ccagagcaca g atctgtttc 1500
gtgcattgga agaccccacc caagcttggc agccgagctc gtgtatcctg gggctccctt 1560
catctccagg gagtcccctc cccggcccta ccagcgcccg ctggctgagc ccctaccca 1620
caccaggccg tcttcccggg ccctcccttg gaaacctgcc ctgcctgagg gccctctgc 1680
ccagcttggg cccagctggg ctctgc cacc ctacctgttc agtgtcccgg gcccgttgag 1740
gatgaggccg ctagaggcct gaggatgagc tggaaggagt gagaggggac aaaaccacc 1800
ttgttggagc ctgcagggtg gtgctgggac tgagccagtc ccaggggcat gtattggcct 1860
ggaggtgggg ttgggattgg gggctggtgc cagccttcct ctgcagctga cctctgttgt 1920
cctccccttg ggcggctgag agcccagct gacatggaaa tacagttgtt ggcctccggc 1980
ctcccctc 1988

<210> 129

<211> 385

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(385)

<223> 5' terminal sequence. insulin -like growth
factor 1 receptor (IGF1R) gene.

<400> 129

gtggcggcac tcattgttct cgggtgcacgc ccgcttccca cagtgcttg tggcacattt 60
tctggcagcg gtttgtggtc cagcagcggg agttgtactc at tgttgatg gtggtcttct 120
cacacatcgg cttctcctcc atggtccctg gacacaggtc cccacattcc tttgggggct 180
tattccccac aatgtagtta ttggacaccg catccaggat cagggaccag tccacagtng 240
agaggttaaca gaggtcagca tttttctcaa tcctgatggc cccccgagta atgttcctca 300
ggttgtaaag cccaatatcc ttgaggatgg gtcaatcttc gaaggatgaa ccaggggcnt 360
aggttnttg gaaggagntt ttcca 385

<210> 130

<211> 4989

<212> DNA/RNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(4989)

<223> insulin-like growth factor 1 receptor
(IGF1R) gene.

<400> 130

ttttttttt ttttgagaaa gggaatttca tccaaataa aaggaatgaa gtctggctcc 60
ggaggagggt cccgacctc gctgtggggg ctctgttct tctccggcg gctctcgctc 120
tggccgacga gtgga gaaat ctgcggggcca ggcacgaca tccgcaacga ctatcagcag 180
ctgaagcgcc tggagaactg cacgggtgatc gagggctacc tccacatcct gctcatctcc 240
aaggccgagg actaccgcag ctaccgcttc cccaagctca cggtcattac cgagtacttg 300
ctgctgttcc gagtggctgg cctcgagagc ctccggagacc tcttcccaa cctcagc gtc 360
atccgcggtt ggaaactctt ctacaactac gccctggtca tcttcgagat gaccaatctc 420
aaggatattg ggctttacaa cctgaggaaac attactcggg gggccatcag gattgagaaa 480
aatgctgacc tctgttacct ctccactgtg gactggtccc tgatcctgga tgcgggtgctc 540
aataactaca ttgtggggaa taagcccca aagga atgtg gggacctgtg tccagggacc 600

atggaggaga agccgatgtg tgagaagacc accatcaaca atgagtacaa ctaccgctgc 660
 tggaccacaa accgctgcca gaaaatgtgc ccaagcacgt gtgggaagcg ggcgtgcacc 720
 gagaacaatg agtgctgcca ccccgagtgc ctgggcagct gcagcgcgcc tgacaacgac 780
 acggcctgtg tagcttgccg ccactactac tatgccggtg tctgtgtgcc tgccctgccg 840
 cccaacacct acaggtttga gggctggcgc tgtgtggacc gtgacttctg cgccaacatc 900
 ctcaagcgcg agagcagcga ctccgagggg tttgtgatcc acgacggcga gtgcatgcag 960
 gagtgcacct cgggcttcat ccgcaacggc agccagagca tgtactgcat ccctt gtgaa 1020
 ggtccttgcc cgaaggtctg tgaggaagaa aagaaaaaa agaccattga ttctgttact 1080
 tctgtcaga tgcocaagg atgcaccatc ttcaagggca atttgctcat taacatccga 1140
 cgggggaata acattgcttc agagctggag aacttcatgg ggctcatcga ggtggtgacg 1200
 ggctacgtga agatccgcca ttctcatgcc ttgtctctt tgccttctt aaaaaacctt 1260
 cgcctcatcc taggagagga gcagctagaa ggaattact ctttctacgt cctcgacaac 1320
 cagaacttgc agcaactgtg ggactgggac caccgcaacc tgaccatcaa agcagggaaa 1380
 atgtactttg ctttcaatcc caaattatgt gtttccgaaa ttaccgcat ggaggagtg 1440
 acggggacta aaggcgcca aagcaaaggg gacataaaca ccaggaacaa cggggagaga 1500
 gcctcctgtg aaagtgcagc cctgcatttc acctccacca ccacgtcgaa gaatcgcatc 1560
 atcataacct ggcacgggta cgggccccct gactacaggg atctcatcag cttcaccgtt 1620
 tactacaagg aagcaccctt taagaatgtc acagagtatg atg ggcagga tgcctgcggc 1680
 tccaacagct ggaacatggt ggacgtggac ctcccgcca acaaggacgt ggagccggc 1740
 atcttactac atgggctgaa gccctggact cagtacgcg tttacgtcaa ggctgtgacc 1800
 ctaccatgg tgagaacga ccatatccgt ggggccaaaga gtgagatctt gtacattcgc 1860
 accaatgctt cagtctctt ccttcccttg gacgttctt cagcatcgaa ctctcttct 1920
 cagttaatcg tgaagtggaa cctccctct ctgcccaacg gcaacctgag ttactacatt 1980
 gtgcgtggc agcggcagcc tcaggacggc tacctttacc ggcacaatta ctgctccaaa 2040
 gacaaaatcc ccatcaggaa gtatgccgac ggcaccatcg acattgagga ggtcaca gag 2100
 aacccaaga ctgaggtgtg tgggtgggag aaagggcctt gctgcgcctg ccccaaaact 2160
 gaagccgaga agcaggccga gaaggaggag gctgaatacc gcaaagtctt tgagaatttc 2220
 ctgcacaact ccatcttctg gccagacct gaaaggaagc ggagagatgt catgcaagt 2280
 gccaaacca ccatgtccag ccgaagcagc aacaccagc cgttctttg agagcagagt ggataacaag 2340
 accgccccg aagagctgga gacagagtac ccttctttg agagcagagt ggataacaag 2400
 gagagaactg tcattttctaa ccttcggcct ttacattgt accgcatcga tatccacagc 2460
 tgcaaccacg aggtgagaa gctgggctgc agcgcctcca acttctctt tgcaaggact 2520
 atgccgcgag aaggagcaga tgacattcct gggccagtga cctgggagcc aaggcctgaa 2580
 aactccatct ttttaaagtg gccggaacct gagaatccca atggattgat tctaattgat 2640
 gaaataaaat acggtacaca agttgaggat cagcgagaat gtgtgtccag acaggaatac 2700
 aggaagtatg gaggggccaa gctaaaccgg ctacaccgg ggaac tacac agcccgatt 2760
 caggccacat ctctctctg gaattggctg tggacagatc ctgtgttctt ctatgtccag 2820
 gccaaaacag gatataaaaa cttcatccat ctgatcatcg ctctgccgt cgtgtcctg 2880
 ttgatcgtg gagggttggt gattatgctg tacgtcttcc atagaaagag aaataacagc 2940
 aggtcgggga atggagtgt gtatgcctct gtaaccgg agtacttcag cgtgtctgat 3000
 gtgtacgttc ctgatgagt ggaggtggct cgggagaaga tcaccatgag ccgggaactt 3060
 gggcaggggt cgtttgggt ggtctatgaa ggggttgcca aggtgtggt gaaagatgaa 3120
 cctgaaacca gagtggccat taaaacagt aacgagccg caagcatgag tgagaggat t 3180
 gagtttctca acgaagcttc tgtgatgaag gagttcaatt gtcaccatgt ggtgcgattg 3240
 ctgggtgtgg tgcaccaagg ccagccaaca ctggtcatca tggaaactgat gacacggggc 3300
 gatctcaaaa gttatctccg gtctctgagg ccagaaatgg agaataatcc agtcctagca 3360
 cctccaagcc tgagcaagat gatccagatg gcc ggagaga ttgcagacgg catggcatac 3420
 ctcaacgcca ataagttcgt ccacagagac cttgtgccc ggaattgcat ggtagccgaa 3480
 gatttcacag tcaaaatcgg agattttggt atgacgcgag atatctatga gacagactat 3540
 taccggaaag gaggcaaagg gctgctgccc gtgcgctgga tgtctcctga gtccctcaag 3600
 gatggagtct tcaccactta ctcggaagtc tggctcttgc gggctcgtct ctgggagatc 3660
 gccacactgg ccgagcagcc ctaccagggc ttgtccaaag agcaagtctt tcgcttcgtc 3720
 atggagggcg gcctctgga caagccagac aactgtcctg acatgctgtt tgaactgatg 3780
 cgcatgtgct ggcagtataa cccaagatg aggccttctt tcttga gat catcagcagc 3840
 atcaaaagg agatggagcc tggtctccg gaggtctct tctactacag cgaggagaa 3900
 aagctgcggc agccggagga gctggacctg gcgccagaga acatggagag cgtccctctg 3960
 gacctcggc cctcctgctc ctccctgcca ctcccgaca gacactcagg acacaaggcc 4020
 gagaacggcc cgggccctg ggtgctggtc ctccgcgcca gcttcgacga gagacagcct 4080
 tacgcccaca tgaacggggg ccgcaagaac gagcgggctt tgccgctgcc ccagtcttgc 4140
 acctgtgat ccttgatcc tgaatctgtg caaacagtaa cgtgtgcgca cgcgcagcgg 4200
 ggtggggggg gagagagagt ttaacaatc cattacaag cctcctgtac ctcatggat 4260

87/292

```

cttcagttct gcccttgctg cccgcgggag acagcttctc tgcagtaaaa cacatttggg 4320
atgttccttt tttcaatatg caagcagctt tttattccct gcccaaacc ttaactgaca 4380
tgggccttta agaaccttaa tgacaacact taatagcaac agagcacttg agaaccagtc 4440
tcctcactct gtccctgtcc ttccctgttc tccct ttctc tctcctctct gcttcataac 4500
ggaaaaataa ttgccacaag tccagctggg aagccctttt tatcagtttg aggaagtggc 4560
tgtccctgtg gccccatcca accactgtac acaccgcct gacaccgtgg gtcattacaa 4620
aaaaacacgt ggagatggaa atttttacct ttatctttca cttttctagg gacatgaaat 4680
ttacaaaggy ccatcgttca tccaagctg ttaccatttt aacgctgcct aattttgcca 4740
aaatcctgaa cttttctccct catcggccg gcgctgattc ctcgtgtccg gaggcattgg 4800
tgagcatggc agctggttgc tccatttgag agacacgctg gcgacacact cgtccatcc 4860
gactgcccct gctgtgtgc tcaaggccac aggcacacag gtctcattg c ttctgactag 4920
attattattt gggggaactg gacacaatag gtctttctct cagtgaaggt ggggagaagc 4980
tgaaccggc                                     4989

```

<210> 131

<211> 470

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(470)

<223> 5' terminal sequence. insulin receptor
(INSR) gene.

<400> 131

```

gggcaacaat ctggcagctg agctagaagc caacctcggc ctcatgaag aaatttcagg 60
gtatctaaaa atccgccgat cctacgctct ggtgtcactt tccttc ttcc ggaagttacg 120
tctgattcga ggagagacct tggaattng gaactactcc ttctatgcct tggacaacca 180
gaacctaaag cagctctggg actggagcaa acacaacctc accatcactc aggggaaact 240
cttcttcac tataaccoca aactctgctt gtcagaaatc cacaagatgg gaaggaaatt 300
tcagggaacc aaggggncgc cagg aggaga aacgacattt nccctggaag gaccaatggg 360
gggaccaggg catcctgtgg aaaaatggag tttactttaa anttttgctt taacattngg 420
gacntttttt tggacaagtt ttttgttgaa gttggggagc cctnattttg 470

```

<210> 132

<211> 4691

<212> DNA/RNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(4691)

<223> insulin receptor (INSR) gene.

<400> 132

```

gagaaggacg cgcgccccc agcgtctctg ggggcgcct cggagcatga ccccgcggg 60
ccagcgccgc gcgcctgatc cgaggagacc ccgcgtccc gcagc catgg gcaccggggg 120
ccggcggggg gcggcgccg cgccgtgct ggtggcgtg gccgcgtgc tactggggcg 180
cgcgggccac ctgtacccc gagaggtgtg tcccgcatg gatatccga acaacctcac 240
taggttgcat gagctggaga attgctctgt catcgaagga cacttcaga tactcttgat 300
gttcaaaacg agggccgaag att tccgaga cctcagtttc cccaaactca tcatgatcac 360
tgattacttg ctgctcttcc gggctatgg gctcgagagc ctgaaggacc tgtccccaa 420

```


cctcacggtc atccggggat cagcactgtt ctttaactac gcgctggcca tcttcgagat 480
 gggtcacctc aaggaaactcg gcctctacaa cctgatgaac atcacccggg gttctgtccg 540
 catcgagaag aacaatgagc tctgttactt ggccactatc gactgggtccc gtatcctgga 600
 ttccgtggag gataatcaca tcgtgttgaa caaagatgac aacgaggagt gtggagacat 660
 ctgtccgggt accgcgaagg gcaagaccaa ctgccccgcc accgtcatca acgggcagtt 720
 tgtcgaaacga tgttgactc atagtcaactg ccagaaagtt tgc ccgacca tctgtaagtc 780
 acacggctgc accgcgaag gcctctgttg ccacagcgag tgccctgggca actgttctca 840
 gcccagcacg cccaccaagt gcgtggcctg ccgcaacttc tacctggacg gcagggtgtg 900
 ggagacctgc ccgccccgt actaccactt ccaggactgg cgctgtgtga acttcagctt 960
 ctgccaggac ctgcaccaca a atgcaagaa ctgcggaggg cagggtgcc accaatacgt 1020
 cattcacaac aacaagtga tccctgagt tccctccggg tacacgatga attccagcaa 1080
 cttgctgtgc acccatgcc tgggtccctg tcccaagggtg tgccacctcc tagaaggcga 1140
 gaagaccatc gactcgggtga cgtctgcccc ggagctccga ggatgcaccg tcatcaacgg 1200
 gagtctgac atcaacattc gaggaggcaa caatctggca gctgagctag aagccaacct 1260
 cggcctcatt aagaaattt cagggtatct aaaaatccgc cgatcctacg ctctgggtgc 1320
 actttccttc ttccggaaagt tacgtctgat tgcaggagag accttgaaa ttgggaacta 1380
 ctcttctat gccttggaac accagaacct aaggc agctc tgggactgga gcaaacacaa 1440
 cctcaccacc actcagggga aactcttctt ccactataac cccaaactct gcttgtcaga 1500
 aatccacaag atggaagaag tttcagggaac caaggggccc caggagagaa acgacattgc 1560
 cctgaagacc aatggggaca aggcacccctg tgaaaatgag ttacttaaat tttcttacat 1620
 tcggacatct tttgacaaga tcttctgag atgggagccg tactggcccc ccgacttccg 1680
 agacctcttg gggttcagtc tgttctacaa agaggccctt tatcagaatg tgacggagtt 1740
 cgatgggcag gatcgctgtg ttccaacag ttggacgggtg gtagacattg acccaccct 1800
 gaggtccaac gaccccaaat cacagaacca cccagggtgg ctgatgcgg g gtctcaagcc 1860
 ctggaccacg tatgccatct ttgtgaagac cctggtcacc ttttcggatg aacgccggac 1920
 ctatggggcc aagagtgaac tcatctatgt ccagacagat gccaccaacc cctctgtgcc 1980
 cctggtacca atctcagtg ctaactcatc atcccagatt attctgaagt ggaaaccacc 2040
 ctccgacccc aatggcaaca tca cccacta cctggttttc tgggagaggc aggcggaaga 2100
 cagtgaagctg ttccagctgg attattgcct caaagggtg aagctgcct cgaggacctg 2160
 gtctccacca ttccagctcg aagattctca gaagcacaac cagagtgaat atgaggattc 2220
 ggccggcgaa tgctgctct gtccaaagac agactctcag atcctgaagg agctggagga 2280
 gtccctcgtt aggaagacgt ttgaggatta cctgcacaac gtggttttcg tcccagaaa 2340
 aacctctca ggactgggtg ccgaggaccc taggccatct cggaaacgca ggtcccttg 2400
 cgatgttggg aatgtgacgg tgcccggtgc caggtggca gctttcccca acacttctc 2460
 gaccagcgtg ccacagagtc cggaggagca caggcct ttt gagaaggtg tgaacaagga 2520
 gtccgtggtc atctccgct tgcgacactt cagggtctat cgcacgagc tgcaggcttg 2580
 caaccaggac acccctgagg aacgggtgcag tgtggcagcc tacgtcagtg cgaggacct 2640
 gcctgaagcc aagcgtgatg acattgttg cctgtgacg catgaaatct ttgagaacaa 2700
 cgctgctcac ttgatgtggc aggagccgaa ggagcccaat ggtctgatcg tgctgtatga 2760
 agtgagttat cggcgatatg gtgatgagga gctgcattc tgctctccc gcaagcactt 2820
 cgctctgga cggggtgcga ggctgcgtg gctgtcaccg gggaaactaca gcgtgcgaat 2880
 ccgggcctac tcccttgccg gcaacggctc ttggacggaa ccacactatt tctacgtgac 2940
 agactattta gacgtcccg caaatattgc aaaaattatc atcgccccc tcatcttctg 3000
 ctttctcttc agtgtgtga ttggaagtat ttatctatc ctgagaaaga ggcagccaga 3060
 tgggcccgtg ggaccgctt acgcttcttc aaacctgag tatctcagtg ccagtgtgt 3120
 gtttccatgc tctgtgtacg tgccg gacga gtgggagggtg tctcgagaga agatcaccct 3180
 ccttcgagag ctggggcagg gctccttcg catggtgtat gagggcaatg ccagggacat 3240
 catcaagggt gaggcagaga cccgcgtggc ggtgaagacg gtcaacgagt cagccagtct 3300
 ccgagagcgg attgagttcc tcaatgaggc ctccgtcatg aagggttca cctgccatca 3360
 cgtggtgcgc ctccgtggag tgggtgtccaa gggccagccc acgctggtg tgatggagct 3420
 gatggctcac ggagacctga agagctacct ccgttctctg cggccagagg ctgagaataa 3480
 tccctggcgc cctcccccta ccttcaaga gatgattcag atggcgccag agattgtctga 3540
 cgggatggcc taactgaacg ccaagaagtt tgtgcacg g gacctggcag cgagaaactg 3600
 catggtcgcc catgatttta ctgtcaaaat tggagacttt ggaatgacca gagacatcta 3660
 tgaacggat tactaccgga aagggggcaa gggctgtctc cctgtacggt ggatggcacc 3720
 ggagtccctg aaggatggg tcttcaccac ttctctgac atgtggtcct ttggcgtggt 3780
 ccttgggaa atc accagct tggcagaaca gccttaccaa ggctgtcta atgaacaggt 3840
 gttgaaattt gtcatggatg gaggggtatct ggatcaaccc gacaactgtc cagagagagt 3900
 cactgacctc atgcgcatgt gctggcaatt caaccccaag atgaggccaa ccttccctgga 3960
 gattgtcaac ctgctcaagg acgacctgca cccagcttt ccagaggtgt cg ttcttcca 4020
 cagcaggagg aacaaggctc ccgagagtga ggagctggag atggagtttg aggacatgga 4080

89/292

```

gaatgtgcc ctggaccgtt cctcgcactg tcagagggag gaggcggggg gccgggatgg 4140
agggctcctcg ctgggtttca agcggagcta cgaggaacac atcccttaca cacacatgaa 4200
cggaggcaag aaaaacgggc ggattct gac ctgacctcg tccaatcctt cctaacagtg 4260
cctaccgtgg cgggggcggg caggggttcc cattttcgct ttctcttggt ttgaaagcct 4320
ctggaaaact caggattctc acgactctac catgtccagt ggagttcaga gatcgttcct 4380
atacatttct gttcatctta aggtggactc gtttggttac caatttaact agtcctgcag 4440
aggatttaac tgtgaacctg gagggcaagg ggtttccaca gttgctgctc ctttggggca 4500
acgacggttt caaaccagga ttttggtttt ttctggtccc cccacccgcc ccagcagat 4560
ggaaagaaag cacctgtttt taaaaattct tttttttttt tttttttttt tttttttgct 4620
ggtgtctgag cttcagtata aaagacaaaa cttcctgttt gtggaacaaa atttcgaaag 4680
aaaaaaccaa a                                     4691

```

<210> 133

<211> 451

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(451)

<223> 5' terminal sequence. forkhead box ola
(rhabdomyosarcoma) (FOXO1A) gene.

<400> 133

```

naaggagtgt ctgactttct actctcctcc ccataatgac attatgacac cagttgatcc 60
tggggtagcc cagcccaaca gccgggttct gggccagaac gtcattgatg gccctaattc 120
ggtcatgtca acctatggca gccaggcatc tcataacaaa atgatgaatc ccagctccca 180
taccacccct ggnacatgct cagcagacat ctgcagttaa cgggcgtccc ctgcccaca 240
cggtaagcac catgcccac acctcgggta tgaaccgcct gaccaagtg aagacacctg 300
tacaagtgcc tcttggccca ccccatggca gatgagtgcc tgggggggtt aacttccttc 3 60
cgtgaggcag ctggcaatgg gttatgggca ggatggggcc tttttccacc aggagaagct 420
tcccaagtgt attttggatg ggctttttt t                                     451

```

<210> 134

<211> 5723

<212> DNA/RNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(5723)

<223> forkhead box ola (rhabdomyosarcoma) (FOXO1A)
gene.

<400> 134

```

gcagccgcca cattcaacag gcagcagcgc agcgggcgcg ccgctgggga gagcaagcgg 60
cccgcggcgt ccgtccgtcc ttccgtccgc ggccctgtca gctggagcgc ggcgcag gct 120
ctgccccggc ccggcggtc tggccggccg tccagtccgt gcggcgacc ccgaggagcc 180
tcgatgtgga tgccccgcg aagttaagtt ctgggctcgc gcttccactc cgcgcgcct 240
tctcccagt ttccgtccgc tcgcccacc ggcttcgttc ccccaaatct cggaccgtcc 300
cttcgcgcc cctcccgcgc cgcgccagc gctgc gttct cccctctttg gctctcctgc 360
ggctggggga ggggcggggg tcaccatggc cgaggcgcc caggtggtgg agatcgacc 420
ggacttcgag ccgtgcccc ggccgcgctc gtgcacctgg ccgctgcca ggccggagtt 480

```

tagccagtc aactcggcca cctccagccc ggcgcgcgcg ggcagcgcgcg ctgccaaccc 540
cgacgcgcgcg gcg ggcctgc cctcggcctc ggcgcgcgcg gtcagcgcgcg acttcatgag 600
caacctgagc ttgtcggagg agagcggagg cttcccgcag gcgcccggct ccgtggcggc 660
ggcgggtggc gcggcggccg ccgcggcgcg caccgggggg ctgtgcgggg acttccaggg 720
cccggaggcg ggcgcgcctgc acccagcgcg acccagcgcg ccgcccggcg ggccg ctgtc 780
gcagcaccgc ccgtgcgcgc ccgcgcgcgc tgggcgcgcg gcggggcagc cgcgcaagag 840
cagctcgtcc cgcgcgaacg cgtggggcaa cctgtcctac gccgacctca tcaccaaggc 900
catcgagagc tcggcggaga agcggctcac gctgtgcgag atctacgagt ggatggtcaa 960
gagcgtgccc tacttcaagg ataagggtga cag caacagc tcggcgggct ggaagaattc 1020
aattcgtcat aattcgtccc tacacagcaa gttcattcgt gtgcagaatg aaggaaactg 1080
aaaaagttct tgggtggatgc tcaatccaga ggggtggcaag agcgggaaat ctccataggag 1140
aagagctgca tccatggaga acaacagtaa atttgctaag agccgaagcc gagctgcca 1200
taagaaagca tctctccagt ctggccagga ggggtgctggg gacagccctg gatcacagt 1260
ttccaaatgg cctgcgaacc ctggcctcga cagcaatgat gactttgata actggagtac 1320
atttcgcctc cgaactagct caaatgctag tactattagt gggagactct caccattat 1380
gaccgaacag gatgatcttg gagaagggga tgtgcattct atggtgt acc cgcctctgc 1440
cgcaagatg gcctctactt taccagctct gtctgagata agcaatcccg aaaacatgga 1500
aaatcttttg gataatctca acctctctc atcaccaaca tcattaactg tttcgacca 1560
gtctcacct ggcaacctga tgcagcagc gccgtgctac tcgtttgcgc caccaaacac 1620
cagtttgaat tcacccagcc c aaactacca taaatataca tatggccaat ccagcatgag 1680
ccctttgccc cagatgccta tacaacact tcaggacaat aagtcgagtt atggaggtat 1740
gagtcagtat aactgtgcgc ctggaactct gaaggagttg ctgactctg actctcctc 1800
ccataatgac attatgacac cagttgatcc tggggtagcc cagcccaaca gccgggttct 1860
gggcagagac gtcatgatgg gccctaattc ggtcatgtca acctatggca gccaggcatc 1920
tcataacaaa atgatgaatc ccagctccca taccaccct ggacatgctc agcagacatc 1980
tgcagttaac ggcgcgcctc tgcgccacac ggtaagcacc atgcccaca cctcgggtat 2040
gaaccgcctg aaccaagtga agacacctgt acaag tgcct ctgcccacc ccatgcagat 2100
gagtgccctg ggggctact cctccgtgag cagctgcaat ggctatggca gaatgggct 2160
tctccaccag gagaagctcc caagtgaact ggatggcatg ttcattgagc gcttagactg 2220
tgacatggaa tccatcattc ggaatgacct catggatgga gatacattgg attttaactt 2280
tgacaatgtg ttgcccaccc aaagcttccc acacagtgct aagacaacga cacatagctg 2340
gggtgcaggc tgagggttag tgagcagggt acacttaaaa gtacttcaga ttgtctgaca 2400
gcaggaactg agagaagcag tccaaagatg tctttacca actccctttt agttttcttg 2460
gttaaaaaaa aaaaacaaaa aaaaaaccct ccttttttc ctttctca g acttggcagc 2520
aaagacattt ttcctgtaca ggatgtttgc ccaatgtgtg caggttatgt gctgctgtg 2580
ataaggactg tgccattgga aatttcatta caatgaagt ccaaactcac tacaccatat 2640
aattgcagaa aagattttca gatcctgggt tgctttcaag ttttgtatat aagcagtaga 2700
tacagattgt atttgtgtgt gtt tttgggt tttctaaata tccaattggt ccaaggaaag 2760
tttatactct ttttgtataa ctgtgatggg cctcatgtct tgataagta aactttgtt 2820
tgtactacct gtttctgcg gaactgacgg atcacaaaga actgaatctc cattctgcat 2880
ctccattgaa gcgccttgga cctgttcacg ttgccacaga attcacatga gaaccaagta 29 40
gcctgttacc aatctgctaa attaatggac ttgttaaaact tttggaaaaa aaaagattaa 3000
atgccagctt tgtacagggtc ttttctattt tttttgttt attttgttat ttgcaaat 3060
gtacaaacat ttaaattggt ctaatttcca gataaatgat ttttgatgtt attgttggga 3120
cttaagaaca tttttggaat agatattgaa ctgtaat aat gttttcttaa aactagagtc 3180
tactttgtta catagtcagc ttgtaaattt tgtggaacca caggatattg gggcagcatt 3240
cataatttct attttgtatt ctaactggat tagtactaat tttatacatg ctttaactggt 3300
ttgtacactt tgggatgcta cttagtgtg tttctgacta atcttaaatc attgtaatta 3360
gtacttgcac attcaacggt tcaggccctg gttgggcagg aaagtgtgt atagtattg 3420
acactttgcg tttcttattt aggataactt aatatgttt tatgtatgta ttttaagaa 3480
atttcatctg cttctactga actatgcgta ctgcatagca tcaagtctc tctagagacc 3540
tctgtagtcc tgggaggcct cataatgttt gtagatcaga aaaggagat ctgcatctaa 3600
agcaatggc ctttgcctaa cgagggattt tgatccactt caccattttg agttgagctt 3660
tagcaaaagt tccctctat aattccttgc tcttgttca gtccaggtgg aggttgggtt 3720
tgtagtctg ccttgaggaa ttatgtcaac actcatactt catctcattc tccctctgc 3780
cctgcagatt agattactta gcaca ctgtg gaagtttaag tgggaaggag gaatttaaaa 3840
atgggacttg agtggtttgt agaatttgt ttcataagtt cagatgggtg gcaaatggaa 3900
tagaacttac ttaaaaattg gggagattta tttgaaaacc agctgtaagt tgtgcattga 3960
gattatgtta aaagccttg cttaagaatt tgaaaatttc tttagcctgt agcaacctaa 4020
actgtaattc ctatcattat gttttattac tttccaatta cctgtaactg acagaccaa 4080
ttaattggct ttgtgtccta tttagtcct cagtattttc aagtcagtg gaaagcccaa 4140

agtcatacaca atgaagagaa caggtgcaca gcaactgttcc tcttgtgttc ttgagaagga 4200
tctaattttt ctgtatatag cccacatcac acttgcttt g tcttgtatgt taattgcac 4260
ttcattggct tggatattcc taaatgttta acaagaacac aagtgttcc gataagattt 4320
cctacagtaa gccagctgta ttgtaagctt cccaccgtga tgatcatttt tttgaagatt 4380
cattgaacag ccaccactct atcatcctca ttttggggca gtccaagaca tagctgggtt 4440
tagaaaccca agt tctctcta agcacagcct cccgggtatg taactgaact tgggtccaaa 4500
gtacttgtgt actaatttct attactacgt actgtcactt tcctcccggt ccattactgc 4560
atcataatac aaggaacctc agagccccc tttgttcatt aaagaggcaa ctacagccaa 4620
aatcactgtt aaaatcttac tacttcatgg agtagctctt aggaaaatat at ctctctcc 4680
tgagtctggg taattatacc tctcccaagc cccattgtg tgttgaaatc ctgtcatgaa 4740
tccttggtag ctctctgaga acagtgaagt ccagggaag gcactctggtc tgtctggaaa 4800
gcaaacatta tgtggcctct ggtagtttt ttctgtgaag aatactgact ttctggagta 4860
atgagtatat atcagttatt gtacatg att gctttgtgaa atgtgcaa at gatcacct 4920
atgcagcctt gtttgattta ttttctctgg tttgtactgt tattaanaagc atattgtatt 4980
atagagctat tcagatatat taaatataaa gatgtattgt ttccgtaata tagacgtatg 5040
gaatatattt aggtaataga tgtattactt ggaaggttct gctttgacaa actgacaaa 5100
tctaaatgag cacatgtatc ccagtgcga gtaaatcaat ggaacatccc aagaagagga 5160
taaggatgct taaaatggaa atcattctcc aacgatatac aaattggact tgttcaactg 5220
ctggatatat gctaccaata accccagccc caacttaaaa ttcttacatt caagctccta 5280
agagttctta atttataact aattttaaaa gagaagtttc ttttctggtt ttagtttggg 5340
aataatcatt cattaataaaa atgtattgt ggtttatgcg aacagaccaa cctggcatta 5400
cagttggcct ctcttgagg tgggcacagc ctggcagtggt ggccaggggt ggccatgta 5460
gtcccatcag gacgtatgca tgcctctgc atttctgac ccgagtttag taacagtga 5520
gattccacgt tcttg tctcg atactctgag aagtgccctga tgtgatgta ctacagaca 5580
caagaacaat ctttgcata attgtataaa gccataaatg tacataaatt atgtttaaat 5640
ggcttgggtg ctttctttt taattatgca gaataagctc tttattagga atttttgtg 5700
aagctattaa atacttgagt taa 5723

<210> 135

<211> 466

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(466)

<223> 3' terminal sequence. epidermal growth
factor receptor (avian erythroblasti c leukemia
viral (v-erb-b) oncogene homolog) (EGFR) gene.

<400> 135

tcaaatatac cntttgaaa gataaatttc tgctcaaagg gacaatattc ttgctggatg 60
cgtttctgta aatgcttcac agtttgaaga caaaggaatg caactccca aaatgtgcc 120
gaggtggaag tacttctctg ctagtccgtg taaacgt tgc aaaaccagtc tgtgggtcta 180
agagctaattg cngcatggc tgttgggatg gaggacctgc tgtggcttgg tctgggtat 240
cgaaagagtc tggattttta gggctcatac tatcctccgt ggtcatgctc caataaattc 300
actgctttgt ggcgcgaccc ttaggtattc tgcattttca gctntggagc ccttaaagat 360
gccatttggc ttggccttcc ttgggaaaga agtcctgctg gtagtcaggg ttttccaggg 420
taatttgggtg gctgcctttt ctgggccag tnggaggggc ttttgc 466

<210> 136

<211> 450

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(450)

<223> 5' terminal sequence. epidermal growth
factor receptor (avian erythroblastic leukemia
viral (v-erb-b) oncogene homolog) (EGFR) gene.

<400> 136

```
cgctcctngaa tggatgaaga agacatggac gacgtggtgg atgccgacga gtacctcatc 6 0
ccacagcagg gcttcttcag cagccccctcc acgtcacgga ctccccctct gagctctctg 120
agtgaacca gcaacaattc caccgtggct tgcattgata gaaatgggct gcaaagtgtc 180
ccatcaagga agacagcttc ttgcagcgat acagctcaga cccacaggc gccttgactg 240
aggacagcat agacgacacc ttctctccag tgcctgaata cataaaccag tccgttcca 300
aaaggccgcg tggcttctgt gcagaatcct gttctattca caattcagcc ttttgaaccc 360
cggcggccca gcaggaggac ccacacttac cagggacccc cacaggcant gcagtggggc 420
aaccgcgagt ttttcaaca ttgttccagt 450
```

<210> 137

<211> 5532

<212> DNA/RNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(5532)

<223> epidermal growth factor receptor (avian
erythroblastic leukemia viral (v-erb-b) oncogene
homolog) (EGFR) gene.

<400> 137

```
gccgcgctgc gccggagtcc cgagctagcc cggcgccgc cgccgccag accggacgac 60
aggccacctc gtcggcgctcc gcccgagtcc ccgcctcgcc gccaacgcca caaccaccgc 120
gcacggcccc ctgactccgt ccagtattga tcgggagagc cggagcgagc tcttcgggga 180
gcagcgatgc gacctc cgg gacggccggg gcagcgctcc tggcgctgct ggctgcgctc 240
tgcccgcgca gtcgggctct ggaggaaaag aaagtttgcc aaggcacgag taacaagctc 300
acgcagttgg gcatctttga agatcatttt ctacgcctcc agaggatgtt caataactgt 360
gagtggtgcc ttgggaattt ggaaattacc tatgtgcaga ggaattatga tcttccct c 420
ttaagacca tccaggaggt ggctgggtat gtctcattg cctcaacac agtggagcga 480
attcctttgg aaaacctgca gatcatcaga ggaaatatgt actacgaaa ttctatgcc 540
ttagcagctc tatctaacta tgatgcaaat aaaaccggac tgaaggagct gcccatgaga 600
aatttacagg aaatcctgca tggcgccgtg cggttca gca acaacctgc cctgtgcaac 660
gtggagagca tccagtgccg ggacatagtc agcagtgact ttctcagcaa catgtcgatg 720
gacttccaga accacctggg cagctgccaa aagtgtgac caagctgtcc caatgggagc 780
tgctggggtg caggagagga gaactgccag aaactgacca aaatcatctg tgcccagcag 840
tgctccgggc gctgc cgtgg caagtccccc agtgactgct gccacaacca gtgtgctgca 900
ggctgcacag gccccggga gagcgactgc ctggtctgcc gcaaattccg agacgaagcc 960
acgtgcaagg acacctgccc cccactcatg ctctacaacc ccaccacgta ccagatggat 1020
gtgaacccc agggcaaata cagctttggt gccacctgcy tgaagaagtg tccccg taat 1080
tatgtgtgta cagatcacgg ctgctgcgtc cgagcctgtg gggccgacag ctatgagatg 1140
gaggaagacg gcgtccgcaa gtgtaagaag tgogaagggc cttgccgcaa agtgtgtaac 1200
ggaataggta ttggtgaatt taaagactca ctctccataa atgctacgaa tattaacac 1260
ttcaaaaact gcacctccat cagtggcgat ctccacatcc tgccggtggc atttaggggt 1320
gactccttca cacatactcc tcctctggat ccacaggaaac tggatattct gaaaaccgta 1380
aaggaaatca cagggttttt gctgattcag gcttggcctg aaaacaggac ggacctccat 1440
gcctttgaga acctagaaat catacgcggc aggaccaagc aacatggtca gttttctctt 1500
```

gcagtcgtca gcctgaacat aacatccttg ggattacgct ccctcaagga gataagtgat 1560
ggagatgtga taatttcagg aaacaaaaat ttgtgctatg caaatacaat aaactggaaa 1620
aaactgtttg ggacctccgg tcagaaaacc aaaattataa gcaacagagg tgaaaacagc 1680
tgcaaggcca caggccaggt ctgccatgcc ttgtgctccc ccga gggctg ctggggcccg 1740
gagcccaggg actgcgtctc ttgccggaat gtcagccgag gcagggaatg cgtggacaag 1800
tgcaagcttc tggagggtga gccaaaggag tttgtggaga actctgagtg catacagtgc 1860
caccagagt gcctgcctca ggccatgaac atcacctgca caggacgggg accagacaac 1920
tgtatccagt gtgcccact a cattgacggc ccccactgcg tcaagacctg cccggcagga 1980
gtcatgggag aaaacaacac cctggtcttg aagtacgcag acgccggcca tgtgtgccac 2040
ctgtgccatc caaactgcac ctacggatgc actgggccag gtcttgaagg ctgtccaacg 2100
aatgggcta agatcccgtc catcgccact gggatggttg gggccctcct cttgctgc tg 2160
gtggtggccc tgggagtcgg cctcttcatt cgaaggcgcc acatcgttcg gaagcgacg 2220
ctgcccaggc tgcgcagga gagggagctt gtggagcctc ttacaccagc tggagaagct 2280
cccaaccaag ctctcttgag gatcttgaag gaaactgaat tcaaaaagat caaagtgtctg 2340
ggctccggtg cgttcggcac ggtgtataag gg actctgga tcccagaagg tgagaaagtt 2400
aaaattcccg tcgtatatca ggaattaaaga gaagcaacat ctccgaaagc caacaaggaa 2460
atcctcgatg aagcctacgt gatggccagc gtggacaacc ccacagtgtg ccgctgtctg 2520
ggcatctgcc tcacctccac cgtgcaactc atcacgcagc tcatgccctt cggtgcctc 2580
ctggactatg tccgggaaca caaagacaat attggctccc agtacctgtc caactggtgt 2640
gtgcagatcg caaagggcac gaactacttg gaggaccgtc gcttggtgca ccgcgacctg 2700
gcagccagga acgtactggt gaaaacaccg cagcatgtca agatcacaga ttttgggctg 2760
gccaaactgc tgggtgcgga agagaaagaa taccatgcag aaggag gcaa agtgcctatc 2820
aagtggatgg cattggaatc aattttacac aatatctata ccaccagag tgatgtctgg 2880
agctacgggg tgaccgtttg ggagttgatg acctttggat ccaagccata tgacggaatc 2940
cctgccagcg agatctctc catcctggag aaaggagaac gcctccctca gccaccata 3000
tgtaccatcg atgtctacat gatcatggtc aagtgtctga tgatagacgc agatagtgc 3060
ccaaagttcc gtgagttgat catcgaattc tccaaaatgg cccgagaccc ccagcgctac 3120
cttgcctatc agggggatga aagaatgcac ttgccaaagc ctacagactc caactctac 3180
cgtgccctga tggatgaaga agacatggac gacgtggtg atgccgacga gtacctcact 3240
ccacagcagg gcttcttcag cagccctcc acgtcacgga ctccctcct gagctctctg 3300
agtgaacca gcaacaattc caccgtggct tgcattgata gaaatgggct gcaaagctgt 3360
cccatcaagg aagacagctt ctgcagcga tacagctcag accccacagg cgccttgact 3420
gaggacagca tagacgacac ctctctccca gtgc ctgaat acataaacca gtccgttccc 3480
aaaaggcccg ctggctctgt gcagaatcct gtctatcaca atcagcctct gaaccccgcg 3540
cccagcagag acccacacta ccaggacccc cagtgggcaa ccccgagtat 3600
ctcaacactg tccagccac ctgtgtcaac agcacattcg acagccctgc ccactgggccc 3660
cagaaaggca gccaccaaat tagcctggac aaccctgact accagcagga cttctttccc 3720
aaggaaagca agccaaatgg catctttaag ggctccacag ctgaaaatgc agaataccta 3780
agggtcgcgc cacaagcag tgaatttatt ggagcatgac cacggaggat agtatgagcc 3840
ctaaaaatcc agactctttc gataccagg accaagccac agcaggtc ct ccatcccaac 3900
agccatgcc gcttagctc tttagccac agactggtt tgcaacgttt acaccgacta 3960
gccaggaagt acttccacct cgggcacatt ttgggaagtt gcattccttt gtcttcaaac 4020
tgtgaagcat ttacagaaac gcatccagca agaatttgt cctttgagc agaaatttat 4080
ctttcaaga ggtatattt aa aaaaaaa aaaaagtata tgtgaggatt tttattgatt 4140
gggatcttg gagtttttca ttgtcgctat tgatttttac ttcaatggg tcttccaaca 4200
aggaagaagc ttgctggtag cacttgctac cctgagttca tccaggccca actgtgagca 4260
aggagcacia gccacaagtc ttccagagga tgcttgattc cagtggttct gcttcaaggc 4320
ttccactgca aaacactaaa gatccaagaa ggccttcag gccccagcag gccggatcgg 4380
tactgtatca agtcatggca ggtacagtag gataagccac tctgtccctt cctgggcaaa 4440
gaagaaacgg aggggatgaa ttcttcttga gacttacttt tgtaaaaatg tccccacggt 4500
acttactccc cactgatgga ccagtgggtt ccagtc atga gcgttagact gacttgtttg 4560
tcttccattc cattgttttg aaactcagta tgccgcccct gtcttgctgt catgaaatca 4620
gcaagagagg atgacacatc aaataataac tcggattcca gccacattg gattcatcag 4680
catttggacc aatagcccac agctgagaat gtggaatacc taaggataac accgcttttg 4740
ttctcgcaaa aacgtatctc ctaatttgag gctcagatga aatgcacag gtcctttggg 4800
gcatagatca gaagactaca aaaatgaagc tgctctgaaa tctcctttag ccatcacc 4860
aaccocccaa aattagtttg tgttacttat ggaagatagt tttctccttt tacttcaact 4920
caaaagcttt ttactcaaag agtatatgtt ccctccaggt cagctgcccc caaacccct 4980
ccttacgctt tgtcacacaa aaagtgtctc tgccttgagt catctattca agcacttaca 5040
gctctggcca caacagggca ttttacaggt gcgaatgaca gtagcattat gagttagtg 5100
aattcaggta gtaaatatga aactagggtt tgaaattgat aatgctttca caacatttgc 5160

94/292

agatgtttta gaaggaaaaa agtt ccttcc taaaataatt tctctacaat tggaagattg 5220
gaagattcag ctagttagga gccattttt tcctaactctg tgtgtgccct gtaacctgac 5280
tggttaacag cagtcctttg taaacagtgt tttaaactct cctagtcaat atccacccca 5340
tccaatttat caaggaagaa atggttcaga aaatattttc agcctacagt tatgttcagt 540 0
cacacacaca tacaaaatgt tccttttgct tttaaagtaa tttttgactc ccagatcagt 5460
cagagccoct acagcattgt taagaaagta tttgattttt gtctcaatga aaataaaaact 5520
atattcattt cc 5532

<210> 138

<211> 378

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(378)

<223> 3' terminal sequence. tek tyrosine kinase,
endothelial (venous malformations, multiple
cutaneous and mucosal) (TEK) gene.

<400> 138

ggatnagant ttanaggcaa gacatttatt cactcatgat atatcagtgc aaagtgtgcc 60
tacagtatac aaggtaaact cacaactcat caaaactaaa actttttaca atgtgcaata 120
catgtaggga tattaattca atatataaat gtcacatgtc tcccaaatgt caccaggt 180
ttctgttatt tcttaaaata tacaagtcaa t attaccaga gaaaagataa gaaaatccca 240
ttattttata ctaaaacttat gtatacttct ctaaagattc ttagggcttg taagcaatga 300
ggtttaaggc natttttttag gatgttagca tcccggggct gacttngccg ggctgtggga 360
acccaggn cggagtgg 378

<210> 139

<211> 447

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(447)

<223> 5' terminal sequence. tek tyrosine kinase,
endothelial (venous malformations, multiple
cutaneous and mucosal) (TEK) gene.

<400> 139

gctttcactg gcatgggaga cccttgacac ctgtgagaa aacatgcctc tgccaaagga 60
tgtgatatat aagtgtacat atgtgctgta cacctgggac cttcaccact gtatgccca 120
tgcatggatc tatgtagat gctctgactc taataggact gtatatactg ttttaagaat 180
gggctgaaat cagaatgcct gtttgtggtt tcatatgcaa taatatattt ttttaaaaat 240
gtggacttca taggaaggcg tgagtacaat tagtataatg cataactcat tgttgccta 300
ggatattttg atatttacct ttatgttga atgctattaa atgttttccn gtgtccaaag 360
taaaatattg ttttaataaac ctaacaatgg accccgatag tacag ggta agtgagggga 420
accttatgga ttctaacaag tcctagg 447

<210> 140

<211> 4138

<212> DNA/RNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(4138)

<223> tek tyrosine kinase, endothelial (venous malformations, multiple cutaneous and mucosal) (TEK) gene.

<400> 140

```
cttctgtgct gttccttctt gcctctaact tgtaacaag acgtactagg acgatgctaa 60
tggaagtc acaaccgctg ggtttttgaa aggatccttg ggacctcatg cac atttgtg 120
gaaactggat ggagagattt ggggaagcat ggactcttta gccagcttag ttctctgtgg 180
agtcagcttg ctcccttctg gaactgtgga aggtgccatg gacttgatct tgatcaattc 240
cctacctctt gtatctgatg ctgaaacatc tctcacctgc attgcctctg ggtggcgccc 300
ccatgagccc atcaccatag gaagggaactt t gaagcctta atgaaccagc accaggatcc 360
gctggaaagt actcaagatg tgaccagaga atgggctaaa aaagttgttt ggaagagaga 420
aaaggctagt aagatcaatg gtgcttattt ctgtgaagg cgagttcgag gagaggcaat 480
caggatacga accatgaaga tgcgtcaaca agcttctctc ctaccagcta ctttaactat 540
gactgtggac aaggagata acgtgaacat atctttcaaa aaggtattga ttaaagaaga 600
agatgcagtg atttacaaaa atggttctct catccattca gtgccccggc atgaagtacc 660
tgatattcta gaagtacacc tgcctcatgc tcagccccag gatgctggag tgtactcggc 720
caggatataa ggaggaaccc tcttcacctc ggcttccacc aggtgatag t ccggagatg 780
tgaagccag aagtggggac ctgaatgcaa ccatctctgt actgcttgta tgaacaatgg 840
tgtctgccat gaagatactg gagaatgcat ttgcccctct gggtttatgg gaaggacgtg 900
tgagaaggct tgtgaactgc acacgtttgg cagaacttgt aaagaaagg gcagtgagca 960
agagggatgc aagtcttatg tgttctgtct ccctgacccc tatgggtgtt cctgtgccac 1020
aggctggaag ggtctgcagt gcaatgaagc atgccaccct gggtttttacg ggccagattg 1080
taagcttagg tgcagctgca acaatgggga gatgtgtgat cgcttccaag gatgtctctg 1140
ctctccagga tggcaggggc tccagtgtga gagagaaggc ataccgagga tgaccccaa 1200
gatagtggat ttgccagatc atatagaagt aaacagtggt aaatttaatc ccatttgcaa 1260
agcttctggc tggccgctac ctactaatga agaaatgacc ctggtgaagc cggatgggac 1320
agtgtcccat ccaaaagact ttaaccatac ggatcatttc tcagtagcca tattcaccat 1380
ccaccggatc ctccccctg actcaggagt ttgggtctgc agt gtgaaca cagtggctgg 1440
gatggtggaa aagcccttca acatttctgt taaagttctt ccaaagcccc tgaatgcccc 1500
aaacgtgatt gacactggac ataactttgc tgtcatcaac atcagctctg agccttactt 1560
tgggatgga ccaatcaaat ccaagaagct tctatacaaa cccgttaatc actatgaggc 1620
ttggcaacat attcaagt ga caaatgagat tgttacctc aactatttgg aacctcggac 1680
agaatatgaa ctctgtgtgc aactggtccg tcgtggagag ggtggggaag ggcactcctg 1740
acctgtgaga cgcttcacaa cagcttctat cggactccct cctccaagag gtctaaatct 1800
cctgcctaaa agtcagacca ctctaaattt gacctggcaa ccaatatttc caagctc gga 1860
agatgacttt tatgttgaag tggagagaag gtctgtgcaa aaaagtgatc agcagaatat 1920
taaaagttcca ggcaacttga cttcgggtgct acttaacaac ttacatccca gggagcagta 1980
cgtggtccga gctagagtca acaccaaggc ccagggggaa tggagtgaag atctcactgc 2040
ttggaccctt agtgacattc ttcctctca a ccagaaaa atcaagattt ccaacattac 2100
acactcctcg gctgtgattt cttggacaat attggatggc tattctattt cttctattac 2160
tatccgttac aaggttcaag gcaagaatga agaccagcac gttgatgtga agataaagaa 2220
tgccaccatc attcagtatc agctcaaggg cctagagcct gaaacagcat accagggtga 2280
catttttgca gagaacaaca tagggtcaag caaccagcc ttttctcatg aactggtgac 2340
cctccagaa tctcaagcac cagcggacct cggagggggg aagatgctgc ttatagccat 2400
ccttgctctc ctggaatga cctgctgac tgtgctgttg gcctttctga tcatattgca 2460
attgaagagg gcaaatgtgc aaaggagaat ggcccaagcc ttcca aaacg tgagggaaga 2520
accagctgtg cagtccaact cagggactct ggccctaaac aggaaggtea aaaacaacc 2580
agatcctaca atttatccag tgcttgactg gaatgacatc aaatttcaag atgtgattgg 2640
ggagggcaat ttggccaag ttcttaaggc gcgcatcaag aaggatgggt tacggatgga 2700
tgctgccatc aaaagaatga aagaatatgc ctccaaagat gatcacagg actttgcagg 2760
```


96/292

```
agaactggaa gttctttgta aacttggaca ccatccaaac atcatcaatc tcttaggagc 2820
atgtgaacat cgaggtact tgtacctggc cattgagtag gcgccccatg gaaaccttct 2880
ggacttcctt cgcaagagcc gtgtgctgga gacggaccca gcatttgcca ttgccaata g 2940
caccgcgtcc aactgtcct cccagcagct ccttcacttc gctgccgacg tggccccggg 3000
catggactac ttgagccaaa aacagtttat ccacagggat ctggctgcca gaaacatttt 3060
agttgtgtaa aactatgtgg caaaaatagc agattttgga ttgtcccagag gtcaagagg 3120
gtacgtgaaa aagacaatgg gaaggctccc agt gcgctgg atggccatcg agtcactgaa 3180
ttacagtgtg tacacaacca acagtgtgt atggtcctat ggtgtgttac tatgggagat 3240
tgtagctta ggaggcacac cctactgcgg gatgacttgt gcagaactct acgagaagct 3300
gccccagggc tacagactgg agaagcccct gaactgtgat gatgagggtg atgatctaat 3360
gagacaatgc tggcgggaga agccttatga gaggccatca ttgtcccaga tattggtgtc 3420
cttaaacaga atgttagagg agcgaaagac ctacgtgaat accacgcttt atgagaagtt 3480
tacttatgca ggaattgact gttctgctga agaagcggcc taggacagaa catctgtata 3540
ccctctgttt ccctttcact ggcatgggag acccttgaca actgctg aga aaacatgcct 3600
ctgcccagg atgtgatata taagtgtaca tatgtgctgg aattctaaca agtcataggt 3660
taataattaa gacactgaaa aatctaagt atataaatca gattcttctc tctcatttta 3720
tccctcacct gtagcatgcc agtcccgttt catttagtca tgtgaccact ctgtcttgtg 3780
tttccacagc ctgcaagttc a gtccaggat gctaacatct aaaaatagac ttaaattctca 3840
ttgcttaca gcctaagaat ctttagagaa gtatacataa gtttaggata aaataatggg 3900
atcttcttt ctttctctg gtaatatga cttgtatatt ttaagaaata acagaaagcc 3960
tgggtgacat ttgggagaca tgtgacattt atatattgaa ttaatatccc tacatgtatt 4020
gcacattgta aaaagtttta gtttgatga gttgtgagtt taccttgat actgtaggca 4080
cactttgcac tgatatatca tgagtgaata aatgtcttgc ctactcaaaa aaaaaaaaa 4138
```

<210> 141

<211> 395

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(395)

<223> 3' terminal sequence. tumor necrosis factor
receptor superfamily, member 6 (TNFRSF6) gene.

<400> 141

```
taattccaaa cacaaggggc aaaaaaatcc tccataaatg gaagttcttt aggtggttcc 60
aggnatctgc ttcagtttat aa ctatcttc acagtttaca ttacagaaa tataaatatt 120
atttcttaaa attcacattt aatacaaaact ttcaaagata tttaaacgta ggatagtagt 180
aaggagaatc ttaaattctta gaaacttggg ggtatgacaa gagcaattcc taaatccaga 240
tgatgatttt accattgcta tgtataagct gccatttgta ggcaggtttt acatggggac 300
attattgaac atttccgggg ggtgggggga aaaataaggn atctatttta tccatctttg 360
gattggcaaa cctgggggtt angacatgtt caca 395
```

<210> 142

<211> 461

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(461)

<223> 5' terminal sequence. tumor necrosis factor

receptor superfamily, member 6 (TNFRSF6) gene.

<400> 142

```
tcgtaattgg catcaacttc atggaagaa agaagcgtat gacacattga ttaaagatct 60
caaaaaagcc aatctttgta ctcttgcag a gaaaattcag actatcatcc tcaaggacat 120
tactagtgcac tcagaaaatt caaacttcag aaatgaaatc caaagcttgg tctagagtga 180
aaaacaacaa attcagttct gagtatatgc aattagtgtt tgaaaagatt cttaatagct 240
ggctgtaaat actgcttggg tttttactgg gtacatttta tcatttatta gcgctgaaga 300
gccacatat ttgtagggtt ttaatatctc catggattct gcctccaagg gtgtttaaaa 360
tctagttagg ggaacaacac ttcttcaag ggttaaagtc ngtggcctgg ctaagtaccc 420
ccattaggga gtgtttgccg ggggttgnaa ggtttaggtt t 461
```

<210> 143

<211> 2551

<212> DNA/RNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(2551)

<223> tumor necrosis factor receptor superfamily,
member 6 (TNFRSF6) gene.

<400> 143

```
gcaagagtga cacacaggtg ttcaaagacg cttctgggga gtgagggaa g cggtttacga 60
gtgacttggc tggagcctca ggggcgggca ctggcacgga acacaccctg aggccagccc 120
tggctgcccga ggcgagctg cctcttctcc cgcgggttgg tggaccctgt cagtacggag 180
ttgggggaagc tctttcactt cggaggattg ctcaacaacc atgctgggca tctggaccct 240
cctacctctg gttcttacgt ctgttgct ag attatcgctc aaaagtgtta atgccccagt 300
gactgacatc aactccaagg gattggaatt gaggaagact gttactacag ttgagactca 360
gaacttggaa ggccctgcac atgatggcca attctgccat aagccctgtc ctccagggtga 420
aaggaaagct agggactgca cagtcaatgg ggatgaacca gactgcgtgc cctgccaaaga 480
agggaaaggag tacacagaca aagcccattt ttcttccaaa tgcagaagat gtagattgtg 540
tgatgaagga catggccttag aagtggaaat aaactgcacc cggaccacga ataccaagt 600
cagatgtaaa ccaactttt tttgttaact tactgtatgt gaacactgtg acccttgcac 660
caaatgtgaa catggaatca tcaaggaatg cacactcacc agcaacac ca agtgcaaaaga 720
ggaaggatcc agatctaact tggggtggct ttgtcttctt cttttgcca ttccactaat 780
tgtttgggtg aagagaaaag aagtacagaa aacatgcaga aagcacagaa aggaaaacca 840
aggttctcat gaatctccaa ccttaaatcc tgaaacagtg gcaataaatt tatctgatgt 900
tgacttgagt aaatatatca cacta ttgc tggagtcagt aactaagtc aagttaaagg 960
ctttgttcga aagaatggtg tcaatgaagc caaaatagat gagatcaaga atgacaatgt 1020
ccaagacaca gcagaacaga aagttcaact gcttcgtaat tggcatcaac ttcattgaaa 1080
gaaagaagcg tatgacacat tgattaaaga tctcaaaaaa gccaatcttt gtactcttgc 1140
agagaaaatt cagactatca tctcaagga cattactagt gactcagaaa attcaaat 1200
cagaaatgaa atccaaagct tgggtctagag tgaaaaacaa caaattcagt tctgagtata 1260
tgcaattagt gtttgaaaag attcttaata gctggctgta aatactgctt gggtttttac 1320
tgggtacatt ttatcattta ttacgctga agagccaaca tttttgtaga tttttaatat 1380
ctcatgattc tgccctcaag gatgtttaaa atctagttag gaaaacaaac ttcattcaaga 1440
gtaaatgcag tggcatgcta agtaccacaa taggagtgtg tgcagaggat gaaagattaa 1500
gattatgctc tggcatctaa catatgattc tgtatgtatg atgtaatcag tgtatgttag 1560
tacaaatgtc tatccacagg ctaacccac aatagaagaa gctatgacct 1620
tttgctgaaa tatcagttac tgaacaggca ggccactttg cctctaaatt acctctgata 1680
attctagaga ttttaccata tttctaaact ttgtttataa ctctgagaag atcatattta 1740
tgtaaagtat atgtatttga gtgcagaatt taaataaggc tctacctcaa agac ctttgc 1800
acagtttatt ggtgtcatat tatacaatat ttcaattgtg aattcacata gaaaacatta 1860
aattataatg tttgactatt atatatgtgt atgcatttta ctggctcaaa actacctact 1920
tctttctcag gcatcaaaag cattttgagc aggagagtat tactagagct ttgccacctc 1980
```

98/292

```

tccatttttg ctttggtgct catcttaat g gcctaata gca ccccaaaaca tggaaatata 2040
accaaaaaat acttaaatagt ccacaaaag gcaagactgc ccttagaaat tctagcctgg 2100
tttgagata ctaactgctc tcagagaaag tagctttgtg acatgtcatg aacccatgtt 2160
tgcaatcaaa gatgataaaa tagattctta tttttccccc acccccgaat atgttcaata 2220
atgtcccatg taaaacctgc tacaaatggc agcttataca tagcaatggt aaaatcatca 2280
tctggattta ggaattgctc ttgtcatacc cccaagtttc taagatttaa gattctcctt 2340
actactatcc tacgttttaa tatctttgaa agtttgtatt aaatgtgaat ttttaagaaat 2400
aatatttata tttctgtaaa tgtaaaactgt gaagatagtt at aaactgaa gcagatacct 2460
ggaaccacct aaagaacttc catttatgga ggattttttt gccccttggtg tttggaatta 2520
taaaatatag gtaaaagtac gtaattaaat a 2551

```

<210> 144

<211> 434

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(434)

<223> 3' terminal sequence. cyclin -dependent
kinase inhibitor 1a (p21, cip1) (CDKN1A) gene.

<400> 144

```

aaagtcacta agaatacttt atnagcacc tgctgtatat tcagcattgt gggaggagct 60
gtgaaagaca cagaacagta cagggtgtgg tccctgccct cgagagggtt acagtctagg 120
tggaagaaac ggaaccagga cacatgggga gccgagagaa aacagtcacg gccagtatgt 180
tacaggagct ggaaggtnnt tggggtcaga cccaataact ccaagtacac taagcacttc 240
agtccttcca ggggtcaaac gttagtcca ggaagacaa ctactcccag ccccatatga 300
gcccacgtgg catgccctgt ccatagcctc tactgccacc atcttaaaat gtctgactcc 360
ttgttccgct ggctaattca aagtgaatg aactggggag ggatgggggt gatgaggaag 420
gttcgntgga cgtt 434

```

<210> 145

<211> 257

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(257)

<223> 5' terminal sequence. cyclin -dependent
kinase inhibitor 1a (p21, cip1) (CDKN1A) gene.

<400> 145

```

cttgtgctgc ntncagggg a gcaggctgaa gggccccag gtggacctgg agactctcag 60
ggtcgaaaac ggcgcagac cagcatgaca gatttctacc actccaaacg ccggctgac 120
ttctcaaga ggaagcccta atccgccac aggaagcctg cagtccctga agcgcgaggg 180
cctcaaaggc cntnctnaca tcttctgcct tagtctcagt ttgtgtgtct taattattat 2 40
ttgtgtttta aattttt 257

```

<210> 146

<211> 2121

<212> DNA/RNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(2121)

<223> cyclin-dependent kinase inhibitor 1a (p21,
cip1) (CDKN1A) gene.

<400> 146

```
gccgaagtca gttccttgtg gagccggagc tgggcgcgga ttgcgccagg caccgaggca 60
ctcagaggag gcgccatgtc agaaccggct ggggatgtcc gtcagaacc atgcggcagc 120
aaggcctgcc gcgcctctt cggccagtg gacagcgagc agctg agccg cgactgtgat 180
gcgctaattg cgggctgcat ccaggaggcc cgtgagcgat ggaacttcga ctttgtcacc 240
gagacaccac tggagggtga cttgccttg gagcgtgtgc ggggccttgg cctgcccagg 300
ctctaccttc ccacggggcc ccggcgaggc cgggatgagt tgggaggagg caggcggcct 360
ggcacctcac ctgctctgct gca ggggaca gcagaggaa accatgtgga cctgtcactg 420
tcttgtacc ttgtgcctcg ctcaggggag caggctgaag ggtccccagg tggacctgga 480
gactctcagg gtcgaaaacg gcggcagacc agcatgacag atttctacca ctccaaacgc 540
cggctgatct tctccaagag gaagccctaa tccgcccaca ggaagcctgc agtcctggaa 600
gcgcgagggc ctcaaaggcc cgctctacat cttctgcctt agtctcagtt tgtgtgtctt 660
aattattatt tgtgttttaa tttaaacacc tctcatgta cataccctgg ccgccccctg 720
ccccccagcc tctggcatta gaattattta acaaaaaact aggcgggttg atgagagggt 780
cctaagagtg ctgggcattt ttattttatg aaatactatt taa agcctcc tcatcccgtg 840
ttctcctttt cctctctccc ggaggttggg tgggcgggct tcatgccagc tacttctccc 900
tccccacttg tccgctgggt ggtaccctct ggaggggtgt ggctccttcc catcgctgtc 960
acaggcgggt atgaaattca ccccttttcc tggacactca gacctgaatt ctttttcatt 1020
tgagaagtaa acagatggca ctttgaagg gcctcacoga gtgggggcat catcaaaaac 1080
tttgagtgcc cctcacctcc tctaagggtg gcagggtga ccctgaagtg agcacagcct 1140
agggctgagc tggggacctg gtaccctcct ggctottgat acccccctct gtcttgtgaa 1200
ggcaggggga aggtggggtg ctggagcaga ccaccccgcc tgcctcatg gccctctga 1260
cctgcactgg ggagcccgtc tcagtgttga gccttttccc tctttggctc ccctgtacct 1320
tttgaggagc cccagcttac ccttcttctc cagctgggct ctgcaattcc cctctgctgc 1380
tgtccctccc ctttgtctt ccttcagta ccctctcatg ctccagggtg ctctgaggtg 1440
cctgtcccac ccccacccc agctcaatgg actg gaaggg gaagggacac acaagaagaa 1500
gggcacccca gttctacctc aggcagctca agcagcgacc gccccctct ctagtgtgg 1560
gggtgagggt cccatgtggg gccacaggcc cccttgagt gggttatctc tgtgttaggg 1620
gtatatgatg ggggagtaga tctttctagg agggagacac tggccctca aatcgtccag 1680
gcaccttct catccacccc atccctcccc agttcattgc actttgatta gcagcggaac 1740
aaggagtcag acattttaag atggtggcag tagaggctat ggacagggca tgccacgtgg 1800
gctcatatgg ggctgggagt agttgtctt cctggcacta acgttgagcc cctggaggca 1860
ctgaagtgtc tagtgtactt ggagtattgg ggtctgacct caaacacc tt ccagctcctg 1920
taacatactg gcctggactg ttttctctcg gctcccatg tgtcctggtt ccggtttctc 1980
cacctagact gtaaacctct cgagggcagg gaccacacc tgtactgttc tgtgtctttc 2040
acagctcttc ccacaatgct gaataacag caggtgtcca ataatgatt cttagtgtgact 2100
ttaaaaaaaa aaaaaaaaaa a 2121
```

<210> 147

<211> 452

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(452)

<223> 3' terminal sequence. phospholipase a2,
group iia (platelets, synovial fluid) (PLA2G2A)
gene.

<400> 147

```
gatttgctaa ttgctttatt cagaagagac cccocggagt acagcttctt tggttaagca 60
cggagttgag gtggaggaga gcagtagaag gctggaaatc tgctggatgt ctcattctgg 120
gtgggtatag aagggtcctt gcctggcctc taggatgggt gagggatgct ttctgcatgg 180
ccaaggaact tggtaggggt agggagggag ggtatgagag agggaaattc agcactgggt 240
ggaaggtttc cagggaagag gggactcagc aacgaggggt gctccctctg cagtntttat 300
tggaatagta ctggtacttt ttattgtagg tcgtcttntt tctagcaaaa cagggtngca 360
gcagccttat cacacttca c acagttgact tctgcaggag tccnttttt gcacaggttg 420
attctgctcc ccgaagttac taaacttttt tt 452
```

<210> 148

<211> 379

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(379)

<223> 5' terminal sequence. phospholipase a2,
group iia (platelets, synovial fluid) (PLA2G2A)
gene.

<400> 148

```
tggagtctct tgagagagcc accaaggagg agcagggggag cgacggccgg ggcagaagtt 60
gagaccaccc agcagaggag ctaggccagt ccatctgc at ttgtcaccca agaactctta 120
ccatgaagac cctoctactg ttggcagtga tcatgatctt tggcctactg caggcccatg 180
ggaatttggg gaatttccac agaatgatca agttgacgac aggaaggaa gccgcactca 240
gttatggctt ctacggctgc cactgtggcg tgggttgacag aggatcccc aaggatgcaa 300
cggattcgct gctgtg tcac tcatgactgt ttgtctacaaa cgtctgggag aaacgtgggt 360
tnttggcacc aaatttttt 379
```

<210> 149

<211> 854

<212> DNA/RNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(854)

<223> phospholipase a2, group iia (platelets,
synovial fluid) (PLA2G2A) gene.

<400> 149

```
gaattcccaa ctctggagtc ctctgagaga gccaccaagg aggagcaggg gagcgacggc 60
cggggcagaa gttgagacca ccagcagag gagctaggcc agtccatctg catttgtc ac 120
ccaagaactc ttacatgaa gaccctccta ctgttggcag tgatcatgat ctttggccta 180
ctgcaggccc atgggaattt ggtgaatttc cacagaatga tcaagttgac gacaggaaag 240
gaagccgcac tcagttatgg cttctacggc tgccactgtg gcgtgggtgg cagaggatcc 300
```

cccaaggatg caacggatcg ctgctgtgtc actcat gact gttgctacaa acgtctggag 360
aaacgtggat gtggcaccac atttctgagc tacaagttta gcaactcggg gagcagaatc 420
acctgtgcaa aacaggactc ctgcagaagt caactgtgtg agtgtgataa ggctgctgcc 480
acctgttttg ctagaaacaa gacgacctac aataaaaagt accagtacta ttccaataaa 540
cactgcagag ggag cacccc tcgttgctga gtccccctt ccttggaac cttccacca 600
gtgctgaatt tccctctctc ataccctccc tccctaccct aaccaagttc cttggccatg 660
cagaaagcat ccctcaccca tcctagaggc caggcaggag cccttctata cccaccaga 720
atgagacatc cagcagattt ccagccttct actgctctcc tccacctcaa ctccgt gctt 780
aaccaaagaa gctgtactcc ggggggtctc ttctgaataa agcaattagc aaatcaaaaa 840
aaaaaaagga attc 854

<210> 150
<211> 224
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer

<220>
<221> misc_feature
<222> (1)..(224)
<223> 3' terminal sequence.
glyceraldehyde-3-phosphate dehydrogenase (GAPD)
gene.

<400> 150
ggttgagcac agggactttt attgatgna catgacaagg tgcggctccc taggcccctc 60
ccctnttcaa ggggtctaca tggcaact nt gaggaggga gattcagtgt ggtgggggac 120
tgagtntggc agggactccc cagcagttag ggtctctctc ttcctcttnt gctcttntctg 180
gggntggtgg nccagggnntn ttactccttg gaggccatnt gggc 224

<210> 151
<211> 359
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer

<220>
<221> misc_feature
<222> (1)..(359)
<223> 5' terminal sequence.
glyceraldehyde-3-phosphate dehydrogenase (GAPD)
gene.

<400> 151
gcgctgagta cgtcgtggag tccactggcg tcttcaccac catggagaag gctggggctc 60
atttgcaggg gggagccaaa agggatcatca tctctgcccc ctctgctgat gcccccatgt 120
tcgtcatggg tgtgaacctt gagaagtatg acaacagcct caagatcatc agcaatgcct 180
cctgcaccac caactgctta gcaccctgg gccagggtca tccatgacaa ctttggatc 240
gtggaaggac tcatgaccac agtccatgcc atcactgcca c ccagaagac tgtggatggc 300
ccctncggga aactgtgggc gtgatggccg cggggttctt tcagaacatc atccctgcc 359

<210> 152
<211> 1283
<212> DNA/RNA

102/292

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(1283)

<223> glyceraldehyde -3-phosphate dehydrogenase
(GAPD) gene.

<400> 152

```
ctctctgctc ctctgttcg acagtcagcc gcattcttctt ttgcgtcgcc agccgagcca 60
catcgctcag acaccatggg gaagggtgaag gtccggagtca acggatttgg tcgtattggg 120
cgccctggta ccagggtctg ttttaactct ggta aagtgg atattgttgc catcaatgac 180
cccttcattg acctcaacta catgggtttac atgttccaat atgattccac ccattggcaa 240
ttccatggca ccgtcaaggc tgagaacggg aagcttgtca tcaatggaaa tcccatcacc 300
atcttccagg agcgagatcc ctccaaaatc aagtggggcg atgctggcgc tgagtacgtc 360
gtggagtcca ctggcgtctt caccacatg gagaaggctg gggctcattt gcagggggga 420
gccaaaaggg tcatcatctc tgcccccctc gctgatgcc ccattgtcgt catgggtgtg 480
aaccatgaga agtatgacaa cagcctcaag atcatcagca atgcctcctg caccaccaac 540
tgcttagcac ccctggccaa ggtcatccat gacaactttg gtatcgtgga agga ctcatg 600
accacagtcc atgccatcac tgccaccag aagactgtgg atggccctc cgggaaactg 660
tggcgtgatg gccgcggggc tctccagaac atcatccctg cctctactgg cgctgccaag 720
gctgtgggca aggtcatccc tgagctgaac gggaagtcca ctggcatggc cttccgtgtc 780
cccactgcca acgtgtcagt ggtggacctg ac ctgccgtc tagaaaaacc tgccaaatat 840
gatgacatca agaagggtgt gaagcaggcg tcggagggcc cctcaaggg catcctgggc 900
tacactgagc accagggtgt ctctctgac ttcaacagcg acaccactc ctccacctt 960
gacgtctggg ctggcattgc cctcaacgac cactttgtca agtcatttc ctggtatgac 1020
aacgaatttg gctacagcaa cagggtgttg gacctcatg ccacatggc ctccaaggag 1080
taagaccctt ggaccaccag cccagcaag agcacaagag gaagagagag accctcactg 1140
ctggggagtc cctgccacac tcagtcccc accacactga atctccctc ctacagtgtg 1200
ccatgtagac ccctgaaga ggggaggggc ctaggagacc gcacctgt c atgtaccatc 1260
aataaagtac cctgtgctca acc 1283
```

<210> 153

<211> 361

<212> DNA

<213> Artificial Sequence.

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(361)

<223> 3' terminal sequence. jun b proto-oncogene
(JUNB) gene.

<400> 153

```
tacttaata gattcaatan aaagaacaaa cacacacaaa cacaacacg tcttaaaata 60
aactctttag agactaagtg cgtgtttctt ttccacagta cgggtgcagag aggggagggc 120
agggggcggg ggtcccttcc caatgtcccc gcgggcttga gta ccaggcg gcggggccag 180
ctccntant ncgccccctc ttccctccc tgttaaatac acaaataat tatattcaat 240
ntgaatcng tctntttcca gcagaaaaaa aacatacaaa aaaaagtggg aagggggggg 300
cttntttaa cgttcgangg ttggaaggnc tttggggcnc aggggtaggg angggccgag 360
t 361
```

<210> 154

<211> 401
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<220>
<221> misc_feature
<222> (1)..(401)
<223> 5' terminal sequence. jun b proto -oncogene
(JUNB) gene.

<400> 154
agcgcatcaa agtngagcgc angccttgcg gaaccggctn gcggccacca agtgccggaa 60
gcggaantgg gagcgcatcg ggcttgggag gacaaggtga agacgctcaa ggccgagaac 120
gcgggngtgt cgagtaccgc cggcttcctc cgggagcagg tggcccagct caaacagaag 180
gtcatgaccc acgtnagcaa cggctnctnag ctgctgcttn gggtaaggag acacgccttc 240
tggaacgttc cctgcccctt tacgggacac ccccttcgtt tnggacggtt nggcacacgg 300
tttcccactn gggttccaagg gtacgaggcg gtggggnacc cacctggggg acntaggggg 360
cgnccgcaaa ccacattngg atttcgggcc ttcttaacct t 401

<210> 155
<211> 1797
<212> DNA/RNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<220>
<221> misc_feature
<222> (1)..(1797)
<223> jun b proto -oncogene (JUNB) gene.

<400> 155
ccagcaggga gctgggagct gggggaaacg acgc caggaa agctatcgcg ccagagaggg 60
cgacgggggc tcgggaagcc tgacagggtc ttgcgcac gctgccggct ggctgctacc 120
cgcccgcgcc agccccgag aacgcgcgac caggcaccca gtccggtcac cgcagcggag 180
agctcgccgc tcgctgcagc gaggcccgga gcggcccgcc agggaccctc cccagaccgc 240
ctgggcccgc cggatgtgca ctaaaatgga acagcccttc taccacgacg actcatacac 300
agctacggga tacggccggg cccctgggtg cctctctcta cagactaca aactcctgaa 360
accgagcctg gcggtcaacc tggccgaccc ctaccggagt ctcaaagcgc ctggggctcg 420
cggaccgcgc ccagaggcg gcggtggcgg cagctacttt tctggtcagg gctcg gacac 480
cggcgctct ctcaagctcg cctcttcgga gctggaacgc ctgattgtcc ccaacagcaa 540
cggcgatgc acgacgacgc ctacaccccc gggacagtac ttttaccccc gcgggggtgg 600
cagcggtgga ggtgcaggg gcgcagggg gcggcgccacc gaggagcagg agggcttcgc 660
cgacggcttt gtcaaagccc tggacgatct gca caagatg aaccacgtga cccccccaa 720
cgtgtccctg ggcgctaccg gggggccccc ggctggggcc gggggcgctt acgcccggcc 780
ggagccacct cccgtttaca ccaacctcag cagctactcc ccagcctctg cgtcctcggg 840
aggcgccggg gctgcccgtc ggaccgggag ctgctaccgc acgaccacca tcagctacct 900
cccacacgc cgcgcccttg ccggtggcca cccggcgag ctgggcttgg gccgcggcgc 960
ctccaccttc aaggaggaac cgcagaccgt cgcgagggcg cgcagccggg acgccacgcc 1020
gccggtgtcc cccatcaaca tgggaagacca agagcgcatc aaagtggagc gcaagcggct 1080
gcggaaccgg ctggcgcca ccaagtgcg gaagcgggag ctggagcgca t cgcgcgcct 1140
ggaggacaag gtgaagacgc tcaaggccga gaacgcggg ctgtcgagta ccgcccgcct 1200
cctccgggag caggtggccc agctcaaaca gaaggtcatg acccagctca gcaacggctg 1260
tcagctgctg cttgggggtca agggacacgc cttctgaacg tccccgtccc ctttacggac 1320
accccctgc ttggacgggt gggcac acgc ctcccactgg ggtccaggga gcaggcgggtg 1380
ggcaccaccc ctgggacctt ggggcgcgc aaaccacact ggactccggc cccctaccc 1440

104/292

tgcgccagct ccttccacct cgacgtttac aagccccccc ttccactttt ttttgtatgt 1500
 tttttttctg ctggaaacag actcgattca tattgaatat aatatatttg tgtatttaac 1560
 agggagggga agagggggcg atcgcgccgg agctggcccc gccgcctggg actcaagccc 1620
 gcggggacat tgggaagggg acccccgcgc cctgccctcc cctctctgca ccgtactgtg 1680
 gaaaagaaac acgcacttag tctctaaaga gtttatttta agacgtgttt gtgtttgtgt 1740
 gtgtttgttc tttttattga atctatttaa gtaaaaaaaaa aattggttct ttattaa 1797

<210> 156

<211> 335

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(335)

<223> 3' terminal sequence. cellular retinoic
 acid-binding protein 2 (CRABP2) gene.

<400> 156

aagcatttta ataaaattaa caataaata ttctaaactg tataggctac agggacaaaag 60
 ggtagaagct agagggccag tctttcctgc tcaggccctc aagtcctctt tagagagacc 120
 ctgctctggg ctggtttggg gctaggactg ctgacttggg gaggcgggga gtgaaccggg 180
 aatgggtgat ctgggctctt gcagccattc ctctttgttg gtgtagggga ggagagaaga 240
 ggtcaaagaa agcaagaccc tgcaagaggc atccagtgga cccccagaag tgactggggg 300
 aaggggagcg ctatcctagg anggtggggg tgggt 335

<210> 157

<211> 481

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(481)

<223> 5' terminal sequence. cellular retinoic
 acid-binding protein 2 (CRABP2) gene.

<400> 157

gcctggactt gtcttgggtt ccagaacctg acgacccggc gacgcgacgt ctct ttgac 60
 taaaagacag tgtccagtgc tccagcctag gactctacgg ggaccgcctc ccgcgcccgc 120
 accatgccca acttctcttg caactggaaa atcatccgat cggaaaactt cgaggaattg 180
 ctcaaagtgc tnggggtgaa tgtgatgctg aggaagattg ctgtggctnc agcgtccaag 240
 ccagcagtng agatcaaaca ggagggagac act ttctaca tcaaaacctc caccaccgtg 300
 cggcaccaca gagattaact tcaagggtng ggaggagttt gagggagcag antgtgggtg 360
 gggaggccct gttaaggagc ngggtgaaat ggggagagtg aggattaaat ggtcttttga 420
 gcagaagttc ctgaagggng aggggcccga agacntcttg gaccngagaa tttccccacg 480
 t 481

<210> 158

<211> 969

<212> DNA/RNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(969)

<223> cellular retinoic acid-binding protein 2
(CRABP2) gene.

<400> 158

```
agctttgggg ttgtccctgg acttgtcttg gttccagaac ctgacgaccc ggcgacggcg 60
acgtctcttt tgactaaaag acagtgtcca gtgctccagc ctaggagtct acggggaccg 120
cctcccgcgc cgccaccatg cccaacttct ctggcaactg gaaaatcatc cgatcggaaa 180
acttcgagga attgctcaaa gtgctggggg tgaatgtgat gctgaggaag attgctgtgg 240
ctgcagcgtc caagccagca gtggagatca aacaggaggg agacactttc tacatcaaaa 300
cctccaccac cgtgcgcacc acagagatta acttcaaggt tggggaggag tttgaggagc 360
agactgtgga tgggaggccc tgtaagagcc tggtgaaatg ggagag tgag aataaaatgg 420
tctgtgagca gaagctcctg aaggggagag gccccaagac ctcgtaggacc agagaactga 480
ccaacgatgg ggaactgatc ctgaccatga cggcggatga cgttgtgtgc accaggggtct 540
acgtccgaga gtgagtggcg acaggtagaa ccgcggccga agcccaccac tggccatgct 600
caccgcctg cttcactgcc ccct ccgtcc caccocctcc ttctaggata gcgtcccct 660
taccocagtc acttctgggg gtactgga tgccctttgc aggtctttgc tttctttgac 720
ctcttctctc ctcccctaca ccaacaaaga ggaatggctg caagagccca gatcacccat 780
tccgggttca ctcccgcct cccaagtca gcagtcctag ccccaaacca gccagagca 840
gggtctctct aaaggggact tgagggcctg agcaggaaaag actggccctc tagcttctac 900
cctttgtccc tgtagcctat acagtttaga atatttattt gttaatttta ttaaaatgct 960
ttaaaaaaa                                     969
```

<210> 159

<211> 344

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(344)

<223> 3' terminal sequence. activin a receptor
type ii-like 1 (ACVRL1) gene.

<400> 159

```
cgcgnttga ggggaggtgg ccccgntcc gccgangaan tcgccccg cc acccgagag 60
cncncagagg gaccattgac cttgggctcc cccaggaaaag gccttctgat gctgctgatg 120
gccttggtga ccaggggaga cctgtgaag cgtctcggg gccgctggt gacctgcacg 180
tgtgagagcc cacattgcaa ggggcctacc tgccgggggg cctgggtgca cagtagtgct 240
tgggtgcggg agggggggag gcacccc cag ggaacattcg gggntgcggg aantttgcac 300
aggagantct tgcagggggg gcgcccacc gatttcgttc aacc                                     344
```

<210> 160

<211> 416

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>
<221> misc_feature
<222> (1)..(416)
<223> 5' terminal sequence. activin a receptor
type ii-like 1 (ACVRL1) gene.

<400> 160
gtcagtctcc cggaaccagg actgttcatc cctcgaggag aagatcttga cggccacact 60
ctcaccgtgc cacaagcccc gccacacttc gccatagcgc cttttccac acactccacc 120
aaggcaacct gccgtngcca ctgtcctctg caccagggaa ggggagccct gagccactcc 180
ctgtgggtgg cagtcaactgt ccaggagggt ccccaacat gctgttcgcc ctgcttcaga 240
tgcttttcag ggatgaggat gggattttcc cagcttcgct gttgcagggc cagttgctt 300
tttccttgcc tncgttcggg acatggccac agggcccagg ggacaaccag g gggccacca 360
gggggnccag gcaanggcca agncacgggg ggcccagggt ttnaaggggc cagttt 416

<210> 161
<211> 1970
<212> DNA/RNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<220>
<221> misc_feature
<222> (1)..(1970)
<223> activin a receptor type ii-like 1 (ACVRL1)
gene.

<400> 161
aggaacagggt ttattaggag ggagtgggtg agctgggcca ggcaggaaga cgctggaata 60
agaaacattt ttgtccagc ccccatccca gtcccgggag gctgccgcgc cagctgcgcc 120
gagcagcccc ctcccgggt ccagcccgggt ccggggccgc gccggaccc c agcccggcgt 180
ccagcgctgg cggtgcaact gcggcgcgc ggtggagggg aggtggcccc ggtccgccga 240
aggctagcgc ccgccacce gcagagcggg ccagaggga ccatgacctt gggctcccc 300
aggaaggcc ttctgatgct gctgatggcc ttggtgacct agggagacct tgtgaagccg 360
tctcggggcc cgctggtgac ctgcaog tgt gagagccac attgcaaggg gcctacctgc 420
cggggggcct ggtgcacagt agtgcgtggt cgggaggagg ggaggcacc ccaggaacat 480
cgggctgcg ggaacttgca cagggagctc tgcagggggc gccccaccga gttcgtcaac 540
cactactgct gcgacagcca cctctgaac cacaactgt ccttggtgct ggaggccacc 600
caacctcctt cggagcagcc gggaacagat gccagctgg cctgatcct gggccccgtg 660
ctggccttgc tggccctggt ggccctgggt gtccctgggc tgtggcatgt ccgacggagg 720
caggagaagc agcgtggcct gcacagcgag ctgggagagt ccagtctcat cctgaaagca 780
tctgagcagg gcgacacgat gttgggggac ctccctggaca gtgactg cac cacagggagt 840
ggctcagggc tccccttctt ggtgcagagg acagtggcac ggcaggttgc cttggtggag 900
tgtgtgggaa aaggccgcta tggcgaagtg tggcggggct tgtggcacgg tgagagtgtg 960
gccgtcaaga tcttctctc gagggatgaa cagtcttgg tccgggagac tgagatctat 1020
aacacagtat tgctcagaca cgac aacatc ctaggcttca tgcctcaga catgacctcc 1080
cgcaactcga gcaogcagct gtggtcatc acgcactacc acgagcacgg ctccctctac 1140
gactttctgc agagacagac gctggagccc catctggctc tgaggctagc tgtgtccgcg 1200
gcatcgggcc tggcgacact gcacgtggag atcttcggt caccagggcaa accagccatt 126 0
gccccccgcg acttcaagag ccgcaatgtg ctggtcaaga gcaacctgca gtgttgcatc 1320
gccgacctgg gcctggctgt gatgactca cagggcagcg attacctgga catcggaac 1380
aaccgagag tgggaccaa gcggtacatg gcaccgagg tgctggacga gcagatccgc 1440
acggactgct ttgactccta caagtggact gacatctg gg cctttggcct ggtgctgtg 1500
gagattgccc gccggacat cgtgaatggc atcgtggagg actatagacc acccttctat 1560
gatgtggtgc ccaatgacct cagctttgag gacatgaaga aggtggtgtg tgtggatcag 1620
cagaccccca ccatccctaa ccggtggct gcagaccgg tcctctcagg cctagctcag 1680
atgatgcggg agtgctggtg cccaaacccc tctgcccag tcaccgcgct gcggatcaag 1740
aagacactac aaaaaattag caacagtcca gagaagccta aagtgattca atagcccagg 1800

107/292

agcacctgat tcctttctgc ctgcaggggg ctgggggggt ggggggcagt ggatggtgcc 1860
ctatctgggt agaggtagtg tgagtgtggt gtgtgctggg gatgggcagc t gcgcctgcc 1920
tgctcggccc ccagcccacc cagccaaaaa tacagctggg ctgaaacctg 1970

<210> 162

<211> 407

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(407)

<223> 5' terminal sequence. lim domain protein
(RIL) gene.

<400> 162

gtgaccctgc gcgggccttc gccctggggc ttccgcctgg tngggccgng gacttcagcg 60
cgccctcac catctcagcg gtccatgctg gcagcaaggc tcatntggct gccctgtgcc 120
caggagacct gatccaggcc atcaatggtg agagcacaga gtcctgac a cacctggang 180
cacagaaccg catcaagggc tgccacgac accctcacact gtctgtgagc aggcctgagg 240
gcaggagctg gccagtgcc cctgatgaca gcaaggctca ggcacacagg atccacatcg 300
ntcctgagat ccaggacggc agcccaaca ccagcaggcg gccctcaggc accgggactt 360
gggccagaag atnngcagan caagnct ggg gtttttncat atggaca 407

<210> 163

<211> 1130

<212> DNA/RNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(1130)

<223> lim domain protein (RIL) gene.

<400> 163

tgagagtccg gctcaggctc cggtgcggc tccagcccgc gatgcccac tccgtgacc 60
tgcgcgggcc ttgcacctgg ggcttccgcc tgggtgggccc ggacttcagc gcgcccctca 120
ccatctcacg ggtccatgct ggcagcaagg cctcattggc tgccctgtgc ccaggagacc 180
tgatccaggc catcaatggt gagagcacag agctcatgac acacctg gag gcacagaacc 240
gcatcaaggc ctgccacgat cacctcacac tgtctgtgag caggcctgag ggcaggagct 300
ggcccagtg cctgatgac agcaaggctc aggcacacag gatccacatc gatcctgaga 360
tccaggacgg cagcccaaca accagcaggc ggcctcagg caccgggact gggccagaag 420
atggcagacc aagcctggga tctcc atatg gaaaaccccc ttgctttcca gtccctcaca 480
atggcagcag cgaggccacc ctgccagccc agatgagcac cctgcatgtg tctccacccc 540
ccagcgctga ccagcagag gcctcccgcg gagccgggag cagagtcgac ctgggctccg 600
aggtgtacag gatgctgcgg gagccggccg agcccgtggc cgcggagccc aagcagtcag 660
gtccttccg ctacttgacg ggcattgctag aggcgggca gggcggggat tggcccgggc 720
ctggcgggcc ccggaacctc aagccacgg ccagcaagct gggcgctccg ctgagcggcc 780
tgcaagggct ccccgagtgc acgcgtgct gccacggaat cgtgggcacc atcgtcaagg 840
aacgggacaa gctctacat cccgagtgt tcatgtgcag tgact gcggc ctgaacctca 900
agcagcgtgg ttacttcttt ctggacgagc ggctctactg tgagagccac gccaaaggcg 960
gcgtgaagcc gcccgagggc tacgacgtgg tggcggtgta cccaatgcc aaggtggaac 1020
tcgtctgagc tgggaccctg ctcccacccc tgcttcttaa ggtccctgct cgcccggtgt 1080

108/292

aaatatgttt caccctgtcc c tctaataaa gtcctctgtc tcaaaaaaaaa

1130

<210> 164

<211> 310

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(310)

<223> 5' terminal sequence. shc (src homology 2 domain-containing) transforming protein 1 (SHC1) gene.

<400> 164

anattcggaa cgagggatcc ctctatgtc aacgtccaga acctagacaa ggcccggcaa 60
gcagtgggtg gtgctgggcc cccaatcct gctatcaatg gcagtgcacc ccgggacctg 120
tttgacatga agccttcga agatgctctt cgctgc ctc cacctcccca gtcggtgtcc 180
atgntcgagc agtccgagg ggagccctgg gttccatggg aagctgagcc ggccggaggc 240
tgaggcactg ctggcagctt caatggggat ttccnggtac gggagagcac gaccacacng 300
gggcaatatg 310

<210> 165

<211> 3664

<212> DNA/RNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(3664)

<223> shc (src homology 2 domain -containing) transforming protein 1 (SHC1) gene.

<400> 165

atggggcctg aaactgtctg ggtctgagct ggggagcgga agccacttgt ccctctccct 60
ccccaggact tctgtgactc ctgggccaca gaggtccaac cagggttaagg gcctggggat 120
accctctgcc tggccccctt gccaaaactg gcaggggggc caggctgggc agcagccccct 180
ctttcacctc aactatggat ctctgcccc ccaagcccaa gtacaatcca ct ccggaatg 240
agtctctgtc atcgtggag gaaggggctt ctgggtccac cccccggag gagctgcctt 300
ccccatcagc ttcateccctg gggcccatcc tgctcctct gctggggac gatagtcca 360
ctaccctgtg ctcttcttc ccccgatga gcaacctgag gctggccaac ccgctgggg 420
ggcgcccagg gtctaagggg gagccaggaa gggcagctga tgatggggag gggatcgatg 480
ggcgagccat gccagagtca ggccccctac ccctcctcca ggacatgaac aagctgagtg 540
gaggcgggcg gcgcaggact cgggtggaag ggggccagct tggggcgag gagtggaccc 600
gccacgggag ctttgtcaat aagcccacgc ggggctggct gcatcccaac gacaaagtca 660
tgggaccggg ggtttcctac ttggttcggt acatgggttg tgtggaggtc ctccagtcaa 720
tgctgcccct ggacttcaac acccgactc aggtcaccag ggaggccatc agtctggtgt 780
gtgaggctgt gccgggtgct aagggggcga caaggaggag aaagccctgt agccgcccgc 840
tcagctctat cctggggagg agtaacctga aatttctggt aatgccaatc actctcaccg 900
tctccaccag cagcctcaac ctcatggccg cagactgcaa acagatcatc gccaacccacc 960
acatgcaatc tatctcattt gcatccggcg gggatccgga cacagccgag tatgtgcctt 1020
atgttgccaa agaccctgtg aatcagagag cctgccacat tctggagtggt cccgaagggc 1080
ttgcccagga tgtcatcagc accattg gcc aggccttcga gttgcgcttc aaacaataacc 1140

109/292

```

tcaggaaccc acccaactg gtcaccctc atgacaggat ggctggcttt gatggctcag 1200
catgggatga ggaggaggaa gagccacctg accatcagta ctataatgac ttcccgggga 1260
aggaaccccc cttggggggg gtggtagaca tgaggcttcg ggaaggagcc gctccagggg 1320
ctgctcgacc cactgcaccc aatgccaga ccccagcca cttgggagct acattgcctg 1380
taggacagcc tgttggggga gatccagaag tccgcaaaca gatgccacct ccaccaccct 1440
gtccaggcag agagcttttt gatgatccct cctatgtcaa cgtccagaac ctagacaagg 1500
cccggcaagc agtgggtggt gctgggcccc ccaatcctgc tatcaatggc agtgcacccc 1560
gggacctgtt tgacatgaag cccttcgaag atgctcttcg ggtgcctcca cctccccagt 1620
cgggtgtccat ggctgagcag ctccgagggg agccctgggt ccatgggaag ctgagccggc 1680
gggaggctga ggcactgctg cagctcaatg gggacttctt ggtacgggag agcacgacca 1740
cacctggcca gtatg tgctc actggcttgc agagtgggca gcctaagcat ttgctactgg 1800
tggacctga ggggtgtggt cggactaagg atcacgctt tgaaagtgtc agtcacctta 1860
tcagctacca catggacaat cacttgccca tcatctctgc gggcagcga cgtgtgtctac 1920
agcaacctgt ggagcggaaa ctgtgatctg ccctagcgct ctcttcaga agat gccctc 1980
caatcctttc caccctattc cctaactctc gggacctcgt ttgggagtgt tctgtgggct 2040
tggccttctg tcagagctgg gactgtgggt ttcatatcca gctgagtga 2100
agggtttgag tcaaaagcct ggggtgagaat cctgcctctc cccaaacatt aatcaccaaa 2160
gtattaatgt acagagtggc ccctcacct g ggcctttcct gtgccaacct gatgccctt 2220
ccccaagaag gtgagtgtt gtcatggaaa atgtcctgtg gtgacaggcc cagtggaaaca 2280
gtcaccttc tgggcaagg ggaacaaatc acacctctg gcttcagggt atccagacc 2340
cctctcaaca cccgcccccc ccatgtttaa actttgtgcc tttgaccatc tcttaggtct 2400
aatgatattt tatgcaaaca gttcttggac ccctgaattc ttcaatgaca gggatgccaa 2460
caccttcttg gcttctggga cctgtgttct tctgtgacac cctctccggt ttgggttggg 2520
ataacagagg caggagtggc agctgtcccc tctccctggg gatatgcaac ccttagagat 2580
tgccccagag cccactccc ggcaggcgg gagatggacc cc tcccttgc tcagtgcctc 2640
ctggccgggg cccctcacc caaggggtct gtatatacat ttcataaggc ctgccctccc 2700
atgttgcatg cctatgtact ctgcgcaaaa gtgcagccct tccctcctgaa gctctgccc 2760
tgctccctt tctgggaggg cgggggtggg gtgactgaat ttgggcctct tgtacagtta 2820
actctcccag gtgatt ttg ttgaggtgag aaaaggggca ttgagactat aaagcagtag 2880
acaatcccc cataccatct gtgagtttg aactgcattc ttttaaagtt ttatatgcat 2940
atattttagg gctgctagac ttactttcct attttctttt ccattgctta ttcttgagca 3000
caaaatgata atcaattatt acattttatac atcacctttt tgacttttcc aagccc tttt 3060
acagctcttg gcattttcct cgctaggcc tgtgaggtaa ctgggatcgc accttttata 3120
ccagagacct gaggcagatg aaattttatt ccatctagga ctagaaaaac ttgggtctct 3180
taccgcgaga ctgagaggca gaagtcagcc cgaatgcctg tcagtttcat ggaggggaaa 3240
cgcaaaacct gcagttcctg agtaccttct acaggcccgg ccagcctag gccgggggtg 3300
gccacaccac agcaagccgg cccccctct tttggccttg tggataaggg agagttgacc 3360
gttttcatcc tggcctcctt ttgctgtttg gatgtttcca cgggtctcac ttataccaaa 3420
gggaaaactc ttcattaaag tccgtatttc ttctaaaaaa aaaaaaaaaa aaatacattt 3480
atacatcacc tttttgactt ttccaagccc ttttacagct cttggcattt tcctcgcta 3540
ggcctgtgag gtaactggga tcgcaccttt tataccagag acctgaggca gatgaaattt 3600
atttccatct aggactagaa aaacttgggt ctcttaccgc gagactgaga ggcagaagtc 3660
agcc 3664

```

<210> 166

<211> 449

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(449)

<223> 3' terminal sequence.

glyceraldehyde-3-phosphate dehydrogenase (GAPD)
gene.

<400> 166

110/292

```
gagcacaggg tncctttattg atggtacatg acaagggtgcg gctccctagg cccctcccct 60
cttcaagggg tctacatgga aactgtgagg aggggagatt cagtgtggtg ggggactgag 120
tntggcaggg actccccagc agtgagggtc tctctcttcc tcttgtgctc ttgctggggc 180
tggtggtcca ggggt cttac tccttgagg ccattgtggc atgagggtcca ccacctgtt 240
gctgtagcca aattcggtgt cataccaggg aatgagctt gacaaagtgg tcgttgagg 300
caatgccagc cccagccttc gaagggtgag gantgggttt cgctnttgaa gtcagaggag 360
accacctggg tgctcagttt agcccaggga tgcccttgag ggggccctcc gacgttt ttt 420
tcaccacctt tttgatntca tcatntttt 449
```

<210> 167

<211> 467

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(467)

<223> 5' terminal sequence.

glyceraldehyde-3-phosphate dehydrogenase (GAPD)
gene.

<400> 167

```
tggttcagac tcagccgcat cttcttttgc gtcgccagcc gagccacatc gctgagacac 60
catggggaag gtgaaggctcg gagtcaacgg atttggtcgt attgggcgcc tggtcaccag 120
ggctgctttt aactctggta aagtggata t tggtgccatc aatgaccctt tcattgacct 180
caactacatg gtttacatgt tccaatatga ttccacccat gggcaaattc catgggcacc 240
gtcaaggctg agaacgggaa gcttgtcatc aatgggaaat cccattcacc atcttcagg 300
gagcgagatc cctccaaaat tcaagtggg ggcgatgctg ggcgcttgag ttacgttcgt 360
gggagttcca ctgggccttc tttcaaccac ctttgagaa gggtttggg gttcatttn 420
caaggggggg gagcccaaan ggtcttcat tttttggccc ccttttt 467
```

<210> 168

<211> 316

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(316)

<223> 3' terminal sequence. desmin (DES) gene.

<400> 168

```
ggcttgtgtt tntntctctt ttattgtttc tctccagagc ccctgcagca ggggagggga 60
gggcgtgggg aggtgggcgc cctcccacc agcctgagac cgctctctgc ctctctctc 120
tcctctcttc tccagcatct cac ccacttt ctctccttct naatctcctg ctcccacctc 180
cagcaccttc ggggattccc tctttagacc cctgctttct aagtccacc ggggctgggg 240
aaaggaaagt aagagaccac ggggacaatt tcaagcccc cagntccac aggggctagt 300
cccctgggnt acctgc 316
```

<210> 169

<211> 440

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(440)

<223> 5' terminal sequence. desmin (DES) gene.

<400> 169

```
atctcccat ccagacctac tctgccctca acttccgag a aaccagccct gagcaaagg 60
gttctgaggt ccataccaag aagacgggtga tgatcaagac catcgagaca cgggatggg 120
aggctcgtcag tgaggccaca cagcagcagc atgaagtgt ctaaagacag agaccctctg 180
ccaccagaga ccgtcctcac ccctgtcctc actgtccct gaagccagcc ttcttccatc 240
ccagggacac cacaccca gc cttcagtct ccccttcaca gcctctggac ccctcctcac 300
tgggccattc cctcgtggtt ccccaacagc ggacataggc ccctccttgc tgggttcaca 360
ggggcatggc cccgggccac ttnttgcggg aaccacagtt gttgaggctt tgggtgtttg 420
ggcagttgag ttgaggcttt                                     440
```

<210> 170

<211> 2218

<212> DNA/RNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(2218)

<223> desmin (DES) gene.

<400> 170

```
cctcgccgca tccactctcc ggccggccgc ctgccgcgc cctcctcc gt gcgccgccca 60
gcctcgcccg cgcgctcacc atgagccagg cctactcgtc cagccagcgc gtgtcctcct 120
accgccgcac cttcggcggc gccccgggct tcccgcctcg ctccccgctg agctcgcccg 180
tgttcccgcg gccgggtttc ggtcttaagg gctcctccag ctccgtgacg tcccgcgtgt 240
accaggtgtc gcgcacgtcg ggccggg ccg ggggcctggg gtcgctgcgg gccagccggc 300
tggggaccac ccgcacgcc tctcctacg gcgcaggcga gctgtggac ttctacttg 360
ccgacgcggt gaaccaggag ttcttgacca cgcgcaccaa cgagaagggt gagctgcagg 420
agctcaatga ccgcttcgcc aactacatcg agaagggtcg cttcctggag cagcagaacg 480
cgctcgccgc cgaagtgaac cggctcaagg gccgcgagcc gacgcgagtg gccgagctct 540
acgaggagga gctgcgggag ctgcggcgcc aggtggaggt gctcactaac cagcgcgcg 600
gcgtcgacgt cgagcgcgac aacctgctcg acgacctgca gcggctcaag gccaaagtgc 660
aggaggagat tcagttgaag gaagaagcag agaacaattt ggctgcc ttc cgagcggacg 720
tggtgcagc tactctagct cgattgacc tggagcgcag aattgaatct ctcaacgagg 780
agatcgcggt ccttaagaaa gtgcattgag aggatccg tgagttgcag gctcagcttc 840
aggaacagca ggtccaggtg gagatggaca tgtctaagcc agacctcact gccgcctca 900
gggatatccg ggtcagtat gagac catcg cggctaagaa catctctgaa gctgaggagt 960
ggtacaagtc gaagggtgtc gacctgacc aggcagccaa caagaacaac gacgccctgc 1020
gccaggccaa gcaggagatg atggaatacc gacaccagat ccagtcctac acctgcgaga 1080
ttgacgccct caagggcact aacgattccc tgatgaggca gatgcgggaa ttggaggacc 1140
gatttgccag tgaggccagt ggctaccagg acaacattgc gcgcctggag gaagaaatcc 1200
ggcacctcaa ggatgagatg gcccgccatc tgccgcgagta ccaggacctg ctcaacgtga 1260
agatggccct ggatgtggag attgccacct accggaagct gctggaggga gaggagagcc 1320
ggatcaatct ccccatccag acctactctg cctcaactt ccgagaaacc agccctgagc 1380
aaaggggttc tgaggtccat accaagaaga cggatgatga caagaccatc gagacacggg 1440
atggggaggt cgtcagttag gcgacacagc agcagcatga agtgctctaa agacgagaga 1500
ccctctgcca ccagagaccg tctcaccgcc tgtctcact gctccctgaa gccagcctt 1560
```


112/292

```

cttccatccc agga caccac acccagcctc agtcctcccg tcacagcctc tgacccctcc 1620
tcactggcca tccctcgtgg tccccaacag cgacatagcc catccctgcc tggtcacagg 1680
catgccccgg ccacctctgc ggaccccagc tgtgagcctt ggctgttggc agtgagttag 1740
cctggctctt gtgctggatg gagcccaggc gggagcgggtg gccctgtccc tcc cacctct 1800
gtgacctgag gcctacgctt tggctctgga gatagcccca gagcagggtg ttgggatact 1860
gcagggccag gactgagccc cgcagacctc cccagcccct agcccaggag agagaaagcc 1920
aggcaggtag cctgggggac tagccctgtg gagactgggg ggcttgaat tgtccccgtg 1980
gtctcttact ttcttttccc cagcccag gg tggacttaga aagcaggggc tacaagaggg 2040
aatccccgaa ggtgctggag gtgggagcag gagattgaga aggagagaaa gtgggtgaga 2100
tgctggagaa gagagaggag gagagaggca gagagcggtc tgaggctggg gggaggggag 2160
cccacctccc cagccctccc cccccctgc tgcaggggct ctggagagaa acaataaa 2218

```

<210> 171

<211> 367

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(367)

<223> 5' terminal sequence. casein kinase 2, beta polypeptide (CSNK2B) gene.

<400> 171

```

gatccaagcc cgctacatcc ttaccaaccg tggcatcgcc agatgttggg aaagtaccag 60
caaggagact ttgggttactg tcctcgtgtg tactgtgaga accagccaat gcttccatt 120
ggcctttcag acatcccagg tgaagccatg gtgaagctct actgcccacaa gtgcatggat 180
gtgtacacac ccaagtcatc aagacacatc cacacggatg ggcgcctac t ttcggcactg 240
gtttccctca catgctcttc atgggtgcat cccgagtacc ggcccaaggg gaccttgcca 300
accagtttgt gccaggggtt ttacggtttt caaggttcca tncggtgggg cttaccagg 360
tgcaggt 367

```

<210> 172

<211> 1128

<212> DNA/RNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(1128)

<223> casein kinase 2, beta polypeptide (CSNK2B) gene.

<400> 172

```

gcttctcggt gtgccccgcc cgcaagcgcc ctctccggg ccttc gtgac agccagggtg 60
tgcgcggggt atcctgggat tggtagttcg ctttctctca tttagccagt ttctttctct 120
accggggact cegtgtcccg gcatccaccg cggcacctga ccttgggcgc ttgcgtgttg 180
ccctcttccc caccctccct aatttccact cccccaccc cacttcgcct gccgcggtcg 240
ggtccgcggc ctgcgctgta gcgg tcgccc cegtccctg gaagtagcaa cttccctacc 300
ccacccagct cctgggtccc gtccagccgc tgacgtgaag atgagcagct cagaggagg 360
gtcctggatt tcctggttct gtgggctccg tggcaatgaa ttcttctgtg aagtggatga 420
agactacatc caggacaaat ttaattctac tggactcaat gagcagggtc ctcactatcg 480
acaagctcta gacatgatct tggacctgga gcctgatgaa gaactggaag acaaccccaa 540

```

113/292

```

ccagagtgc ctgattgagc aggcagccga gatgctttat ggattgatcc acgcccgccta 600
catccttacc aaccgtggca tgcgccagat gttggaaaag taccagcaag gagactttgg 660
ttactgtcct cgtgtgtact gtgagaacca gccaatgctt ccca ttggcc ttccagacat 720
cccagtgtaa gccatggtga agctctactg cccaagtgc atggatgtgt acacacccaa 780
gtcatcaaga caccatcaca cggatggcgc ctacttcggc actggtttcc ctcacatgct 840
cttcattggtg catcccagat accggcccaa gagacctgcc aaccagtttg tgcccaggct 900
ctacggtttc aagatccatc cg atggccta ccagctgcag ctccaagccg ccagcaactt 960
caagagccca gtcaagacga ttcgctgatt cctccccc cctgtcctgc agtctttgtc 1020
ttttccttcc ttttttgcca cctttcagg aacctgtat ggtttttagt ttaaattaaa 1080
ggagtcgtta tcgtgggtgg aatatgaaat aaagtagaag aaaaggcc 11 28

```

<210> 173

<211> 475

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(475)

<223> 3' terminal sequence. golgi apparatus
protein 1 (GLG1) gene.

<400> 173

```

gggttttttt ctnaaaaaaa cctttgagtt gcaggtcagg tnaagttggtt ctggaagtac 60
cggaagttct gttggnatga gagagacttg tctacaggca ggnaaaccca agtttgccaa 120
acaaaggcag taaccccagc gaccagctgc tgctgtgca cggtagaggag gaggaggaca 180
ccatggacac gagtggaggc tggatgggac aacgcagtgg acatctgcta atg ctctaac 240
acggggttgg ngtcacttct gagaagagcg aggttnagtgg ggaatnctata caagagggtt 300
ntacaaactg gggcactggg atagggtagt tcctttgggn gggtaaggt gggctctacc 360
ccgtccnttg agctctngtg tncactncgc ttggggggtc cntcccaca cattcagggc 420
cantcaggna caattttacc aggtgntccc a ctgtttcac agggggattt aagtt 475

```

<210> 174

<211> 483

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(483)

<223> 5' terminal sequence. golgi apparatus
protein 1 (GLG1) gene.

<400> 174

```

ggtcatctct tgcctgaagc tgagatatgc tgaccagcgc ctgtcttcag actgtgaaga 60
ccagatccga atcattatcc aggagtccgc cctggactac cgcctggatc ctgagctcca 120
gctgcaactgc tcagacgaga tctccagtct atgtgctgaa gaagcagcag cccaagagca 180
gacaggtcag gtggaggagt gcc tcaaggc caacctgctc aagatcaaaa cagaattgtg 240
taaatnggaa gtgctaaaca tgctgaagga aagcaaagca gacatctttg ttgacccggt 300
acttcatact tgcttgtgcc ctgggacatt aaacaccact gcgcagcatt caccctgggc 360
cgcgggcggt caaattgttc ctgtnttcat gggaaggcac tgggagggtt aaggcgggtt 420
gaggtttaca gcccgagttg caaaaaggcg cttcattgac ccggtttgag gtgttggtt 480
ttt 483

```

<210> 175
<211> 3909
<212> DNA/RNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<220>
<221> misc_feature
<222> (1)..(3909)
<223> golgi apparatus protein 1 (GLG1) gene.

<400> 175
ggcagcaggc tcgcgcggga ctcaagatgg cggcgtgtgg acgtgtacgg aggatgttcc 60
gcttgtcggc ggcgctgcat ctgctgctgc tattcgcggc cgggggcaga aactccccgg 120
ccaggcgctc ccacagccag ggccagggtc ccggggccaa ctttgtgtcc ttctagggc 180
aggccggagg cggcgccccg gcgggtcagc agctgcccc a gctgcctcag tcctgcagc 240
ttcagcagca acagcagcag cagcaacagc aacagcagcc tcagccgccg cagccgcctt 300
tcccgcgggg tgggcctccg cggcggggag gagcgggggc tgggtggggc tggaag ctgg 360
cggagggaaga gtctgcagg gaggacgtga cccgcgtgtg ccctaagcac acctggagca 420
acaacctggc ggtgctcgag tgctgcagg atgtgaggga gcctgaaaat gaaatttctt 480
cagactgcaa tcatttgttg tggaattata agctgaacct aactacagat cccaaatttg 540
aatctgtggc cagagagggt tgcaaatcta ctat aacaga gattaagaa tgtgctgatg 600
aaccggttgg aaaagggttac atggtttcct gcttagtgga tcaccgaggc aacatcactg 660
agtatcagtg ataccagtac attaccaaga tgacggccat catttttagt gattaccgtt 720
taatctgttg cttcatggat gactgcaaaa atgacatcaa cattctgaaa tgtggcagta 780
ttcggcttgg agaaaaggat gcacattcac aagggtgaggt ggtatcatgc ttggagaaag 840
gcctggtgaa agaagcagaa gaaagagaac ccaagattca agtttctgaa ctctgcaaga 900
aagccaattc ccgggtggct gagctgtcat cggatgactt tcaacttagac cggcatttat 960
atthtcttgg ccgagatgat cgggagcggt tttgtgaaaa tacacaagct ggtg agggca 1020
gagtgtataa gtgcctcttt aaccataaat ttgaagaatc catgagtga aagtgtcgag 1080
aagcacttac aaccgcgcaa aagctgattg ccaggatta taaagtcagt tattcattgg 1140
ccaaatctcg taaaagtgaac ttgaagaaat accggtgcaa tgtggaaaac cttccgcgat 1200
cgcgtgaagc caggctctcc tacttgta a tgtgcctgga gtcagctgta cacagagggc 1260
gacaagtcag cagtgaagtgc cagggggaga tgctggatta ccgacgcatg ttgatggaag 1320
acttttctct gagccctgag atcatcctaa gctgtcgggg ggagattgaa caccattgtt 1380
ccgattaca tcgaaaagga cggaccctac actgtctgat gaaggtagtt cgaggggaga 1440
aggggaacct tggaaatgac tgccagcagg cgcttcaaac actgattcag gagactgacc 1500
ctggtgcaga ttaccgcatt gatcgagctt ccaatgaagc ttgtgaatct gtaatccaga 1560
cagcctgcaa acatataaga tctggagacc caatgatctc gtcgtgcctg atggaacatt 1620
tatacacaga gaagatggtg gaagactgtg aacaccgtct ct tagagctg cagtatttca 1680
tctcccgga ttggaagctg gacctgtcc tgtaccgcaa gtgccaggga gacgttctc 1740
gtctttgcca caccacgggt tggaatgaga ccagtgaatt tatgcctcag ggagctgtgt 1800
tctcttgttt atacagacac gcctaccgca ctgaagaaca gggaaggagg ctctcacggg 1860
agtgcgagc tgaagtc caa aggatcctac accagcgtgc catggatgtc aagctggatc 1920
ctgcctcaca ggataagtgc ctgattgatc tgggaaaatg gtgcagtga aaaacagaga 1980
ctggacagga gctggagtgc cttcaggacc atctggatga cttggtggtg gagtgtagag 2040
atatagttgg caacctcact gagttagaat cagaggatat ccaaatagaa gccttg ctga 2100
tgagagcctg tgagcccata attcagacat tctgccacga tgcggataac cagatagact 2160
ctggggacct gatggagtgt ctgatacaga acaaacacca gaaggacatg aacgagaagt 2220
gtgccatcgg agttacccac ttccagctgg tgcagatgaa ggattttcgg tttcttaca 2280
agtttaaat ggctgcaag gaggacgtgt tgaagctttg ccaaacata aaaaagaagg 2340
tggaagtggt gatctgcctg agcacgaccg tgcgcaatga cactctgcag gaagccaagg 2400
agcacagggt gtccctgaag tgccgcaggc agctccgtgt ggaggagctg gagatgacgg 2460
aggacatccg cttggagcca gatctatacg aagcctgcaa gagtgcacac aaaaacttct 2520
gttccgctgt gcaatatggc aacgctcaga ttatcgaatg tctgaaagaa aacaagaagc 2580
agctaagcac ccgctgccac caaaaagtat ttaagctgca ggagacagag atgatggacc 2640
cagagctaga ctacaccctc atgaggggtct gcaagcagat gataaagagg ttctgtccgg 2700

aagcagattc taaaaccatg ttgcagtgt tgaagcaaaa taaa aacagt gaattgatgg 2760
atcccaaagt caaacagatg ataaccaagc gccagatcac ccagaacaca gattaccgct 2820
taaaacccat gttaagaaaa gcctgtaaag ctgacattcc taaattctgt cacggatatcc 2880
tgactaaggc caaggatgat tcagaattag aaggacaagt catctcttgc ctgaagctga 2940
gatatgctga ccagcgccct g tcttcagact gtgaagacca gatccgaatc attatccagg 3000
agtccgcctt ggactaccgc ctggatcctc agctccagct gcaactgctca gacgagatct 3060
ccagtctatg tgctgaagaa gcagcagccc aagagcagac aggtcaggtg gaggagtgcc 3120
tcaagggtcaa cctgctcaag atcaaaacag aattgtgtaa aaaggaagtg ctaaact gc 3180
tgaaggaaag caaagcagac atctttgttg acccggtact tcatactgct tgtgccctgg 3240
acattaaaca ccaactgcga gcaactaccc ctggccgcgg gcgtcaaatg tctgtctca 3300
tggaagcact ggaggataag cgggtgaggt tacagcccga gtgcaaaaag cgcctcaatg 3360
accggattga gatgtggagt tacgcagcaa ag gtggcccc agcagatggc ttctctgatc 3420
ttgccatgca agtaatgacg tctccatcta agaactacat tctctctgtg atcagtggga 3480
gcatctgtat attgttcctg attggcctga tgtgtggacg gatcaccag cgagtgcac 3540
gagagctcaa ggacaggtag agccacctg accaccaaag gaactaccta tccagtgcc 3600
agtttgtaca gccctcttgt atagcatccc cactcacctc gctcttctca gaagtgcac 3660
caaccccgctg tttagagcatt agcagatgtc cactgcgttg tcccatccag cctccactcg 3720
tgtccatggt gtccctctcc tctcaccgt gcagcagcag cagctggctg ctgggggttac 3780
tgcccttctg ttggcaactt ggggttacct gcctgtagac aagtct ctct cataccaaca 3840
gaacttcgg tacttccaga accaactcac ctgacctgca actcaaaggc tttttaaga 3900
aaaccacca 3909

<210> 176

<211> 390

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(390)

<223> 5' terminal sequence. endothelin receptor
type b (EDNRB) gene.

<400> 176

gttaagatca aacctcaca agagaaatag aatgtttgaa aggctatccc aaaagacttt 60
tttgaatctg tcattcacat accctgtgaa gac aatacta tctacaattt tttcaggatt 120
attaaaatct tcttctttca ctatcgtagc ttaaaactctg tttggttttg tcatctgtaa 180
atacttacct acatacactg catgtagatg attaaatgag ggcaggccct gtgctcatag 240
ctttacgatg gagagatgcc agtgacctca taataaagac tgtggaactg cctgggtgca 300
gtgtccacat gacaaagggg caggtaggca ccctctcttc acccatgctg tgggttaa 360
gggtttctag gcatatgtat tatggctatt 390

<210> 177

<211> 4286

<212> DNA/RNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(4286)

<223> endothelin receptor type b (EDNRB) gene.

<400> 177

gagacattcc ggtgggggac tctggccagc ccgagcaacg tggatcctga gagcactccc 60
 aggtaggcat ttgcccgggt gggacgcctt gccagagcag tgtgtggcag gccccctgg 120
 aggatcaaca cagtggctga ac actgggaa ggaactggta cttggagtct ggacatctga 180
 aacttggctc tgaaactgcg cagcggccac cggacgcctt ctggagcagg tagcagcatg 240
 cagccgcctc caagtctgtg cggacgcgcc ctggttgccg tggttcttgc ctgcgccctg 300
 tcgcggtatc ggggagagga gagaggcttc ccgcctgaca gggccactcc gcttttgcaa 360
 accgcagaga taatgacgcc accactaag accttatggc ccaagggttc caacgccagt 420
 ctggcgcggt cgttggcacc aatgaggtg cctaaaggag acaggacggc aggatctccg 480
 ccacgcacca tctccctcc cccgtgccaa ggacccatcg agatcaagga gactttcaaa 540
 tacatcaaca cggttgtgtc ctgccttgtg ttctgtctgg gg atcatcgg gaactccaca 600
 cttctgagaa ttatctacaa gaacaagtgc atgcgaaacg gtcccaatat cttgatcgcc 660
 agcttggctc tgggagacct gctgcacatc gtcattgaca tccctatcaa tgtctacaag 720
 ctgctggcag aggactggcc atttggagct gagatgtgta agctggtgcc tttcatacag 780
 aaagcctccg tgggaatcac tgtgctgagt ctatgtgctc tgagtattga cagatatcga 840
 gctgttgcct ctttggcacc aattaaagga attggtgttc caaatggac agcagtagaa 900
 attgttttga tttgggtggt ctctgtggtt ctggtgttcc ctgaagccat aggttttgat 960
 ataattacga tggactacaa aggaagtatt ctgcgaatct gcttgcttca tcccgttcag 10 20
 aagacagctt tcatgcagtt ttacaagaca gcaaaagatt ggtggctggt cagtttctat 1080
 ttctgcttgc cattggccat cactgcattt ttttatacac taatgacctg tgaaatgttg 1140
 agaaagaaaa gtggcatgca gattgcttta aatgatcacc taaagcagag acgggaagtg 1200
 gccaaaaccg tcttttgcct ggtccttgtc ttgtccc tct gctggcttcc cttcacctc 1260
 agcaggatct tgaagctcac tctttataat cagaatgatc ccaatagatg tgaacttttg 1320
 agctttctgt tggatttga ctatattggt atcaacatgg cttactgaa ttccctgcatt 1380
 aacccaattg ctctgtattt ggtgagcaaa agattcaaaa actgctttaa gtcattgctta 1440
 tgctgctggt gccagtcatt tgaagaaaaa cagtccttgg aggaaaagca gtcgtgctta 1500
 aagttcaaaag ctaatgatca cggatatgac aacttccgtt ccagtaataa atacagctca 1560
 tcttgaagaa agaactatct actgtatttc attttcttta tattggaccg aagtcattaa 1620
 aacaaaatga aacatttggc aaaacaaaac aaaaaactat gtatttgcac agcacactat 1680
 taaaatatta agtgaatta ttttaacact cacagctaca tatgacattt tatgagctgt 1740
 ttacggcatg gaaagaaaat cagtgggaat taagaaaagc tcgtcgtgaa agcacttaat 1800
 tttttacagt tagcacttca acatagctct taacaacttc caggatattc acacaacact 1860
 taggcttaaa aatgagctca ctacg aattt ctattctttc taaaagaga tttattttta 1920
 aatcaatggg actctgatat aaaggaagaa taagtcactg taaaacagaa cttttaaatg 1980
 aagcttaaat tactcaattt aaaattttta aatcctttta acaactttt caattaatat 2040
 tatcacacta ttatcagatt gtaattagat gcaaatgaga gagcagttta gttgttgcat 2100
 ttttcggaca ctggaacat ttaaatgac agggaggagt aacagaaaaga gcaaggctgt 2160
 ttttgaagaa cattacactt tcaactagaag cccaaacctc agcattctgc aatatgtaac 2220
 caacatgtca caaacaagca gcatgtaaca gactggcaca tgtgccagct gaatttaaaa 2280
 tataatactt ttaaaaagaa aattattaca tcttttaca t tcagttaaga tcaaacctca 2340
 caaagagaaa tagaatgttt gaaaggctat cccaaaagac ttttttgaat ctgtcattca 2400
 cataccctgt gaagacaata ctatctacaa ttttttcagg attattaaaa tcttcttttt 2460
 tcactatcgt agcttaaaact ctgtttgggt ttgtcatctg taaataacta cctacatata 2520
 ctgcatgtag atg attaaat gagggcaggc cctgtgctca tagctttacg atggagagat 2580
 gccagtgacc tcataataaa gactgtgaac tgccctggtg agtgtccaca tgacaaaggg 2640
 gcaggtagca ccctctctca cccatgctgt ggttaaaatg gtttctagca tatgtataat 2700
 gctatagtta aaatactatt tttcaaaatc atacagatta gtacatttaa ca gctacctg 2760
 taaagcttat tactaatttt tgtattattt ttgtaaatag ccaatagaaa agtttgcttg 2820
 acatggtgct tttctttcat ctagaggcaa aactgctttt tgagaccgta agaacctctt 2880
 agctttgtgc gttcctgcct aatttttata tcttctaagc aaagtgcctt aggatagctt 2940
 gggatgagat gtgtgtgaaa gtatgta caa gagaaaacgg aagagagagg aatgagggtg 3000
 gggttggagg aaacccatgg ggacagattc ccattcttag cctaacgttc gtcattgcct 3060
 cgtcacatca atgcaaaagg tctgatattt gttccagcaa aacacagtgc aatgttctca 3120
 gagtgacttt cgaaataaat tgggcccagg agctttaact cggctcttaa atatgcccaa 3180
 atttttactt tgtttttctt ttaataggct gggccacatg ttggaataaa gctagtaagt 3240
 ttgttttctg tcaattattg atgtgatggt acagtaaacc aaaaccaaac aatgtggcca 3300
 gaaagaaaga gcaataataa ttaattcaca caccataggt attctattta taaatcacc 3360
 acaaaactgt tctttaattt catoccaatc actttttcag aggcctgtta tcatagaagt 3420
 cattttagac tctcaatttt aaattaattt tgaatcacta atattttcac agttttattaa 3480
 tatatttaat ttctatttaa atttttagatt atttttatta ccatgtactg aatttttaca 3540
 tcttgatacc ctttcttctt ccatgtcagt atcatgttct ctaattatct tgccaaattt 3600
 tgaaactaca cacaa aaagc atacttgcatt tatttataat aaaattgcat tcagtggctt 3660

117/292

```

tttaaaaaaa atgtttgatt caaaacttta acatactgat aagtaagaaa caattataat 3720
ttctttacat actcaaaacc aagatagaaa aagggtgctat cgttcaactt caaaacatgt 3780
ttcctagtag taaggacttt aatatagcaa cagacaaaat tattgttaac atgg atgta 3840
cagctcaaaa gatttataaa agattttaac ctattttctc ccttattatc cactgctaata 3900
gtggatgtat gttcaaacac ctttttagtat tgatagctta catatggcca aaggaatata 3960
gtttatagca aaacatgggt atgctgtagc taactttata aaagtgtaat ataacaatgt 4020
aaaaaattat atatctggga ggatttttt g gttgcctaaa gtggctatag ttactgattt 4080
tttattatgt aagcaaaacc aataaaaatt taagtttttt taacaactac cttattttttc 4140
actgtacaga cactaattca ttaaatacta attgattgtt taaaagaaat ataaatgtga 4200
caagtggaca ttatttatgt taaatataca attatcaagc aagtatgaag ttattcaatt 4260
aaaatgccac' atttctgggc tctggg 4286

```

<210> 178

<211> 462

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(462)

<223> 3' terminal sequence. gran zyme b (granzyme
2, cytotoxic t-lymphocyte-associated serine
esterase 1) (GZMB) gene.

<400> 178

```

acancagaga tccatttatt acagtcctgc aaccccgact gccacccct tgggaattct 60
tgcctctgtc ccagagatgg tcaggcccag aggaagggtta gtctcatgcc tgctgttaga 120
ggcgnntcat tgttctcttt atccagggca ggaagtntga gaccttgatg tagactcctg 180
gggggtgtccc tttttgttt ccataggaga gaataccttg ggctangtcc ttacananga 240
ggggccccc ccagttcccc cttgaaaccg gtctgtgtct tctttggatc cccacacaa 300
atntcagtg gctctgctgt aattgccatg ggaaggagac gggtcac ant gggcagttcc 360
ttctgcactn ttcaggaaca atttctgaa gtgtgggttg ctaaagtgtc cattgagaaa 420
taacccagc ccaggccaaa ttgaaaagtt gcctgggntt tt 462

```

<210> 179

<211> 960

<212> DNA/RNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(960)

<223> granzyme b (granzyme 2, cytotoxic
t-lymphocyte-associated serine esterase 1) (GZMB)
gene.

<400> 179

```

agcagctcca accagggcag ctttctgag aagatgcaac caatcctgct tctgctggcc 60
ttctctctgc tgcccagggc agatgcaggg gagatcatcg ggggacatga ggccaagccc 120
cactcccgcc cctacatggc ttatcttatg atctgggatc agaagtctct gaagaggtgc 180
ggtggcttcc tgatacaaga cgacttctgt ctgacagctg ctcactgttg gggaagctcc 240
ataaatgtca ccttgggggc ccacaatatc aaagaacagg agcc gaccca gcagtttatc 300
cctgtgaaaa gacccatccc ccatccagcc tataatccta agaacttctc caacgacatc 360

```

118/292

atgctactgc agctggagag aaaggccaag cggaccagag ctgtgcagcc cctcaggcta 420
 cctagcaaca agggccaggt gaagccaggg cagacatgca gtgtggccgg ctgggggag 480
 acggccccc tgggaaaaca ct cacaacaca ctacaagagg tgaagatgac agtgcaggaa 540
 gatcgaaagt gcgaatctga cttacgccat tattacgaca gtaccattga gttgtgcgtg 600
 ggggaccag agattaaaaa gacttccttt aagggggact ctggaggccc tcttgtgtgt 660
 aacaagggtg cccaggggcat tgtctcctat ggacgaaaca atggcatgcc tccacgagcc 720
 tgcaccaaag tctcaagctt tgtacactgg ataaagaaaa ccatgaaacg ctactaacta 780
 caggaagcaa actaagcccc cgctgtaatg aaacaccttc tctggagcca agtccagatt 840
 tacactggga gaggtgccag caactgaata aatacctctc ccagtgtaaa tctggagcca 900
 agtccagatt tacactggga gaggtgccag caactgaata aa tacctctt agctgagtgg 960

<210> 180

<211> 471

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(471)

<223> 3' terminal sequence. fibroblast growth
 factor receptor 1 (fms-related tyrosine kinase 2,
 pfeiffer syndrome) (FGFR1) gene.

<400> 180

tnaagcagca gcaattttta ttgagggacc taaactgaaa ataggtttag aacataattt 60
 aaaaaataa aacagcaaaa gtagcaaaaa atatatgacc tttttaaaaa cattttcctt 120
 ttttttcttt ttgtttttta atatatagca actga tgcct cccagccacc agngcatct 180
 taccgatggt gtaaatctct ggtaacgacc cttttaaaaa gacatgtaaa tatatactca 240
 gntttatata ctttgtgttt tcttcatagc tatntacaga gccccagtt tgggctgggc 300
 cagggggccn caacactgcc cccaacctgg gccttcgcct caccatcctc tgggtaccgg 360
 gcntttgggt caggcaaaagc aaactagtnt cgggtttatt angccactgg naccaccttt 420
 ttgggggagc aggtcacctt cattcgaggg cacgangcac tgacctcctt t 471

<210> 181

<211> 463

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(463)

<223> 5' terminal sequence. fibroblast growth
 factor receptor 1 (fms-related tyrosine kinase 2,
 pfeiffer syndrome) (FGFR1) gene.

<400> 181

gctttgtcgc cagccacttc atccccctcc agatgttgga ccaacacccc tccctgccac 60
 caggactgcc tggggggagg agtgggagcc aatgaacagg catgcaagtg agagcttct 120
 gagctttctc ctgtcgggtt ggtctgtttt gccttcaccc ataagcccct cgcaactntgg 180
 tggcaggtgc cttgtcctca gggctacagc agtagggagg tcagtgtctc gtgcctogat 240
 tgaaggtgac ctctgcccca gataggtggt gccagtggct ttattaat tc cgatactagt 300
 ttgctttgct gaccaaagtc ctgggtacca gaggatggtg aggcgaaggc aggttggggg 360
 cagtgttgtg gccngggggc agcccaaaac tgggggcttc tgtatatagc tattgaagaa 420

aacacaaatg tattaatctg agtatatatt ttacatgtnt ttt

463

<210> 182

<211> 4066

<212> DNA/RNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(4066)

<223> fibroblast growth factor receptor 1

(fms-related tyrosine kinase 2, pfeiffer syndrome)

(FGFR1) gene.

<400> 182

```

cctcttgcgg ccacaggcgc ggcgtcctcg gcggcgggcg gcagctagcg ggagccggga 60
cgccggtgca gccgcagcgc gcggaggaac ccgggtgtgc cgggagctgg gcggccacgt 120
ccggacggga ccgagacccc tcgtagcgca ttgcggcgac ctgccttcc ccggccgcga 180
gcgcgccgct gcttgaagg ccgcggaacc caa ggacttt tctccggtcc gagctcgggg 240
cgccccgcag gcgcacggta cccgtgctgc agtcgggcac gccgcggcgc cgggggcctc 300
cgcagggcga tggagccggt ctgcaaggaa agtgaggcgc cgccgctgcg ttctggagga 360
ggggggcaca aggtctggag accccgggtg gcggacggga gccctccccc cgccccgcct 420
ccggggcacc agctccggt ccattgttcc cgcccggtc ggaggcgccg agcaccgagc 480
gccgcctggga gtcgagcgcc ggccgcggag ctcttgcgac ccgcccagga ccgaacaga 540
gcccgggggc ggccggcccg agccggggac gcgggcacac gcccgctcgc acaagccacg 600
gcggactctc ccgaggcgga acctccacgc cgagcgaggg tcagtttgaa aag gaggatc 660
gagctcactg tggagatcc atggagatgt ggagccttgt caccaacctc taactgcaga 720
actgggatgt ggagctggaa gtgcctctc ttctgggctg tgctggtcac agccacactc 780
tgcaccgcta ggccgtgccc gaccttgctt gaacaagccc agccctgggg agccctgtg 840
gaagtggagt ccttctggt ccaccgggt g acctgctgc agttgcgctg tcggtgctgg 900
gacgatgtgc agagcatcaa ctggctgcgg gacgggtgac agctggcgga aagcaaccgc 960
accgcgcatc caggggagga ggtggagggt caggactccg tgcccgcaga ctccggcctc 1020
tatgcttgcg taaccagcag cccctcgggc agtgacacca cctacttctc cgtcaatgtt 1080
tcagatgctc tcccctctc ggaggatgat gatgatgat atgactctc ttcagaggag 1140
aaagaaacag ataacaccaa accaaaccgt atgcccgtag ctccatattg gacatcccca 1200
gaaaagatgg aaaaagaatt gcatgcagt ccggctgcca agacagtga gttcaaatgc 1260
ccttcagtg ggaccccaaa cccacactg cgctgggtga aaaatgg caa agaattcaaa 1320
cctgaccaca gaattggagg ctacaagggt cgttatgcca cctggagcat cataatggac 1380
tctgtggtgc cctctgacaa gggcaactac acctgcattg tggagaatga gtacggcagc 1440
atcaaccaca cataccagct ggatgtcgtg gagcgggtccc ctaccggcc catcctgcaa 1500
gcaggggtgc ccgccaacaa a acagtggcc ctgggtagca acgtggagtt catgtgtaag 1560
gtgtacagtg acccgagcgc gcacatccag tggctaaagc acatcgaggt gaatgggagc 1620
aagattggcc cagacaacct gccttatgcc agatcttga agactgctgg agttaatacc 1680
accgacaaag agatggaggt gcttcactta agaaatgtct cctttgagga cgaggggag 1740
tatactgtct tggcgggtaa ctctatcgga ctctcccatc actctgcatg gttgaccgtt 1800
ctggaagccc tgggaagag gcgggcagtg atgacctcgc cctgtacct ggagatcatc 1860
atctattgca caggggcctt cctcatctcc tgcattgtgg ggtcgggtcat cgtctacaag 1920
atgaagagtg gtaccaagaa gagtgaactc cacag ccaga tggctgtgca caagctggcc 1980
aagagcatcc ctctgcgcag acaggtaaca gtgtctgctg actccagtgc atccatgaac 2040
tctggggttc ttctggttcg gccatcacgg ctctctccca gtgggactcc catgctagca 2100
gggtctctct agtatgagct tcccgaagac cctcgctggg agctgcctcg ggacagactg 2160
gtcttaggca aaccctggg agagggctgc tttgggcagg tgggtgttgc agaggctatc 2220
gggctggaca aggacaaacc caaccgtgtg accaaagtgg ctgtgaagat gttgaagtgc 2280
gacgcaacag agaaagactt gtcagacctg atctcagaaa tggagatgat gaagatgatc 2340
gggaagcata agaatatcat caacctgctg ggggcctgca cgcaggatg g tcccttgtat 2400
gtcatcgtgg agtatgcctc caagggcaac ctgcgggagt acctgcaggc ccggaggccc 2460
ccagggctgg aatactgcta caacccagc cacaaccagc aggagcagct ctctccaag 2520

```


120/292

```

gacctggtgt cctgcgccta ccaggtggcc cgaggcatgg agtatctggc ctccaagaag 2580
gtgtggaacc tgaaggctcc cct ggtgcat acaccgagac ctggcagcca ggaatgtcct 2640
ggtgacagag gacaatgtga tgaagatagc agactttggc ctgcacggg acattcacca 2700
catcgactac tataaaaaga caaccaacgg ccgactgcct gtgaagtgga tggcaccgga 2760
ggcattatct gaccggatct acaccacca gagtgatgtg tggctcttcg ggggtgctcct 28 20
gtgggagatc ttcactctgg gcggctcccc ataccocggg gtgcctgtgg aggaactttt 2880
caagctgctg aaggagggtc accgcatgga caagcccagt aactgcacca acgagctgta 2940
catgatgatg cgggactgct ggcatgcagt gccctcacag agaccacct tcaagcagct 3000
ggtggaagac ctggacgca tcgtggcctt gacctcc aac caggagtacc tggacctgtc 3060
catgccctg gaccagtact cccccagctt tccgcacacc cggagctcta cgtgctcctc 3120
aggggaggat tcggtcttct ctcatgagcc gctgcccag gagccctgcc tgcccgcaca 3180
cccagcccag cttgccaatg gcgactcaa acgcccgtga ctgccacca cacgccctcc 3240
ccagactoca ccgtcagctg taaccctcac ccacagcctg ctgggcccac caoctgtccg 3300
tccctgtccc ctttctgtct ggaggagcc ggtgcctac caggggcctt cctgtgtggc 3360
ctgccttcac cccactcagg tcacctctcc ctccacctc tctccacctg ctggtgagag 3420
gtgcaaaagc gcagatcttt gctgccagcc acttcatccc ctcccagatg ttggaccaac 3480
acccctccct gccacaggca ctgcctggag ggcagggagt gggagccaat gaacaggcat 3540
gcaagtgaga gctttctgag ctttctctg tcggtttggt ctgttttgcc ttcaccata 3600
agcccctgc actctggtgg caggtgcttg tctcagggc tacagcagta gggaggtcag 3660
tgcttctgtc ctgattgaa ggtga cctct gccccagata ggtggtgcca gtggcttatt 3720
aattccgata ctagtttgct ttgctgacca aatgcctggt accagaggat ggtgaggcga 3780
aggccagggt gggggcagtg ttgtgccctg tcccagccca aactgggggc tctgtatata 3840
gctatgaaga aaacacaaag tgtataaatc tgagtatata tttacatgtc tttttaaaag 3900
ggtcgttacc agagatttac ccacgggta agatgctcct ggtggctggg aggcacagct 3960
tgctatatat taaaaacaaa aaagaaaaat tttttaaaaa ggtcatatat 4020
tttttctac ttttctgtgt ttattttttt aaattatgtt ctaaac 4066

```

<210> 183

<211> 415

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(415)

<223> 5' terminal sequence. protein phosphatase 2
(formerly 2a), catalytic subunit, alpha isoform
(PPP2CA) gene.

<400> 183

```

cagttatata cctccatcac tagctggtga gctctagaca ccaacgtgag gccattggat 60
tgattaaatg tctcagaaat atcttgccca aagggtgtaac cagctcctcg aggagatata 120
ccccaaaccac caggtcctac tggatctgac cacagcaagt cacacattgg accctcatgg 180
ggaacttctt gtaggcgatc aagtgtctctg atatgatcca gtgtat ctat agatggcgag 240
agaccaccat gttagacagaa gatctgcccc tccaccaagg cagttagagg aagatagtca 300
aaaagatctg taaaatattt ccaaacattt ggcatttcca tattttctta aacattcatt 360
ctaggaaacc ttaaacttgt gtgnatctgt cnggtcttct ggtttccctg gagga 415

```

<210> 184

<211> 2181

<212> DNA/RNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(2181)

<223> protein phosphatase 2 (formerly 2a),
catalytic subunit, alpha isoform (PPP2CA) gene.

<400> 184

```
agagagccga gctctggagc ctcagcgagc ggaggaggag gcgcagggcc gacggccgag 60
tactgcggtg agagccagcg ggccagcgcc agcctcaaca gccgccagaa gtacacgagg 120
aaccggcgcc ggcgtgtgcg tgtaggcccg tgtgcggcg gcgcgcgcg aggagcgcg 180
agcgcgagcc ggctggggcg ggtggcatca tggacgagaa ggtgttcacc aa ggagctgg 240
accagtggat cgagcagctg aacgagtga agcagctgtc cgagtccag gtcaagagcc 300
tctgcgagaa ggctaaagaa atcctgacaa aagaatccaa cgtgcaagag gttcgatgtc 360
cagttactgt ctgtggagat gtgcatgggc aatttcatga tctcatggaa ctgtttagaa 420
ttggtggcaa atcaccagat acaaattact tgtttatggg agattatggt gacagaggat 480
attattcagt tgaacagtt acactgcttg tagctcttaa ggttcgttac cgtgaacgca 540
tcaccattct tcgagggaat catgagagca gacagatcac acaagtttat ggtttctatg 600
atgaatgttt aagaaaatat ggaaatgcaa atgtttggaa atattttaca gatctttttg 660
actatcttcc tctcactgcc ttggtggatg ggcagatctt ctgtctacat ggtggtctct 720
cgccatctat agatacactg gatcatatca gagcaactga tcgcctacaa gaagttcccc 780
atgaggggtcc aatgtgtgac ttgctgtggt cagatccaga tgaccgtggt ggttggggta 840
tatctcctcg aggagctggt tacacctttg ggcaagatat ttctgagaca tttaatcatg 900
ccaatggcct caggttggtg tctagagctc accagctagt gatggaggga tataactggt 960
gccatgaccg gaatgtagta acgattttca gtgctccaaa ctattgttat cgttgttgta 1020
accaagctgc aatcatggaa cttgacgata ctctaaaata ctctttcttg cagtttgacc 1080
cagcacctcg tagaggcgag ccacatg tta ctgctgtac ccagactac ttctgtaat 1140
gaaattttaa acttgtacag tattgccatg aaccatatat cgacctaatg gaaatgggaa 1200
gagcaacagt aactccaaag tgtcagaaaa tagttaacat tcaaaaaact tgttttcaca 1260
tggaccaaaa gatgtgccat ataaaaatac aaagcctctt gtcatacaaa gccgtgacca 1320
ctttagaatg aaccagttca ttgcatgctg aagcgacatt gttggtcaag aaaccagttt 1380
ctggcatagc gctatttgta gttacttttg ctttctctga gagactgcag ataataagat 1440
gtaaacatta acacctgtg aatacaattt aacttcatt tagctatagc tttactcagc 1500
atgactgtag ataaggatag cagcaaacaa tcattggagc ttaatgaaca tttttaaaaa 1560
taattaccaa ggcctccctt ctacttgtga gttttgaaat tgttcttttt attttcaggg 1620
ataccgttta atttaattat atgattgtc tgcaactcagt ttattcccta ctcaaactctc 1680
agccccatgt tgttctttgt tattgtcaga acctggtgag ttgttttgaa cagaactggt 1740
ttttccctt cctgtaagac gatgtgactg cacaagagca ctgcagtgtt tttcataata 1800
aacttgtgaa ctaagaactg agaagggtcaa attttaattg tatcaatggg caagactggt 1860
gctgtttatt aaaaaagtta aatcaattga gtaaatttta gaattttag actttaggt 1920
aaaataaaaa tcaagggcac tacataacct ctctggtaac tccttgacat tctt cagatt 1980
aacttcagga tttatttgta tttcacatat tacaatttgt cacattgttg gtgtgcactt 2040
tgtgggttct tcctgcataat taacttggtt gtaagaaagg aaatctgtgc tgcttcagta 2100
agacttaatt gtaaaacat ataacttgag atttaagtct ttgggttggt ttttaataaa 2160
acagcatggt ttcaggtaga g                                     2181
```

<210> 185

<211> 375

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(375)

<223> 5' terminal sequence. homo sapiens, clone
image:4054156, mrna, partial cds (EST R55460)
gene.

122/292

<400> 185
cgaagaggat gaggaagagc tncgtctgct gcancaagag ctccaggccg ggctgcgcac 60
caaggccctg attgtggatg agtcctgccg gcggtnacca tcttccaaca tagggatata 120
cctccctcct tcttataact gaagatcctg gagccccgaa gattcag ggc agacagaccc 180
tgataatgag cctggcaggg aagggaacc aacatcttgt aacttgcttt cccaccctg 240
tttctggggg cagagcaatt gcccaatttc taccctaate caaagtcctt ggggtgnggt 300
gggggttaaac gtgctggtgc atcctaggtc atccaagagt gaggcgcaa gtctctgagg 360
aagggggcac agaac 375

<210> 186

<211> 542

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(542)

<223> 3' terminal sequence. immunoglobulin kappa
constant (IGKC) gene.

<400> 186
gcaaagattc acaatattta ttnattctcc tccaacatta gcataattaa agccaaggag 60
gaggaggggg gtgaggtgaa agatgagctg gaggaccgca ataggggtag gtcccctgtg 120
gaaaaagggt cagaggccaa aggatgggag ggggtcaggc tgganctgag gagcagggtg 180
gggcacttct ccttctaaca ctctcccctg ttgaagctct ttgtgacggg cgagctcagg 240
ccctgatggg tgacttogca ggcgtagact ttgtgtttct cgtagtctgc ttgtgctcagc 300
gtcagggtgc tgctgaggct ntagggtgct gtccctgctg tctgtctctg tgacactctc 360
ctgggggant taccnattt gggagggcgt tatccacctt ccactgtact ttggc ctctc 420
tggggataga agttttttca gcaggcacac aacagaggca nttccagatt tncaactgct 480
catcagatgg ccgggaagnt gaaggncagt nggtgcagcc acatttcttt tgatccncca 540
ct 542

<210> 187

<211> 296

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(296)

<223> 5' terminal sequence. melanocortin 1
receptor (alpha melanocyte stimulating hormone
receptor) (MCLR) gene.

<400> 187
atcacctgca gctccatgct gtccagctc tgcttctg ggcctatgc gtggaccgct 60
acatctccat cttctacgca ctgnetacca cagcatcgtg accctgccgc gggcgcaag 120
nccgttgagg ccatctgggt ggccagtgtc gtcttcagca cgctcttcat cgcctactac 180
gaccacgtgg ccgtctgct gtgcctcgtg gtcttcttcc tggctatgct ggtgctcatg 240
gccgtgctgt acgtccacat gctggcccgg gcctgccagc acgccaggg cattcg 296

<210> 188

123/292

<211> 1270

<212> DNA/RNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(1270)

<223> melanocortin 1 receptor (alpha melanocyte
stimulating hormone receptor) (MC1R) gene.

<400> 188

```
ggagagggtg tgagggcaga tctgggggtg cccagatgga aggaggcagg catgggggac 60
accaaggcc cctgggcagc accatgaact aagcaggaca cctggagggg aagaactgtg 120
gggacctgga ggctccaac gactccttcc tgcttcctgg acaggactat ggctgtgcag 180
ggatcccaga gaagacttct gggctccctc aactccaccc ccacagccat ccccagctg 240
gggctggctg ccaaccagac aggagcccg gctctggagg tgtccatctc tgacgggctc 300
ttcctcagcc tggggctggt gagcttggtg gagaacgcgc tgggtggt ggc caccatcgcc 360
aagaaccgga acctgcactc acccatgtac tgcttcatct gctgcctggc cttgtcggac 420
ctgctggtga gcgggagcaa cgtgctggag acggccgtca tcctcctgct ggaggccggt 480
gcactggtgg cccgggctgc ggtgctgcag cagctggaca atgtcattga cgtgatcacc 540
tgcagctcca tgctgtccag cctct gcttc ctgggcgcca tcgccgtgga ccgctacatc 600
tccatcttct acgcactgcg ctaccacagc atcgtgaccc tgcgcggggc gcggcaagcc 660
gttgccggca tctgggtggc cagtgtcgtc ttcagcacgc tcttcacgc ctactacgac 720
cacgtggccg tctgtctgtg cctcgtggtc ttcttcctgg ctatgctggt gctcatggcc 780
gtgctgtacg tccacatgct ggcccgggccc tgccagcagc cccagggcac cggccggctc 840
cacaagaggc agcgcggggt ccaccagggc tttggcctta aaggcgtgt caccctcacc 900
atcctgctgg gcattttctt cctctgctgg ggccccttct tcctgcatct cacactcatc 960
gtcctctgcc ccgagcacc cactgctggc tgcatttca agaac ttcaa cctctttctc 1020
gccctcatca tctgcaatgc catcatcgac cccctcatct acgccttcca cagccaggag 1080
ctccgcagga cgtcaagga ggtgctgaca tgctcctggt gagcgcggtg cacgcgcttt 1140
aagtgtgctg ggcagaggga ggtggtgata ttgtgtggtc tggttcctgt gtgaccctgg 1200
gcagttcctt acctccctgg tcccgtttg tcaaagagga tggactaaat gatctctgaa 1260
agtgttgaag                                     1270
```

<210> 189

<211> 336

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(336)

<223> 3' terminal sequence. neuregulin 1 (NRG1)
gene.

<400> 189

```
ccaanaccaa atccgagccc ttggacaaa ctgcctgctg ccgagagccg tccgcgtaga 60
gcctcgtct ccggcgagat gtccgagcgc aaagaaggca gaggcaaagg gaagggaag 120
aagaaggagc gaggtcgcnc aagaagccgg ntcccggggc ggngcagcag gagcccagcc 180
ttgcctcccc aattnaaaga gatgaaaagc caggaatcgg ctgcaggttc caaactagtc 240
cttcggtgtg aaaccagttc tgaatactcc tctctcagat tcaagtgggt caagaatggg 300
gaatgaattg aatcgaaaaa nncannccac aaaatt                                     336
```

124/292

<210> 190
<211> 366
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<220>
<221> misc_feature
<222> (1)..(366)
<223> 5' terminal sequence. neuregulin 1 (NRG1)
gene.

<400> 190
tctcaacaat atgctcactg gaga tgacgt ttttagatac gtattgattc accagctgga 60
cattctcggg gggtnngtta ggatggtag gcccattggc aatgttcac atattgtttc 120
gttcagaccg aagctctgcc agagacggtc atgcagcttt ttccgctgtt tcttggtttt 180
gcagtaggcc accacacaca tgatgccgac cacaaggagg gcgatgcaga tgccggttat 240
ggtcagcaact ctcttctggt acagctcctn cgctncata aattcaatnc caagatgctt 300
gtagaagctg gccattnacg tagttttttg gcagcgattc accagtaaaa cttcatttng 360
gggcac 366

<210> 191
<211> 2490
<212> DNA/RNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<220>
<221> misc_feature
<222> (1)..(2490)
<223> neuregulin 1 (NRG1) gene.

<400> 191
gtggctgcgg ggcaattgaa aaagagccgg cgaggagttc cccgaaactt gttggaactc 60
cgggctcggc cggaggccag gagctgag cg gcggcggtg cgggacgatg ggagcgtgag 120
caggacggtg ataacctctc ccgacgcggg ttgcgagggc gccgggcaga ggccaggagc 180
cgagccgcca gcggcgggac ccacgcgaga ctcccgggg cgacaggagc agccccgaga 240
gccaggggcga gcgcccgttc caggtggccg gacgcggcgc cgcgtccgag ccgcgtctcc 300
tgaggagcaac gggagacgcc cccgcgcagc gcgagcgctt cagcgcgggc gctcgtctctc 360
cccacgcagg gacaaacttt tcccaaaccg gatccgagcc cttggacca actcgcctgc 420
gccgagagcc gtccgcgtag agcgcctcgt ctccggcgag atgtccgagc gcaaagaagg 480
cagaggcaaa gggaagggca agaagaagga gcgaggctcc ggcaagaa gc cggagtccgc 540
ggcgggcagc cagagcccag ccttgccctc ccaattgaaa gagatgaaa gccaggaaac 600
ggctgcaggt tccaaactag tccctcggtg tgaaaccagt tctgaatact cctctctcag 660
attcaagtgg ttcaagaatg ggaatgaatt gaatcgaaaa aacaaaccac aaaatatcaa 720
gatacaaaaa aagccaggga agtcag aact tcgcattaac aaagcatcac tggtgattc 780
tgagaggtat atgtgcaaag tgatcagcaa attaggaaat gacagtgcct ctgccaatat 840
caccatcggt gaatacaacg agatcatcac tggatgcca gcctcaactg aaggagcata 900
tgtgtcttca gagtctccca ttagaatatc agtatccaca gaaggagcaa atacttcttc 960
atctacatct acatccacca ctgggacaag ccactttgta aatgtgcgg agaaggagaa 1020
aactttctgt gtgaatggag gggagtgtt catggtgaaa gaccttcaa acccctcgag 1080
atacttgtgc aagtgcctca atgagtttac tggatgacgc tgccaaaact acgtaattggc 1140
cagcttctac aaggcggagg agctgtacca gaagagagt ctg accataa ccggcatctg 1200
catcgccctc cttgtggtcg gcatcatgtg tgtggtggcc tactgcaaaa ccaagaaaca 1260
gcggaaaaag ctgcatgacc gtcttcggca gagccttcgg tctgaacgaa acaatatgat 1320
gaacattgcc aatgggcctc accatcctaa cccaccccc gagaatgtcc agctggtgaa 1380

125/292

```

tcaatacgtatctctaaaaa cgtcatctccagtgagcatattgttgagagagaagcagagac 1440
atcctttttccaccagtcactatacttccacagcccatcac tccactactgtcaccagac 1500
tcctagccacagctggagcaacggacacac tgaagcatcctttccgaaa gccactctgt 1560
aatcgtgatgtcatccgtagaaaacagtaggcacagcagccaaactgggggcccaagagg 1620
acgtcttaattggcacaggagggcctcgtgatgtaacagcttctcaggcatgccagaga 1680
aaccctgatctctaccgagactctcctcatagttaaaggatgtgtcagccatgaccac 1740
cccggctcgtatgtcacctgtagatttccacacgccaagctccccaaatcgcccccttc 1800
ggaaatgtctccaccgtgtccagcatgacggtgtccaagccttccatggcggtcagccc 1860
cttcatggaaagagagacctctacttctcgtgacacca ccaaggctgcgggagaagaa 1920
gtttgaccatcacctcagcagttcagctcttccaccacaaccccgcgcatgacagtaa 1980
cagcctccctgctagcccttgaggatagtgaggatgagagtatgaaa cgaccaaga 2040
gtacgagccagcccaagagcctgttaaagaaactcgccaatagccggcgggccaaaagaac 2100
caagcccaatggccacattgctaacagattggaagtggacagcaacacaa gctcccagag 2160
cagtaactcagagagtgaacagagatgaagagtaggtgaagatacgctttcctggg 2220
catacagaaccccctggcagccagtccttgaaggcaacacctgcctccgctggctgacag 2280
caggactaacccagcaggccgcttctcgacacaggaagaaatccaggcca ggctgtctag 2340
tgtaattgctaaccaagaccctattgctgtataaaacctaaataaacacatagattcacc 2400
tgtaaaactttatttttatataataaagtattccaccttaaattaaacaatttattttatt 2460
ttagcagttctgcaataaaaaa 2490

```

<210> 192

<211> 453

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(453)

<223> 5' terminal sequence. ciliary neurotrophic factor receptor (CNTFR) gene.

<400> 192

```

cagatgctacgccgggaaggagtagcattatccagggtggcagccaaggacaatnagattgg 60
gacatggagtgactggagcgtaccgcccacgctacgccctggactgaggaaccgagacac 120
ctcaccacaggaggcccaggctgcggagaccacgaccagcaccaccagctcctggcacc 180
ccacctaccaagaatctgtgacctggggagctgggca gggcgggggaccctcggca 240
cccttcttggtcagcgtcccctactctggccctggctgncgtgccgcactgccagc 300
agtctcttga tctgagcccgacccccatgaggacatgagagacctgcagaggancag 360
gaggccggagcttgagcctttagaccccggtttctattt tncacacgggcaggaggant 420
tttgcattnttttnagacacaattttt gga 453

```

<210> 193

<211> 1566

<212> DNA/RNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(1566)

<223> ciliary neurotrophic factor receptor (CNTFR) gene.

<400> 193

126/292

```

gcggcgccag cggaggcgcc ggctccagcc ggcgcgccgc gaggctcggc ggtgggatcc 60
ggcgggcggt gctagctccg cgctccctgc ctgctcgtc gccgggggcg gtcggaaggc 120
gcggcgccgaa gcccggggtgg cccgagggcg cgactct agc cttgtcacct catcttgccc 180
ccttggtttt ggaagtcttg aagagtttgt ctggaggagg aggaggacat tgatgtgctt 240
ggtgtgtggc cagtgttgaa gagatggctg ctctgtccc gtgggcctgc tgtgtgtgc 300
ttgccgccgc cgccgcagtt gtctacgcc agagacacag tccacaggag gcaccccatg 360
tgcagtacga gcgcc tgggc tctgacgtga cactgccatg tgggacagca aactgggatg 420
ctgcggtgac gtggcggtta aatgggacag acctggcccc tgacctgctc aacggctctc 480
agctggtgct ccatggcctg gaactgggcc acagtggcct ctacgcctgc ttccaccgtg 540
actcctggca cctgcgccac caagtctctg tgcagtgtgg cttgccgcgc cgggagc ctg 600
tgctcagctg ccgctccaac acttacccca agggcttcta ctgcagctgg catctgcccc 660
ccccaccta cattoccaa accttcaatg tgactgtgct gcatggctcc aaaattatgg 720
tctgtgagaa ggacccagcc ctcaagaacc gctgccacat tcgctacatg cacctgttct 780
ccaccatcaa gtacaaggtc tccataagtg tcagc aatgc cctggggccac aatgccacag 840
ctatcacctt tgacgagttc accattgtga agcctgatcc tccagaaaat gtggtagccc 900
ggccagtgcc cagcaaccct cgccggctgg aggtgacgtg gcagaccccc tcgacctggc 960
ctgacctga gtcttttct ctcaagttct ttctgcgcta ccgaccctc atcctggacc 1020
agtggcagca tggtagctg tccgacggca cagcacacac catcacagat gcctacgccg 1080
ggaaggagta cattatccag gtggcagcca aggacaatga gattgggaca tggagtgact 1140
ggagcgtagc cgccacgct acgcccctga ctgaggaacc gcgacacctc accacggagg 1200
cccaggtgc ggagaccacg accagcacca ccagctccct ggcaccccc c ctaccacga 1260
agatctgtga ccctggggag ctgggcagcg gcgggggacc ctcgacacc ttcttggta 1320
gcgtcccat cactctggcc ctggctgccg ctgcgccac tgcagcagt ctcttgatct 1380
gagcccgga ccccatgagg acatgcagag cacctgcaga ggagcaggag gccggagctg 1440
agcctgcaga ccccggtttc tatttt gcac acgggcagga ggacctttt cattctctc 1500
agacacaatt tgtggagacc ccggcgggcc cgggcctgcc gccccccagc cctgccgcac 1560
caagct 1566

```

<210> 194

<211> 349

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(349)

<223> 5' terminal sequence. angiogenin,
ribonuclease, rnase a family, 5 (ANG) gene.

<400> 194

```

ccgtgtacac aactcacac aaggacgcca accccaccta gatgcaaaga ggattcaaaa 60
gaacatcttt gcgttttcta ccggtccccc atcatcgta tagggaggaa gaagcgggtg 120
agaaacaaaa cttctttcca ttgtcctgcc cgtttctgcg gacttgttct gaggccgagg 180
agcctgtgtt ggaagagatg gtgatgggcc tgggcgtttt gttgttggtc ttcgtgctgg 240
gtctgggtct gacccaccg acctggctc aggataactn c aggtacaca cacttctga 300
cccagcacta tgatgcaaaa ccacagggcc ngggatgaca gatactgtg 349

```

<210> 195

<211> 729

<212> DNA/RNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature
<222> (1)..(729)
<223> angiogenin, ribonuclease, rnase a family, 5
(ANG) gene.

<400> 195
atgatgccgt gtcagagagc aaagctcctg tccttttggc ctaatttggt gatgctgttc 60
ttgggtctac cacacctctt tttgccctcc gcaggagcct gtgttggaag agatgggtgat 120
gggcctgggc gttttgttgt tggctctcgt gctg ggtctg ggtctgacct caccgacctt 180
ggctcaggat aactccaggt acacacactt cctgacctag cactatgatg ccaaaccaca 240
gggcggggat gacagatact gtgaaagcat catgaggaga cggggcctga cctcaccctg 300
caaagacatc aacacattta ttcattggca caagcgcagc atcaaggcca tctgtgaaaa 360
caagaatgga aaacctcaca gagaaaacct aagaataagc aagtcttctt tccagggtcac 420
cacttgcaag ctacatggag gttccccctg gcctccatgc cagtaccgag ccacagcggg 480
gttcagaaac gttgtgttgt cttgtgaaaa tggcttacct gtccacttgg atcagtcaat 540
tttccgtcgt ccgtaaccag cgggccccctg gtcaagtgtt ggctctgctg tcct tgcctt 600
ccatttcccc tctgcacca gaacagtggg ggcaacattc attgccaagg gcccaaagaa 660
agagctacct ggaccttttg tttctgttt gacaacatgt ttaataaata aaaatgtctt 720
gatatcagt 729

<210> 196
<211> 452
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<220>
<221> misc_feature
<222> (1)..(452)
<223> 3' terminal sequence. endoglin
(osler-rendu-weber syndrome 1) (ENG) gene.

<400> 196
ngttactcca gccttggacc ggggctgcca ctt ggagagn cgtggcgacc acaaggaggc 60
gcacatcctg agggtcctgc cgggccactc ggcgggcccc ggacgggtga cgggtgaagg 120
ggaactgagc tgcgcacctg gggatctcga tgcctcctc atcctgcagg gtcccccta 180
cgtgtcctgg ctcatcgacg ccaaccacaa catgcagatc tggaccactg gagaatactc 240
cttcaagatc tttccagaga aaaacattcg tggcttcaag ctcccagaca cacctcaagg 300
cctcctgggg ggacgcgngn atgcttcaat gccagcattg tggcatcctt cgtgggagct 360
taccgtggg ccagcattgt cttnatattca ttgccttcca gcttgcggtt gttaggggtg 420
cagaccttaa ccognaccgt ttccagacca tt 452

<210> 197
<211> 379
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<220>
<221> misc_feature
<222> (1)..(379)
<223> 5' terminal sequence. endoglin
(osler-rendu-weber syndrome 1) (ENG) gene.

<400> 197

128/292

```

aggacgagc ctttgcttgt gcaaccagac aggtcagggc tgatgatgtt caagcgcattg 60
aagacagtcc tatggcttcc tggctcttgag acccggtctt gggacgcagg gctaccgtgc 120
agctgagggg gccggttttg ggtatgggta ctgtgtagaa gtggaggagg aagctgaagc 180
gcgggtcacc ctcggggctt ggggacagca ggct cacaca gttgcccttg gccgcccggc 240
cctgggatga gttccacggg gcctccctca ggccccaagt ccagggtggc agctgtctaa 300
ctggagcagg aactcggaga cggatgggga cantctgacc tgcacaaagc ttttnttgcc 360
ccggcttcga tgggtgtttt                                     379

```

<210> 198

<211> 3142

<212> DNA/RNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(3142)

<223> endoglin (osler-rendu-weber syndrome 1)
(ENG) gene.

<400> 198

```

cctggggcgg ccgggctgga tgagccgg ga gctccctgct gccggtcata ccacagcctt 60
catctgcgcc ctggggccag gactgctgct gtcactgcc a tccattggag ccagcaccc 120
cctccccgcc catccttcgg acagcaactc cagcccagcc ccgcgtccct gtgtccactt 180
ctcctgacct ctcgcccgcc accccagaag gctggagcag ggacgcgcgtc gctccggccg 240
cctgtctccc tcgggtcccc gtgcgagccc acgcccggccc cggtgcccgc ccgcagccct 300
gccactggac acaggataag gccacgcgca caggccccca cgtggacagc atggaccgcy 360
gcaagctccc tctggctgtt gccctgctgc tggccagctg cagcctcagc cccacaagtc 420
ttgcagaaac agtccattgt gaccttcagc ctgtggggcc cgagagggg c gaggtgacat 480
ataccactag ccagggtctc aagggtctgc tggctcaggc cccaatgcc atccttgaag 540
tccatgtcct ctctctggag ttcccaacgg gcccgtcaca gctggagctg actctccagg 600
catccaagca aaatggcacc tggccccgag aggtgcttct ggtcctcagt gtaaacagca 660
gtgtcttctc gcatctccag gccctgg gaa tccactgca cttggcctac aattccagcc 720
tggtcacctt ccaagagccc ccgggggtca acaccacaga gctgccatcc ttcccaaga 780
cccagatcct tgagtgggca gctgagaggg gccccatcac ctctgtgct gagctgaatg 840
accocccagag catcctctc cgactgggccc aagcccaggg gtactgtcc ttctgcatgc 900
tggaagccag ccaggacatg ggccgcacgc tgcagtggcg gccgcgtact ccagccttgg 960
tccggggctg ccacttgga ggctggccg gccacaagga ggcgcacatc ctgaggggtcc 1020
tgccggggcca ctcgcccggg ccccggaagg tgacggtgaa ggtggaactg agctgcgcac 1080
ccggggatct cgatgccgtc ctcatcctgc aggttcccc ctacg tgtcc tggctcatcg 1140
acgccaacca caacatgcag atctggacca ctggagaata ctcttcaag atctttccag 1200
agaaaaacat tctgtgcttc aagctcccag acacacctca aggcctctg ggggaggccc 1260
ggatgctcaa tgccagcatt gtggcatcct tctgtgagct accgctggcc agcattgtct 1320
cacttcatgc ctccagctgc ggtggtaggc tgcagacctc acccgccagg atccagacca 1380
ctcctcccaa ggacacttgt agcccgagc tgcctatgtc cttgatccag acaaagtgtg 1440
ccgacgacgc catgaccctg gtactaaaga aagagcttgt tgcgcatttg aagtgcacca 1500
tcacgggcct gaccttctgg gaccccagct gtgaggcaga ggacaggggt gacaagttt g 1560
tcttgccgag tgcctactcc agctgtggca tgcaggtgtc agcaagtatg atcagcaatg 1620
aggcggtgtt caatatctg tgcagctcat caccacagcg gaaaagggtg cactgcctca 1680
acatggacag cctctcttcc cagctggggc tctacctcag cccacacttc ctccaggcct 1740
ccaacaccat cgagccgggg cagcagagct ttg tgcaggt cagagtgtcc ccatccgtct 1800
ccgagttcct gctccagtta gacagctgcc acctggactt ggggcctgag ggaggcaccg 1860
tggaactcat ccaggcccg ggcgcaagg gcaactgtgt gagcctgctg tcccaagcc 1920
ccgaggtgta ccgcgcctc agcttctctc tccacttcta cacagtacct ataccacaaa 1980
ccggcacctc cagctgcaag gtagccctgc gtcccaagac cgggtctcaa gaccaggaag 2040
tccataggac tgtcttcatg cgcttgaaac tcatcagccc tgacctgtct ggttgacaaa 2100
gcaaaggcct cgtcctgccc gccgtgctgg gcatcacctt tggtgccctc ctcatcgggg 2160
ccctgctcac tgctgcactc tggtagatct actgcacac gcgtgag tac ccaggcccc 2220

```

129/292

```

cacagtgagc atgccggggc cctccatcca cccgggggag cccagtgaag cctctgaggg 2280
attgaggggc cctggcagga ccctgacctc cgcccctgcc cccgctcccg ctcccaggtt 2340
ccccagcaa gcgggagccc gtggtggcgg tggctgcccc ggcctcctcg gagagcagca 2400
gcaccaacca cagcatcggg a gcaccaga gcacccctg ctccaccagc agcatggcat 2460
agccccggcc ccccgcgctc gcccagcagg agagactgag cagccgccag ctgggagcac 2520
tgggtgtgaac tcaccctggg agccagtcct ccactcgacc cagaatggag cctgctctcc 2580
gcgcctaccc ttcccgctc cctctcagag gcctgctgcc agtgcagcca ctggcttggg 2640
acaccttggg gtccctccac ccacagaac cttcaacca gtgggtctgg gatattggctg 2700
cccaggagac agaccacttg ccacgctgtt gtaaaaaccc aagtccctgt catttgaacc 2760
tggatccagc actggtgaac tgagctgggc aggaaggagg aacttgaac agattcaggc 2820
cagccagacc agccaacag cactcctccc ctggg aagag aagagggccc agcccagagc 2880
cacctggatc tatccctgcg gcctccacac ctgaacttgc ctaactaact ggcaggggag 2940
acaggagcct agcggagccc agcctgggag cccagagggt ggcaagaaca gtgggcgttg 3000
ggagcctagc tctgcccaca tggagcccc tctgccggtc gggcagccag cagaggggga 3060
gtagccaagc tgcttgtcct ggcctgccc ctgtgtattc accaccaata aatcagacca 3120
tgaaacctga aaaaaaaaaa aa 3142

```

<210> 199

<211> 402

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(402)

<223> 3' terminal sequence. epidermal growth factor (beta-urogastrone) (EGF) gene.

<400> 199

```

tatgtttttg gtgattttat ttaaataatt agaagaaatt catcgttgtc tataatgaaa 60
acaaatcagg caatttactt acaatcttgt aactgaaaat acatacaaa t tctgtgcaat 120
cacaccaaga gggaaaattc tgtaggggaa aaggacagta atgactaaga aactccgaag 180
cctcctgtgt aatattttta aaataaaatg ttttcattca aatattttta aaaataagcc 240
atctaattct gaagaaatca gtttctaat tacatttttc attgattcat cacaactcat 300
tttgcaaaat catcagcatg gaccacg cca atgaggagtt aaatgcctac actgtatctt 360
aacggtattg taatattcca atcatttcat gaaactgata ta 402

```

<210> 200

<211> 4877

<212> DNA/RNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(4877)

<223> epidermal growth factor (beta-urogastrone) (EGF) gene.

<400> 200

```

actgttggga gaggaatcgt atctccatat ttcttctttc agccccaate caagggttgt 60
agctggaact ttccatcagt tcttcctttc tttttcctct ctaagccttt gccttgctct 120
gtcacagtga agtcagcca agcagggtcg ttaaactctg tgaaatttgt cataagggtg 180
tcagggtattt cttactggct tccaaagaaa catagataaa gaaatctttc ctgtggcttc 240

```

```

ccttggcagg ctgcattcag aaggtctctc agttgaagaa agagcttggg ggacaacagc 300
acaacaggag agtaaaagat gcccaggggc tgaggcctcc gctcaggcag ccgcatctgg 360
ggatcaatcat actcaccttg cccggggccat gctccagcaa aatcaagctg ttttcttttg 420
aaagttcaaaa ctcatcaaga ttatgctgct cactcttatac attctgttgc cagtagtttc 480
aaaatttagt tttgttagtc tctcagcacc gcagcactgg agctgtcctg aaggtactct 540
cgcaggaaat ggaatttcta cttgtgtggg tcttgcacc c ttttaattt tctcccatgg 600
aaatagtatc tttaggattg acacagaagg aaccaattat gagcaattgg tgggtggaagc 660
tgggtgtctca gtgatcatgg attttcatta taatgagaaa agaattctatt ggggtggaatt 720
agaaagacaa cttttgcaaa gagtttttct gaatgggtca aggcaagaga gagtatgtaa 780
tatagagaaa aatgttt ctg gaatggcaat aaattggata aatgaagaag ttatttgggtc 840
aaatcaacag gaaggaatca ttacagtaac agatatgaaa ggaaataatt cccacattct 900
tttaagtgtc ttaaaatatac ctgcaaatgt agcagttgat ccagtagaaa ggtttatatt 960
ttggtcttca gaggtggctg gaagccttta tagagcagat ctgagtggtg tgggagtga a 1020
ggctctgttg gacacatcag agaaaaataac agctgtgtca ttggatgtgc ttgataagcg 1080
gctgttttgg attcagtaca acagagaagg aagcaattct cttatttgcct cctgtgatta 1140
tgatggaggt tctgtccaca ttagtaaaaca tccaacacag cataatttgt ttgcaatgtc 1200
cctttttggt gaccgtatct tctattcaac atg gaaaatg aagacaattt ggatagccaa 1260
caaacacact ggaaggaga tggttagaat taacctccat tcatcatttg taccacttgg 1320
tgaactgaaa gtagtgcatc cacttgcaca acccaaggca gaagatgaca cttgggagcc 1380
tgacagaaa ctttgcaaat tgaggaaagg aaactgcagc agcactgtgt gtgggcaaga 1440
cctccagtca cacttgtgca tgtgtgcaga gggatacgcc ctaagtgcag accggaagta 1500
ctgtgaagat gttaatgaat gtgctttttg gaatcatggc tgtactcttg ggtgtaaaaa 1560
cacccttgga tctattact gcacgtgcc tgtaggattt gttctgtctc ctgatgggaa 1620
acgatgtcat caacttgttt cctgtccacg caatgtgtct gaatgca gcc atgactgtgt 1680
tctgacatca gaaggtccct tctgaaggc tcagtgttg agagagatgg 1740
gaaaacatgt agcggttgtt cctcaccgga taatgggtgga tgtagccagc tctgcgttcc 1800
tcttagccca gtatcctggg aatgtgattg ctttccctgg tatgacctac aactggatga 1860
aaaaagctgt gcagcttcag g accacaacc atttttgcctg tttgccaatt ctcaagatat 1920
tcgacacatg cattttgatg gaacagacta tggaaactctg ctcagccagc agatgggaat 1980
ggtttatgcc ctatgatcatg accctgtgga aaataagata tactttgccc atacagccct 2040
gaagtggata gagagagcta atatggatgg ttcccagcga gaaaggctta ttgagggaagg 2100
agtagatgtg ccagaaggctc ttgctgtgga ctggattggc cgtagattct attggacaga 2160
cagagggaaa tctctgattg gaaggagtga tttaaatggg aaacgttcca aaataatcac 2220
taaggagaac atctctcaac cagcaggaat ctgtgttcat ccaatggcca agagattatt 2280
ctggactgat acagggatta atccacgaat tgaaa gttct tccctccaag gccttggccg 2340
tctggttata gccagctctg atctaactctg gccagtgga ataacgattg acttcttaac 2400
tgacaagttg tactggtgcg atgccaagca gtctgtgatt gaaatggcca atctggatgg 2460
ttcaaaacgc cgaagactta cccagaatga tgtaggtcac ccatttgctg tagcagtggt 2520
tgaggattat gtgtggttct cagattgggc tatgccatca gtaataagag taaacaagag 2580
gactggcaaa gataggttac gtctccaagg cagcatgctg aagccctcat cactggttgt 2640
ggttcatcca ttggcaaaac caggagcaga tccctgctta tatcaaaacg gaggctgtga 2700
acatatttgc aaaaagaggc ttggaactgc ttggtgttgc tgtcgtgaa g gttttatgaa 2760
agcctcagat gggaaaacgt gtctggctct ggatgggtcat cagctgttgg caggtggtga 2820
agttgatcta aagaaccaag taacaccatt ggacatcttg tccaagacta gagtgcaga 2880
agataacatt acagaatctc aacacatgct agtggctgaa atcatggtgt cagatcaaga 2940
tgactgtgct cctgtgggat gca gcatgta tgctcgggtg atttcagagg gagaggatgc 3000
cacatgtcag tgtttgaaag gatttgctgg ggatggaaaa ctatgttctg atatagatga 3060
atgtgagatg ggtgtcccag tgtgtccccc tgctctctcc aagtgcatac acaccgaagg 3120
tggttatgtc tgccggtgct cagaaggcta ccaaggagat gggattcact gtcttgatat 31 80
tgatgagtg ccaactggggg tgcacagctg tggagagaat gccagctgca caaatacaga 3240
gggaggctat acctgcatgt gtgctggacg cctgtctgaa ccaggactga tttgccctga 3300
ctctactcca cccctcacc tcagggaaga tgaccaccac tattccgtaa gaaatagtga 3360
ctctgaatgt cccctgtccc acgatgggta ctgcctc cat gatgggtgtg gcatgtatat 3420
tgaagcatgt gcaagatag catgcaactg ttgtgttggc tacatcgggg agcgatgtca 3480
gtaccgagac ctgaagtggg gggaaactgc ccacgctggc cacgggcagc agcagaagg 3540
catcggtgtg gctgtctgcg ttggtggtgct tgtcatgctg ctctctctga gcctgtgggg 3600
ggcccaactac tacaggactc agaagctgct atcgaaaaac ccaaagaatc cttatgagga 3660
gtcgagcaga gatgtgagga gtcgcaggcc tgctgacact gaggatggga tgtcctcttg 3720
ccctcaacct tggtttgttg ttataaaaga acaccaagac ctcaagaatg ggggtcaacc 3780
agtggctggg gaggatggc aggcagcaga tgggtcaatg caaccaactt catggaggga 3840
ggagccccag ttatgtggaa tgggcacaga gcaaggctgc tggattccag tatccagtga 3900

```

131/292

taagggctcc tgtccccagg taatggagcg aagctttcat atgccctcct atgggacaca 3960
gaccttgaa ggggtgtcg agaagcccca ttctctccta tcagctaacc cattatggca 4020
acaaagggcc ctggaccac cacac caaat ggagctgact cagtgaaaac tggaattaaa 4080
aggaaagtca agaagaatga actatgtcga tgcacagtat cttttcttcc aaaagtagag 4140
caaaactata ggttttggtt ccacaatctc tacgactaat cacctactca atgcctggag 4200
acagatacgt agttgtgctt ttgtttgctc ttttaagcag tctcactgca gtcttatttc 4260
caagtaagag tactgggaga atcactaggt aacttattag aaacccaaaat tgggacaaca 4320
gtgctttgta aattgtgttg tcttcagcag tcaatacaaa tagatttttg tttttgttgt 4380
tcctgcagcc ccagaagaaa ttagggtta aagcagacag tcacactggt ttggtcagtt 4440
acaaagtaat ttctttgatc tggacagaac atttatata a gtttcatgaa atgattggaa 4500
tattacaata ccgttaagat acagtgtagg catttaactc ctcatggcg tggccatgc 4560
tgatgatttt gccaaaatga gttgtgatga atcaatgaaa aatgtaattt agaaactgat 4620
ttcttcagaa ttagatggcc ttatttttta aaatatttga atgaaaacat ttatttttta 4680
aaatattaca caggaggcct tcggagtctt ttagtcatca ctgtcctttt cccctacaga 4740
attttccctc ttggtgtgat tgcacagaat ttgtatgtat tttcagttac aagattgtaa 4800
gtaaatggcc tgatttgttt tcattataga caacgatgaa tttcttctaa ttatttaa 4860
aaaatcacca aaacat 4877

<210> 201

<211> 153

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(153)

<223> 3' terminal sequence. hmt1 (hnrnp
methyltransferase, s. cerevisiae) -like 1 (HRMT1L1)
gene.

<400> 201

attagacctc acattagga aaacatcaaa atgancacg cagaccctt gagatcctga 60
ggttggccca gccgagccg tgctcagaag ccccccagct cgggcccga gctgcccga 120
cgcccgccct caccagcagg caggccccca tcc 153

<210> 202

<211> 472

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(472)

<223> 5' terminal sequence. hmt1 (hnrnp
methyltransferase, s. cerevisiae) -like 1 (HRMT1L1)
gene.

<400> 202

agtgaatgc agggagaaga gcctgctgag tncagtgagg cgggtctcct gcaggaggga 60
gtacagccag aggagtttgt ggccatcgcg gactacgtg ccaccgatga gaccagctc 120
agttttttga gaggagaaaa aattcttata ctgagacaaa ccactgcaga ttggtggtgg 180
ggtgagcgtg cgggctgctg tgggtacatt c cggcaaac atgtggggaa gcacgtggat 240
gagtacgacc ccgaggacac gtggcaggat gaagagtact tcggcagcta tggaaactctg 300

132/292

aaactccact tgggagatgt tggcagacca gccacgaaca actaaatacc acagtgttca 360
ttcctgncag gaattaaaga atccctgnac ggnttaaagt tcttcnngg acgtggggct 420
gtggggattt gggatccntc agtctcttnt tgttgacat tttgcgtggc nt 472

<210> 203

<211> 2093

<212> DNA/RNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(2093)

<223> hmt1 (hmrnp methyltransferase, s.
cerevisiae)-like 1 (HRMT1L1) gene.

<400> 203

cactgcgctt gcgcgggttg agggcggttg ctcaagtctc tggaaaggac cgtccacccc 60
tccgcgcttg cgggtgtggac gcggaactca gcggagaaac gcgattgaga aatggaaaag 120
aaaaatgaaat aaatcagcag ttatgaggca gagcctaaga gaactatggc aa catcaggt 180
gactgtccca gaagtgaatc gcagggagaa gagcctgctg agtgacgtga ggcgggtctc 240
ctgcaggagg gactacagcc agaggagttt gtggccatcg cggactacgc tgccaccgat 300
gagaccagc tcagttttt gagaggagaa aaaattctta tcttgagaca aaccactgca 360
gattgtgtgt ggggtgagcg tgcgggctgc tgtgggtaca ttccggcaaa ccatgtgggg 420
aagcacgttg atgagtacga ccccgaggac acgtggcagg atgaagagta cttcggcagc 480
tatggaactc tgaactcca cttggagatg ttggcagacc agccacgaac aactaaatac 540
cacagtgtca tctgcagaa taaagaatcc ctgacggata aagtcacctt ggacgtgggc 600
tgtgggactg ggcacatcag tctcttctgt gcacactatg cgcggcctag agcgggtgtac 660
gcgggtggagg ccagtggagt ggcacagcac acggggcagc tggctcctgca gaacggcttt 720
gctgacatca tcaccgtgta ccagcagaag gtggaggatg tgggtgctgc cgagaagggtg 780
gacgtgtctg tgtctgagtg gatggggacc tgctgtctgt ttgagttcat gatcgagtcc 840
atcctgtatg cccgggatgc ctggctgaag gaggacgggg tcatttggcc caccatggct 900
gcgttgacac ttgtgccctg cagtgtgatg aggattatcg tagccaaggt gctcttctgg 960
gacaacgcgt acgagttcaa cctcagcgct ctgaaatctt tagcagttaa ggagtttttt 1020
tcaaagccca agtataacca ctttttga aa ccagaagact gtctctctga accgtgcact 1080
atattgcagt tggacatgag aaccgtgcaa atttctgac tagagaccct gaggggagag 1140
ctgcgcttcg acatcaggaa ggcggggacc ctgcacggct tcacggcctg gtttagcgtc 1200
cacttcaga gctgcagga ggggcagcgg ccgcaggtgc tcagcacggg gcccttcac 1260
cccaccacac actggaagca gacgtgttc atgatggacg acccagtcct tgtccataca 1320
ggagacgttg tcacgggttc agttgtgttg cagagaaacc cagtgtggag aaggcacatg 1380
tctgtgtctc tgagctgggc tgtcacttcc agacaagacc ccacatctca aaaagttgga 1440
gaaaaagtct tcccactctg gagatgacag ttgatgcttt a tttgaaaag cagtgtgcat 1500
atcttgaggg gtgatgaaca caagcaaacc aagttgcacc tggcttctgc aactcctgc 1560
gaaagtccgt gaacattcac tccacattga cccctcccta gcctggcagg tgacgtcagg 1620
gtccttcaca gacaaacacg cttgggctcg gcaggagctg ccgtggccac ccccgctgcc 1680
cagtgtctgc cctcta gaag taggctgtgt ttccaggtgt tcacccgttg tggccacagt 1740
gccgaccctg ggctgggtcg gagctccatg ttctaagct aggtctaggt ctacactcct 1800
aggacgcacg catatcagcc cgtgtaccct gtgacagtga ctgtcccccac ctcctgtgtt 1860
agtggtgccc ttactgccgt cgctcatcca ctgctgtggg acgtaggatt gcaca gggct 1920
gtgccagtgg cgtgtaggga aactgcctt ggctcagcgt gcgagctaag gtggcgatgt 1980
atgcgatggg actctgcagt ggatagtaca gttgtgtaga cgtcttccaa ataaattatg 2040
tgttgggtgcc atcgacatg ctcaataaat attttaaatg agtgaaaaaa aaa 2093

<210> 204

<211> 431

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(431)

<223> 3' terminal sequence. ets variant gene 4
(ela enhancer-binding protein, elaf) (ETV4) gene.

<400> 204

```
tgggggcctt  tattaaaggtc  tggcagatgt  ggtggagggtg  gaagtacaaa  cccaggcctg  60
ggcctaggaa  agggcagaag  aaaggcaaag  ggtcccttgg  agcaggaacc  catccctctc  120
tgcttatacc  cagcaccctt  catcccaggt  tcctttcttc  aacctccgcc  tgctcttggg  180
aacacagagc  accaagaact  gacaaaccgg  gaccctccag  gggccacagc  gtgggggc  ag  240
agtccagggn  ttctgtctcc  ccgcagtggg  gagatctngg  ggagctcagg  tgaacctcct  300
cancctctg  ccagtatgaa  gttggggaag  cgcttttct  tgtccccag  aacagaacaa  360
actcttgctc  tctgtgggtt  ngggggaaaa  ggtttngggg  ggtttggact  taggggagaa  420
gttnagcttg  a                                     431
```

<210> 205

<211> 435

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(435)

<223> 5' terminal sequence. ets variant gene 4
(ela enhancer-binding protein, elaf) (ETV4) gene.

<400> 205

```
gtccccctgc  cctgcccttg  gacagtogcc  cctacagncc  tttccccggg  cagagaacgg  60
aatttcctga  gatcctcttg  cacctcccag  ccccaccctg  gccatgggta  cctcggggaa  120
catagctccg  tcttcagca  gccctggga  catttgccac  tccttcacat  ctccaggagg  180
gggcggggaa  cccctcccag  gcccctacc  aacaccagct  gtcggagccc  tgcccaccct  240
atccccagca  gagctttaag  caagaatacc  atgatccct  gtatggaaca  gggnggggcc  300
agccaggccg  tgggaaccag  ggtgggggt  tcaatggggg  cacagggtac  ccaggggggn  360
ggggggttg  ttgattcaaa  acagggaaca  gacgggattt  tt  ggnttaag  gatttnaggt  420
tntttaancg  ggttg                                     435
```

<210> 206

<211> 447

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(447)

<223> 5' terminal sequence. annexin a11 (ANXA11)
gene.

<400> 206

```

agacccagct cctctttgac atttatgaga taaaggaagc catcaagggg gttggcactg 60
atgaagcctg cctgattgag atcctcgctt ccgcagcaaa tgagcacatc cgagaattaa 120
acagagccta caaagcagaa ttcaaaaaga ccctggaaga ggcca ttcga agcgacacat 180
cagggcactt ccagcggtc ctcatctctc tctctcaggg aaaccgtgat gaaagcaca 240
acgtggacat gtactcgcc cagagagatg ccaggaggc tgtatgcgn ccggggagaa 300
ccgcctgggg aacagacgag tccaagtttc aattgcggtt tctgtggctt ccggggagcc 360
gggcnccacc tgggtaggca gtt tttcaat gagttaccag agaatgnaca gggcnggac 420
attntagaa gagcatctgc ccggaga 447

```

<210> 207

<211> 1958

<212> DNA/RNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(1958)

<223> annexin all (ANXA11) gene.

<400> 207

```

gctgctgcgc ccgcggctcc ccagtgcgcc gagtgccccg cgggccccgc gagcgggagt 60
gggacccagc cctaggcaga acccaggcgc cgcgccccgg acgccccgcg agagagccac 120
tcccgccac gtccatttc gccctcgcg tcoggagtcc ccgtggc cag atctaaccat 180
gagctaccct ggctatcccc cgcgccagg tggctacca ccagtgcac caggtggtgg 240
tccctgggga ggtgctgect accctcctcc gccagcatg ccccccacg ggctggataa 300
cgtggccacc tatgcggggc agttcaacca ggactatctc tcgggaatgg cggccaacat 360
gtctgggaca tttggaggag ccaac atgcc caacctgtac cctggggccc ctggggctgg 420
ctaccacca gtgccccctg gcggttttg gcagccccc tctgcccagc agcctgttcc 480
tccctatggg atgtatccac cccaggagg aaacccaccc tccaggatgc cctcatatcc 540
gccataccca ggggccccctg tgccgggcca gcccatgcca cccccggac agcagcccc 600
aggggcctac cctgggcagc caccagtgc ctaccctggt cagcctccag tgccactccc 660
tgggcagcag cagccagtgc cagactaccc aggatacccg gggctctgga ctgtcaccoc 720
cgctgtgccc ccaacccagt ttggaagccg aggcaccatc actgatgctc ccggttttga 780
ccccctgcga gatgcccagg tctgcccga ggccatgaa ggctt cggga cggatgagca 840
ggccatcatt gactgcctgg ggagtgcctc caacaagcag cggcagcaga tctactttc 900
cttcaagacg gcttacggca aggatttgat caaagatctg aaatctgaac tgtcaggaaa 960
ctttgagaag acaatcttgg ctctgatgaa gacccagtc ctctttgaca tttatgagat 1020
aaaggaagcc atcaaggggg tt ggcactga tgaagcctgc ctgattgaga tctcgttc 1080
ccgcagcaat gagcacatcc gagaattaaa cagagcctac aaagcagaat tcaaaaagac 1140
cctggaagag gccattcgaa gcgacacatc agggcacttc cagcggctcc tcctctctct 1200
ctctcaggga aaccgtgatg aaagcacaac cgtggacatg tctactgccc agagagatgc 1 260
ccaggagctg tatgcggccg gggagaaccg cctgggaaca gacgagtcca agttcaatgc 1320
ggttctgtgc tcccgagacc gggccaccc ggtagcagtt tcaatgagt accagagaat 1380
gacaggccgg gacattgaga agagcatctg ccgggagatg tccggggacc tggaggaggg 1440
catgctggcc gtgtgaaat gtctcaagaa taccoc agcc ttctttgccc agagggtcaa 1500
caaggccatg aggggggcag gaacaaagga ccggaccctg attcgcatca tgggtgtctc 1560
cagcgagacc gacctcctgg acatcagatc agagtataag cggatgtacg gcaagtgcgt 1620
gtaccacgac atctggggag atacttcagg ggattaccgg aagattctgc tgaagatctg 1680
tggtggcaat gactgaacag tgactggttg ctcaactctg cccacctgcc ggcaacacca 1740
gtgccaggaa aaggccaaaa gaatgtctgt ttctaacaaa tccacaaata gccccgagat 1800
tcacgtctct agagcttagg cctgtcttcc accctcctg acccgatatg tgtgccacag 1860
gacctgggct ggtctagaac tctctcagga tgcttttct accccatccc tcacagcctc 1920
ttgtgcttaa aatagatggt tcatttttct gaaaaaaa 1958

```

<210> 208

<211> 433

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(433)

<223> 5' terminal sequence. platelet-derived
growth factor receptor, beta polypeptide (PDGFRB)
gene.

<400> 208

```
gccagatgaa gcaaggccat ataccctaaa cttccatcct gggggtcagc tnggctcctg 60
ggagattcca gatcacacat cacactctgg ggactcagga accatgcccc ttccccaggc 120
ccccagcaag tctcaagaac acagctgcac aggccttgac ttagagtnac agccggtntc 180
ctggnaagcc cccagcagct gccccaggga catgggaaga ccacgggacc tctttcacta 240
cccacgatga cctccggggg tctcctgggg caaaaggggac aaagagggca aatgagatca 300
cctnctgcag cccaccactt ccagcacctg tgccgagggt ttic gttcga agacagaatt 360
ggacagttga ggacagttat tgtcttntt taaaagnaca aggaagggtt cagnttgggt 420
tacccecaag gag                                     433
```

<210> 209

<211> 5570

<212> DNA/RNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(5570)

<223> platelet-derived growth factor receptor,
beta polypeptide (PDGFRB) gene.

<400> 209

```
ggccccctcag ccctgctgcc cagcacgagc ctgtgctcgc cctgcccac gcagacagcc 60
agaccagagg cggccctctt ggcggtctg ctctcccga aggatgcttg gggagtgagg 120
cgaagctggg cgctcctctc cctacagca gcccccttcc tccatccctc tgttctcctg 180
agccttcagg agcctgcacc agtctgcct gtcccttctac tcagctgtta cccactctgg 240
gaccagcagt ctttctgata actgggagag ggcagtaagg aggacttcct ggaggggggtg 300
actgtccaga gcctggaact gtgcccacac cagaagccat cagcagcaag gacaccatgc 360
ggcttccggg tgcgatgcca gctctggccc tcaaaggcga gctgctgttg ctgtctctcc 420
tgttaacttct ggaaccacag atctctcagg gcctggctgt cacaccccg gggccagagc 480
ttgtctctca tgtctccagc accttggttc tgacctgtc ggggttcagct ccggtgggtg 540
gggaacggat gtcccaggag cccccacagg aaatggccaa ggcccaggat ggcaccttct 600
ccagcgtgct cacactgacc aacctcactg ggctagacac gggagaatac ttttgacccc 660
acaatgactc ccgtggactg gagaccgatg agcggaaacg gctctacatc tttgtgccag 720
atcccaccgt gggcttcc tc cctaattgat ccgaggaact attcatcttt ctacaggaaa 780
taactgagat caccattcca tgccgagtaa cagaccaca gctgggtggg aactgcacg 840
agaagaaaagg gacggttgca ctgcctgtcc cctatgatca ccaacgtggc ttttctggta 900
tctttgagga cagaagctac atctgcaaaa ccaccattgg ggacagggag gtggattctg 960
atgcctacta tgtctacaga ctccaggtgt catccatcaa cgtctctgtg aacgcagtgc 1020
agactgtggg ccgcagggtg gagaacatca cctcatgtg cattgtgatc gggaatgagg 1080
tggtcaactt cgagtggaca taccoccgca aagaaagtgg gcggctgggt gagccggtga 1140
ctgacttcct cttggatatg ccttaccaca tccgc tccat cctgcacatc cccagtgcgg 1200
agttagaaga ctgggggacc tacacctgca atgtgacgga gagtgtgaat gaccatcagg 1260
atgaaaaggc catcaacatc accgtgggtg agagcggcta cgtgcggctc ctgggagagg 1320
```


tgggcacact acaatttgc gagctgcac ggagccggac actgcaggta gtgttcgagg 1380
cctaccacc gccactgtc ctgtggttca aagacaaccg caccctgggc gactccagcg 1440
ctggcgaaat cgccctgtcc acgcgcaacg tgtcggagac ccggtatgtg tcagagctga 1500
cactggttcg cgtgaagggt gcagaggctg gccactacac catgcggggc ttccatgagg 1560
atgctgaggt ccagctctcc ttccagctac agatcaatgt ccctgtccg a gtgctggagc 1620
taagtgaag ccacctgac agtggggaac agacagtccg ctgtcgtggc cggggcatgc 1680
cccaccgaa catcatctgg tctgcctgca gagacctcaa aaggtgtcca cgtgagctgc 1740
cgcccagct gctggggaac agttccgaag aggagagcca gctggagact aacgtgacgt 1800
actgggagga ggagcaggag ttt gaggtgg tgagcaact gcgtctgcag cacgtggatc 1860
ggccactgtc ggtgcgctgc acgtgcgca acgtgtggg ccaggacacg caggaggtca 1920
tcgtggtgcc acactccttg ccttttaagg ttggtggtgat ctcagccatc ctggccctgg 1980
tggtgctcac catcatctcc ctatcatcc tcatcatgct ttggcagaag aagccacgtt 20 40
acgagatccg atggaagggt attgagtctg tgagctctga cggccatgag tacatctacg 2100
tggaccccat gcagctgccc tatgactcca cgtgggagct gccgcgggac cagcttgtgc 2160
tgggacgca cctcggtcgt ggggcctttg ggcaggtggt ggaggccacg gctcatggcc 2220
tgagccattc tcaggccacg atgaaagtgg ccgtcaa gat gcttaaatcc acagccgca 2280
gcagtgaag gcaagccctt atgtcggagc tgaagatcat gagtcacctt gggccccacc 2340
tgaacgtggt caacctgttg ggggcctgca ccaaaggagg acccatctat atcatcactg 2400
agtactgcc ctacggagac ctggtggact acctgcaccg caacaaacac accttctgc 2460
agcaccactc gacaagcgc cgcccgcca gcgcggagct ctacagcaat gctctgcccg 2520
ttgggtctcc cctgcccagc catgtgtcct tgaccgggga gagcgacggt ggctacatgg 2580
acatagcaaa ggacgagtcg ttgactatg tgcccatgct ggacatgaaa ggagacgtca 2640
aatatgcaga catcgagtc tccaactaca tggcccctta cgataactac gttccctctg 2700
ccctgagag gacctgccga gcaactttga tcaacgagtc tccagtgtca agctacatgg 2760
acctcgtgg cttcagctac caggtggcca atggcatgga gtttctggcc tccaagaact 2820
gcgtccacag agacctggcg gctaggaacg tgctcatctg tgaaggcaag ctggtcaaga 2880
tctgtgactt tggcctggct cgaga catca tgcgggactc gaattacatc tcaaaggca 2940
gcacttttt gcctttaaag ttgatggctc cggagagcat cttcaacagc ctctacacca 3000
ccctgagcga cgtgtggtcc ttccggatcc tgctctggga gatcttcacc ttgggtggca 3060
ccccttacc agagctgccc atgaacgagc agttctacaa tgccatcaaa cggggttacc 3120
gcatggcca gcctgccc atgcctcgac agatctatga gatcatgcag aagtgtggg 3180
aagagaagtt tgagattcgg ccccccctt cccagctggt gctgtctctc gagagactgt 3240
tgggcgaagg ttacaaaaag aagtaccagc aggtggatga ggagttctg aggagtgacc 3300
accagccat ccttcggctc caggcccgct tgcctgggt t ccatggcctc cgatctcccc 3360
tggacaccag ctcctgctcc tatactgccg tgcagccaa tgagggtgac aacgactata 3420
tcatccccct gcctgacccc aaaccgagc ttgctgacga gggccactg gaggttccc 3480
ccagcctagc cagctccacc ctgaatgaag tcaacacctc ctcaaccatc tctgtgaca 3540
gccccctgga gcc ccaggac gaaccagagc cagagcccca gcttgagctc caggtggagc 3600
cggagccaga gctggaacag ttgccggatt cgggggtgcc tgcgcctcg gcggaagcag 3660
aggatagctt cctgtagggg gctggccctt acctgcctt gcctgaagct cccccctgc 3720
cagcaccag cctctcctg cctggcctga ccgggcttcc tgtcagccag gc tgcctta 3780
tcagctgtcc cctctggaa gctttctgct cctgacgtgt tgtgccccaa acctggggc 3840
tggcttagga ggcaagaaaa ctgcaggggc cgtgaccagc cctctgcctc caggagggcc 3900
aactgactct gagccagggt tccccaggg aactcagtt tcccatatgt aagatgggaa 3960
agttagctt gatgaccag aatctag gat tctctcctg gctgacaggt ggggagaccg 4020
aatccctccc tgggaagatt ctggagttta ctgaggtggt aaattaactt ttttctgttc 4080
agccagctac cctcaagga atcatagctc tctcctgca ctttttatcc acccaggagc 4140
tagggaagag acctgctgc cctggtgagc ttgctgagct agggcctagc cttgagcagt 4200
gttgctcat ccagaagaaa gccagctctc tccctatgat gccagtcct gcgttccctg 4260
gcccagctg gtctggggcc attaggcagc ctaattaatg ctggaggtg agccaagtac 4320
aggaccccc cagcctgcag cccttgcca gggcacttg agcacacgca gccatagcaa 4380
gtgctgtgt cctgtcctt caggccatc agtctgggg ctttttctt atcacctca 4440
gtcttaatcc atccaccaga gtctagaagg ccagacgggc ccgcctctg tgatgagaat 4500
gtaaatgtgc cagtgtggag tggccacgtg tgtgtgccag tatatggccc tggctctgca 4560
ttggaactgc tatgaggtc tggaggaatc cctcaccctc tctgggctc agtttccct 4620
tcaaaaaat aataa gtccg acttattaac tctgagtgcc ttgccagcac taacattcta 4680
gagtattcca ggtggttgca catttgtcca gatgaagcaa ggccatatac cctaaacttc 4740
catcctgggg gtcagctggg ctccctgggag attccagatc acacatcaca ctctggggac 4800
tcaggaaaca tgcccttcc ccaggcccc agcaagtctc aagaacacag ctgc acaggc 4860
cttgacttag agtgacagcc ggtgtcctg aaagcccaa gcagctgcc cagggacatg 4920
ggaagaccac gggacctct tcaactacca cgatgacctc cgggggtatc ctgggcaaaa 4980

137/292

```

gggacaaaga gggcaaatga gatcacctcc tgcagcccac cactccagca cctgtgccga 5040
ggctctgcgtc gaagacagaa tggacagtg a ggacagttat gtcttgtaaa agacaagaag 5100
cttcagatgg taccccaaga aggatgtgag aggtggccgc ttggagtttg cccctcacc 5160
accagctgcc ccatccctga ggcagcgctc catgggggta tggttttgtc actgccaga 5220
cctagcagtg acatctcatt gtccccagcc cagtgggcat tggagggtgcc aggggagtca 5280
gggttgtagc caagacgccc ccgcacgggg aggggttgga agggggtgca ggaagctcaa 5340
ccctctggg caccaaccct gcattgcagg ttggcacctt acttccctgg gatccccaga 5400
gttggtccaa ggaggagag tgggttctca atacggtacc aaagatataa tcacctagg 5460
ttacaaatat ttttaggact cacgttaact cacatttata ca gcagaaat gctattttgt 5520
atgctgttaa gtttttctat ctgtgtactt ttttttaagg gaaagatttt 5570

```

<210> 210

<211> 406

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(406)

<223> 5' terminal sequence. williams-beuren
syndrome chromosome region 14 (WBSCR14) gene.

<400> 210

```

gaccggcgta tcacacacat ctccggcgac aggaagcggc gcttcaacat caagctgggg 60
tttgacaccc ttcatgggct cgtgagcaca ctcaagtccc agcccagcct caaggtgagc 120
aaagctacca cgctgcagaa gacagctgag tacatcctta tgctacagca ggagcgtgcg 180
ggcttgcaag aggaggccca gcagctgcgg ggatgagatt gaggagctca atgccgccat 240
taacctgtgc cagcagcagc tgcccgccac aggggtaccc attcacacac cagcgttttg 300
accagatgog agacatgttt gatggactac gtccgaaccc gtacgctgca caa ctgggaa 360
gttctggggg ntttcagcat cctnattccg gcctctgttt tgagtc 406

```

<210> 211

<211> 3293

<212> DNA/RNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(3293)

<223> williams-beuren syndrome chromosome region
14 (WBSCR14) gene.

<400> 211

```

ccccgcgctg cgcggagcag ggaccaggcg gttgcggcgg cgacagccat ggccggcgcg 60
ctggcaggtc tggccgcggg cttgcaggtc ccgcgggtcg cgcccagccc agactcggac 120
tcggacacag actcggagga cccgagtcct cggcgagc g cgggcggtt gctccgctcg 180
caggatcatcc acagcggta cttcatggtg tcgtcgccgc acagcgactc gctgccccgg 240
cggcgcgacc aggaggggtc cgtggggccc tccgacttcg ggccgcgcag tatcgacccc 300
acactcacac gcctcttcga gtgcttgagc ctggcctaca gtggcaagct ggtgtctccc 360
aagtgggaaga atttcaa agg cctcaagctg ctctgcagag acaagatccg cctgaacaac 420
gccatctgga gggcctggta tatccagtat gtgaagcggg ggaagagccc cgtgtgtggc 480
ttcgtgaccc ccctgcaggg gcctgaggct gatgcgcacc ggaagccgga ggccgtggtc 540
ctggagggga actactggaa gcggcgcatc gaggtggtga tgcgggaata ccacaagt g 600

```

138/292

```

cgcatctact acaagaagcg gtcocgtaag cccagcaggg aagatgacct cctggcccct 660
aagcaggcgg aaggcagggtg gccgcgcgg gagcaatggt gcaaacagct cttctccagt 720
gtgggtcccc tgctgtggg ggacccagag gaggagccgg gtggggcgca gtccttgac 780
ctcaattgct tttgtccga catctcagac actctct tca ccatgactca gtccggccct 840
tcgcccctgc agtgccggcc tgaggatgcc tacgtcggca atgctgacat gatccagccg 900
gacctgacgc cactgcagcc aagcctggat gacttcatgg acatctcaga tttctttacc 960
aactccccgc tcccacagcc gcccatgcct tcaaacttcc cagagccccc cagcttcagc 1020
cccggtggtg actcctctt cagcagtggg accctgggccc cagaggtgcc cccggcttcc 1080
tcggccatga cccacatctc tggacacagc cgtctgcagg ctcggaacag ctgccctggc 1140
cccttggaact ccagcgccct cctgagttct gatttctctc ttcctgaaga cccaagccc 1200
cggtccccc cccctcctgt acccccacct ctgctgcatt accctcccc tgc caaggtg 1260
ccaggcctgg agcctgccc cccacctccc ttccctccca tggcaccacc cactgcttg 1320
ctgcaggaag agcctctctt ctctcccagg tttcccttcc ccaccgtccc tcctgcccc 1380
ggagtgtctc cgtgcctgc tcctgcagcc tttccaccca cccacagtc tgtccccagc 1440
ccagccccc ccccttccc catagagc tt ctacccttgg ggtattcgga gcctgccttt 1500
gggccttgct tctccatgcc cagaggcaag cccccgccc catcccctag gggacagaaa 1560
gccagcccc ctaccttagc cctgcccact gccagtcccc ccaccactgc ggggagcaac 1620
aaccctgcc tcacacagct gtcacagca gctaagccgg agcaagccct ggagccacca 1680
cttgatcca gcacctcct ccggtcccca ggggtcccg aggagacagt ccctgaattc 1740
ccctgcacat tcttccccc gaccccgccc cctacaccgc ccgggccacc tccaggccc 1800
gccacattgg ccccttccag gccctgctt gtcccaaaag cggagcggct ctcaccccca 1860
gcgcccagcg gcagtgaac gcggtgtca ggggacctca g ctccatgcc aggcctggg 1920
actctgagcg tccgtgtctc tccccgcaa cccatcctca gccggggccg tccagacagc 1980
aacaagaccg agaaccggcg tatcacacac atctccggcg agcagaagcg gcgcttcaac 2040
atcaagctgg ggtttgacac cttcatggg ctggtgagca cactcagtgc ccagcccagc 2100
ctcaaggtga gcaaag ctac cacgtgcag aagacagctg agtacatcct tatgtacag 2160
caggagcgtg cgggcttgca ggaggaggcc cagcagctgc gggatgagat tgaggagctc 2220
aatgccgcca ttaacctgtg ccagcagcag ctgcccgcca caggggtacc catcacacac 2280
cagcgttttg accagatgcg agacatgttt gatgactacg tccgaaccg tacgc tgcac 2340
aactggaagt tctgggtgtt cagcatcctc atccggcctc tgtttgagtc cttcaacggg 2400
atggtgtcca cggaagtgt gcacaccctc cgccagacct cactggcctg gctggaccag 2460
tactgtctc tgccgctct ccggccaact gtctgaact ccctacgcca gctgggcaca 2520
tctaccagta tctgaccga ccggggcgcg atccctgagc aagccacacg ggcagtcaca 2580
gagggcacc ttggcaaac tttatagtcc tggccagacc ctgctgtca ctcagctgcc 2640
ctgggggctg ctttccctgg gcacgggctc cagggatcat ctctgggcac tcccttctg 2700
ccccaggccc tggctctgccc cttccctggg ggttgagca gggtcaggt ttcacacttg 2760
ccacctctg gaggtcaaga agagcagagt ccccgctcct gctctgccac tgtgtccag 2820
caccgtgacc ttgggtgact cgtccgctgt ctttgaccg ctgtgtttca atctgcaaaa 2880
tggttgatgg gaaggttcaa tcagcagatg acccccaggc cttggcagct gtgacattgg 2940
gggcctaggc tggaactcc gggggtcaa cggtggaag agg aggatgc tgtttatctg 3000
tcacctccac ttgctcccc acaggtggg cacagacctc tgttctgag cagagaagca 3060
gaaaaggagg ttcctctct ctgctcctc actgtgacc cagaggggct gcaggatggt 3120
ttccctggg agaggccagg agggcctgat cccaggagac accagggcca gactgaccac 3180
agcagggcag gcatcatg tg tgtgtgtgtg tgtggatgtg tgtgtgtggg ttttgtaaag 3240
aattcttgac caataaagc aaaaactgtc tgtgtgttaa aaaaaaaaaa aaa 3293

```

<210> 212

<211> 207

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(207)

<223> 5' terminal sequence. cd74 antigen

(invariant polypeptide of major histocompatibility complex, class ii antigen-associated) (CD74) gene.

<400> 212

cctttggcct tggcttttct agtcctatct acctgtcagg ctgagccatc tctcttccc t 60
tccccagtc atcactcccc aaggaagagc caatgttttc cacccataat cctttctgcc 120
gacccctagt tccctctgct cagccaagct tgttatcagc tttcagggcc atngttcaca 180
ttagaataaa aggtagtaat taganaa 207

<210> 213

<211> 1304

<212> DNA/RNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(1304)

<223> cd74 antigen (invariant polypeptide of major
histocompatibility complex, class ii
antigen-associated) (CD74) gene.

<400> 213

ttcccagatg cacaggagga gaagcaggag ctgtcgggaa gatcagaagc cagtcattga 60
tgaccagcgc gaccttatct ccaacaatga gcaactgccc atgctggggc gccgccctgg 120
ggccccggag agcaagtga gccgcggagc cctgtacaca ggcttttcca tcctgggtgac 180
tctgctcctc gctggccagg ccaccaccgc ct acttctctg taccagcagc agggccggct 240
ggacaaactg acagtcacct ccagaaacct gcagctggag aacctgcgca tgaagcttcc 300
caagcctccc aagcctgtga gcaagatgag catggccacc ccgctgctga tgcaggcgct 360
gcccatggga gccctgcccc aggggcccac gcagaatgcc accaagtatg gcaacatgac 420
agaggaccat gtgatgcacc tgctccagaa tgctgacccc ctgaagggtgt accgcgcaact 480
gaaggggagc ttcccggaga acctgagaca ccttaagaac accatggaga ccatagactg 540
gaaggtcttt gagagctgga tgcaccattg gctcctgttt gaaatgagca ggcactcctt 600
ggagcaaaaag ccactgacg ctccaccgaa agagtcaact gaactggagg ac cgtcttc 660
tggtctgggt gtgaccaagc aggatctggg ccagtcctcc atgtgagagc agcagaggcg 720
gtcttcaaca tcctgccagc ccacacagc tacagctttc ttgctccctt cagccccag 780
cccctcccc atgtccacc ctgtacctca tcccatgaga cctgggtgcct ggctctttcg 840
tcacccttgt acaagacaaa ccaagtggga acagcagata acaatgcagc aaggccctgc 900
tgcccaatct ccattctgtca acaggggagc gaggtcccag gaagtggcca aaagctagac 960
agatcccggt tccgtacatc acagcagcct ccaacacaag gctccaagac ctaggctcat 1020
ggacgagatg ggaagcaca gggagaaggg ataaccctac acccagacc caggctggac 1080
atgctgactg tcctctcccc tccagccttt ggcttggct tttctagcct atttacctgc 1140
aggctgagcc actctcttcc ctttccccag catcactccc caaggaagag ccaatgtttt 1200
ggaccataa tcctttctgc cgaccctag ttccctctgc tcagccaagc ttgttatcag 1260
ctttcagggc catggttcac attagaataa aaggtagtaa ttag 1304

<210> 214

<211> 355

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(355)

<223> 5' terminal sequence. annexin a7 (ANXA7)
gene.

<400> 214

aggaaactatc cgaccagctg ccaacttcga tgctataaga gatgcagaaa ttcttcgtaa 60
ggcaatgaag ggttttggga cagatgagca ggcaattgtn gatgtngttg ccaaccgttt 120
ccaatgatca gaggcaaaaa attaaagcag catttaagac ctctatggc aaggatttaa 180
tcaaagatct caaatcagag ttaagtngaa atatggaaga actgatcctn ggccctcttc 240
atgcctccta cgtattacga tgctngagc ttacggaaa gcaatncagg gancaggta 300
tcaggancgt tgtatttgat ttgngatttt ngtgcacang atcanattca ggtaa 355

<210> 215

<211> 2176

<212> DNA/RNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(2176)

<223> annexin a7 (ANXA7) gene.

<400> 215

gaaccgcgtc tcccgaaga tggagccggg ttgggctgtg acgctgctgc tggggtcaga 60
atgtcatacc caggctatcc cccaacaggc taccacactt tccctggata tctctctgca 120
ggtcaggagt catcttttcc cccttctggt cagtatcctt atcctagtgg ctttcttcca 180
atgggaggag gtgcctaccc acaagtgcc aagtagtggt acccaggagc tggaggctac 240
cctgcgcctg gaggttatcc agccctgga ggctatcctg gtgcccaca gccaggggga 300
gtctccatct atcccggagt tctccaggc caaggatttg gaggcccacc agg tggagca 360
ggcttttctg ggtatccaca gccacattca cagtcttatg gaggtggtcc agcacagggt 420
ccactacctg gtggctttcc tggaggacag atgccttctc agtatcctgg aggacaacct 480
acttacccta gtcagatcaa tacagattct ttttcttctt atcctgtttt ctctctgtt 540
tctttggatt atagcagtga acctgccaca g tgaactcagg tcaactcaagg aactatccga 600
ccagctgcca acttcgatgc tataagagat gcagaaatc ttcgtaaggc aatgaagggt 660
tttgggacag atgagcaggc aattgtggat gtgttgcca accgttccaa tgatcagagg 720
caaaaaatta aagcagcatt taagacctcc tatggcaagg atttaataca agatctcaa 780
tcagagttaa gtgaaatat ggaagaactg atcctggccc tcttcatgcc tctacgtat 840
tacgatgcct ggaagcttac gaaagcaatg caggagcag gaactcagga acgtgtattg 900
attgagattt tgtgcacaag aacaaatcag gaaatccgag aaattgtcag atgttatcag 960
tcagaatttg gacgagacct tgaaaaggac attaggtcag atacatcagg a cattttgaa 1020
cgtttacttg tgtccatgtg ccagggaat cgtgatgaga accagagat aaaccaccaa 1080
atggctcagg aagatgctca gcgtctctat caagctggtg aggggagact agggaccgat 1140
gaatcttgct ttaacatgat ccttgccaca agaagcttct ctcagctgag agctaccatg 1200
gaggttatt ctaggatggc taatcg agac ttgttaagca gtgtgagccg tgagttttcc 1260
ggatatgtag aaagtgggtt gaagaccatc ttgcagtgtg cctgaaccg ccctgccttc 1320
tttgctgaga ggtctacta tgctatgaaa ggtgctggca cagatgactc caccctgggtc 1380
cggattgttg tcaactogaag tgagattgac cttgtacaaa taaaacagat gttcgtcag 1440
atgtatcaga agactctggg cacaatgatt gcaggtgaca cgagtggaga ttaccgaaga 1500
cttctctctg ctattgtggg ccagtaggag ggattttttt ttttttaatg aaaaaaaaaa 1560
ttctattcat agcttatcct tcagagcaat gacctgcag cagcaatatc aaacatcagc 1620
taaccgaaag agctttctgt caaggaccgt atcagggtaa tgtgcttggg ttgcacatgt 1680
tgttattgcc ttaattctaa ttttattttg ttctctacat acaatcaatg taaagccata 1740
tcacaatgat acagtaatat tgcaatgttt gtaaaccttc attcttacta gtttcattct 1800
aatcaagatg tcaaattgaa taaaaatcac agcaatctct gattctgtgt aataatattg 1860
aataattttt taga aggtta ctgaaagctc tgcttccgg aatccctcta agtctgcttg 1920
atagagtgga tagtatgtta aaactgtgta ctttaaaaaa aaattcaacc tttacatcta 1980
gaataatttg catctcattt tgctaaatt ggttctgtat tcataaacac tttccacata 2040
gaaaatagat tagtattacc tgtggcacct ttaagaaaag ggtcaaatgt tta tatgctt 2100
aagatacata gctcccttt ttttcgcgtt gtttctttt ttttaattga gttatgacaa 2160
ataaaaaatt gcatat 2176

<210> 216
<211> 525
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<220>
<221> misc_feature
<222> (1)..(525)
<223> 3' terminal sequence. thrombospondin 1
(THBS1) gene.

<400> 216
tcctgnanta nctncaacaa ccgatgtgag ggaaaatcgg tccagacacg gacctgccac 60
attcaggagt gtgacaagag atttaaacag gatggtggct ggagcntgng ttccccgtgg 120
tcattctgtt ctgtgacatg tggatgaggt gtgacacaa ggatccggct ctgcaactct 180
cccagcccc agatgaacgg gaaaccctgt gaaggcgaag gcgngagac caaagcctgc 240
aagaaagacg cctgccccag taagtgtgag gtccgctgca agggtagca tgggcagcag 300
ctctgcccag ctggttgctt gggcatct gc agcctgcagt ttcagtgggg tcataggagc 360
aggaagggtta cctacttagg agaaacaaac agaaggcaaa gtcctgcagg ctgagcaact 420
tctttttaat tgaaaaacaa attcacntt ttccccagct ttttttcctt gtgttcaggg 480
gaggcagagg ttttttgaac ggnnttaggg gatttttgc aagtt 525

<210> 217
<211> 5722
<212> DNA/RNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<220>
<221> misc_feature
<222> (1)..(5722)
<223> thrombospondin 1 (THBS1) gene.

<400> 217
ggacgcacag gcattccccg cgcccctcca gccctgcgg ccctcgc cac cgctcccggc 60
cgccgcgctc cggtacacac aggatccctg ctgggcacca acagctccac catggggctg 120
gcctggggac taggcgtcct gttcctgatg catgtgtgtg gcaccaaccg cattccagag 180
tctggcggag acaacagcgt gtttgacatc tttgaactca ccggggccgc ccgcaagggg 240
tctgggcgcc gactggtgaa ggccc cgac cttccagcc cagctttccg catcaggat 300
gccaacctga tccccctgt gcctgatgac aagttccaag acctggtgga tgctgtgcg 360
gcagaaaagg gtttctcct tctggcatcc ctgaggcaga tgaagaagac ccggggcacg 420
ctgctggccc tggagcggaa agaccactct ggccaggtct tcagcgtggt gtccaatggc 480
aaggcgggca ccctggacct cagcctgacc gtccaaggaa agcagcacgt ggtgtctgtg 540
gaagaagctc tcctggcaac cgccagtggt aagagcatca ccctgtttgt gcaggaagac 600
agggcccagc tgtacatcga ctgtgaaaag atggagaatg ctgagttgga cgtccccatc 660
caaaagcgtct tcaccagaga cctggccagc atcccgagac tccgca tcgc aaaggggggc 720
gtcaatgaca atttccaggg ggtgctgcag aatgtgaggt ttgtctttgg aaccacacca 780
gaagacatcc tcaggaacaa aggtgtctcc agctctacca gtgtcctcct cacccttgac 840
aacaacgtgg tgaatggttc cagccctgcc atccgcacta actacattgg ccacaagaca 900
aaggacttgc aagccatctg cggc atctcc tgtgatgagc tgtccagcat ggtcctggaa 960
ctcagggggc tgccgaccat tgtgaccacg ctgcaggaca gcattccgaa agtgactgaa 1020
gagaacaaag agttggccaa tgagctgagg cgccctcccc tatgctatca caacggagtt 1080
cagtacagaa ataacgagga atggactgtt gatagctgca ctgagtgtca ctgtcagaac 1140

tcagttacca tctgcaaaaa ggtgtcctgc cccatcatgc cctgctccaa tgccacagtt 1200
cctgatggag aatgctgtcc tcgctgttgg cccagcgact ctgctggacga tggctgttct 1260
ccatggtccg agtggacctc ctgttctacg agctgtggca atggaattca gcagcgcggc 1320
cgctcctgcg atagcctcaa caaccgatgt gagggctcc t cggctccagac acggacctgc 1380
cacattcagg agtgtgacaa aagattttaa caggatggtg gctggagcca ctggtccccg 1440
tggatcatctt gttctgtgac atgtggtgat ggtgtgatca caaggatccg gctctgcaac 1500
tctcccagcc cccagatgaa tgggaaaccc tgtgaaggcg aagcgcgga gaccaaagcc 1560
tgcaagaaag acgctgccc catcaatgga ggtggggtc cttggtcacc atgggacatc 1620
tgttctgtca cctgtggagg aggggtacag aaacgtagtc gtctctgcaa caaccccgca 1680
ccccagtttg gaggaagga ctgctgttgg gatgtaacag aaaaccagat ctgcaacaag 1740
caggactgtc caattgatgg atgctgttcc aatccctgct ttgcccggct ga agtgtact 1800
agctaccctg atggcagctg gaaatgtggt gcttgtcccc ctggttacag tggaaatggc 1860
atccagtgcg cagatgttga tgagtgcata gaagtgcctg atgctgtctt caaccacaat 1920
ggagagcacc ggtgtgagaa cacggacccc ggctacaact gcctgcctg cccccacgc 1980
ttcaccggct cacagccctt cggccag ggt gtcgaacatg ccacggccaa caaacaggtg 2040
tgcaagcccc gtaacccctg cacggatggg acccagact gcaacaagaa cgccaagtgc 2100
aactacctgg gccactatag cgaccccatg taccgctgcg agtgcaagcc tggctacgct 2160
ggcaatggca tcatctgcgg ggaggacaca gacctggatg gctggcccaa tgagaacctg 2220
gtgtgcgtgg ccaatgcgac ttaccactgc aaaaaggata attgccccaa ccttcccaac 2280
tcagggcagg aagactatga caaggatgga attggtgatg cctgtgatga tgacgatgac 2340
aatgataaaa ttccagatga cagggacaac tgtccattcc attacaacct agctcagtat 2400
gactatgaca gagatgatgt gggagaccgc tgtgacaact gtccctacaa ccacaacca 2460
gatcaggcag acacagacaa caatggggaa ggagacgct gtgctgcaga cattgatgga 2520
gacggtatcc tcaatgaacg ggacaactgc cagtacgtct acaatgtgga ccagagagac 2580
actgatatgg atggggttgg agatcagtgat gacaattgcc ccttgaaca caatccggat 2640
cagctggact ctgac tcaga ccgcattgga gatacctgtg acaacaatca ggatattgat 2700
gaagatggcc accagaacaa tctggacaac tgtccctatg tgcccaatgc caaccaggct 2760
gaccatgaca aagatggcaa gggagatgcc tgtgaccag atgatgaca cgatggcatt 2820
cctgatgaca aggacaactg cagactcgtg cccaatccc accagaagga ctct gacggc 2880
gatggtcgag gtgatgcctg caaagatgat tttgacctg acagtgtgcc agacatcgat 2940
gacatctgtc ctgagaatgt tgacatcagt gagaccgatt tccgccgatt ccagatgatt 3000
cctctggacc ccaaagggac atcccaaat gaccctaact gggttgtacg ccatcagggt 3060
aaagaactcg tccagactgt caactgtga t cctggactcg ctgtaggtta tgatgagttt 3120
aatgctgtgg acttcagtgg caccttcttc atcaacaccg aaaggacga tgactatgct 3180
ggatttgtct ttggctacca gtccagcagc cgcttttatg ttgtgatgtg gaagcaagtc 3240
accagtcctt actgggacac caacccacg agggctcagg gatactcggg cctttctgtg 3300
aaagtgtga actccaccac agggcctggc gagcacctgc ggaacgcct gtggcacaca 3360
ggaaacacc ctggccaggt gcgcacctg tggcatgacc ctctgcacat aggttgaaa 3420
gatttcaccg cctacagatg gcgtctcagc cacaggccaa agacgggtt cattagagtg 3480
gtgatgtatg aagggaagaa aatcatggct gactcaggac cc atctatga taaaacctat 3540
gctggtgga gactagggtt gtttgtcttc tctcaagaaa tgggtgttct ctctgacctg 3600
aatttgcaat gtatagatcc ctaatcatca attgttgat tgaaagactg atcataaacc 3660
aatgctggta ttgcaccttc tggaaactat ggcttgagaa aacccccagg atcacttctc 3720
cttggcttcc ttctttt ctg tgcctgcac agtgtggact cctagaacgt gcgacctgcc 3780
tcaagaaaat gcagttttca aaaacagact catcagcatt cagcctccaa tgaataagac 3840
atcttccaag catataaaca attgcttttg tttcctttt aaaaagcatc tacttgcttc 3900
agttgggaag gtgcccattc cactctgcct ttgtcacaga gcagggtgct attgtg aggc 3960
catctctgag cagtggactc aaaagcattt tcaggcatgt cagagaaggg aggcactcact 4020
agaattagca aacaaaacca cctgacatc ctccctcagg aacacgggga gcagaggcca 4080
aagcactaag gggaggcgc atacccgaga cgattgtatg aagaaaatat ggaggaaactg 4140
ttacatgttc ggtactaagt cattttcagg ggattgaaag actattgctg gatttcatga 4200
tgctgactgg cgttagctga ttaacccatg taaataggca cttaaataga agcaggaaaag 4260
ggagacaaag actggcttct ggacttctc cctgatcccc acccttactc atcaccttgc 4320
agtggccaga attagggaaat cagaatcaaa ccagtgtgag gcagtgtggt ctgccattgc 4380
ctggtcacat tgaatttggg ggcttcattc tagatgtagc ttgtgcagat gtagcaggaa 4440
aataggaaaa cctaccatct cagtgcctc cagctgcctc ccaaaggag ggagcgctg 4500
cttatatttt tatggttaca atggcacaaa attattatca acctaaacta aacattcctt 4560
ttctcttttt tccgtaatta ctaggtagtt ttctaattct ctct ttgga agtatgattt 4620
ttttaaagtc ttacgatgt aaaatattta ttttttactt attctggaag atctggctga 4680
aggattatc atggaacagg aagaagcgta aagactatcc atgtcatctt tgttgagagt 4740
cttcgtgact gtaagattgt aaatacagat tatttattaa ctctgttctg cctggaaatt 4800

143/292

```

taggcttcat acggaagt g tttgagagca agtagttgac atttatcagc aaatctcttg 4860
caagaacagc acaaggaaaa tcagtctaata aagctgctct gccocttggtg ctcagagtgg 4920
atgttatggg attccttttt tctctgtttt atcttttcaa gtggaattag ttggttatcc 4980
atgtgcaa atgttttaatt gcaaagaaag ccatgagggtc ttcaatactg ttttaccc ca 5040
tcccttggtc atatttccag ggagaaggaa agcatataca cttttttctt tcatttttcc 5100
aaaagagaaa aaaatgacaa aaggtgaaac ttacatacaa atattacctc atttggtgtg 5160
tgactgagta aagaattttt ggatcaagcg gaaagagttt aagtgtctaa caaacttaaa 5220
gctactgtag tacctaaaaa gtcagtgttg ta catagcat aaaaactctg cagagaagta 5280
ttcccaataa ggaaatagca ttgaaatgtt aaatacaatt tctgaaagtt atgttttttt 5340
tctatcatct ggtataccat tgctttattt ttataaatta ttttctcatt gccattggaa 5400
tagaatattc agattgtgta gatagctat ttataaatt tatcaggaaa tactgcctgt 5460
agagtttagt tttctatttt tatataatgt ttgcacactg aattgaagaa ttgttggttt 5520
tttctttttt ttgttttttt tttttttttt tttttttttg cttttgacct cccattttta 5580
ctatttgcca ataccttttt ctaggaatgt gctttttttt gtacacattt ttatccattt 5640
tacattctaa agcagtgtaa gttgtatatt actgtttctt atgtac aagg aacaacaata 5700
aatcatatgg aaatttatat tt 5722

```

<210> 218

<211> 397

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(397)

<223> 3' terminal sequence. protein tyrosine
phosphatase, non-receptor type 2 (PTPN2) gene.

<400> 218

```

ttaatgctgc caaaaagtat aaaaatacag taggaatggc agtacaatac aaagtaatct 60
ctcctaattt atttcttgta catctttcta catctcatac actcattaac aacacttaac 120
acatccaatt aaagggtctg caaagtcttc tgctgggtggg tgctcttcat cccctgggnt 180
gtaaagttta ctttgtaaac aaacaactgt gaggncaatc tagagggtta ggcgagcctc 240
actttagttt ccggagtggg gcttcagggt cttgctttgc acatcaatgg gttcaaaatt 300
tataggctgc aggaatatcc tcaagggtcat ggaatattag ggngtctggt ncaat cttgg 360
ggcccttttt tcttttttcg ttncatttct ccattta 397

```

<210> 219

<211> 338

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(338)

<223> 5' terminal sequence. protein tyrosine
phosphatase, non-receptor type 2 (PTPN2) gene.

<400> 219

```

ggctccttga accctgacca tgggcctgcg gtgatccact gtagtgcagg cattgggcgc 60
tctggcacct tctctctggt agacacttgt cttgttttga tggaaaaagg agatgatatt 120
aacataaac aagtgttact gaac atgaga aaataccgaa tgggtcttat tcagaccca 180
gatcaactga gattctcata catggctata atagaaggag caaatgtat aaaggagat 240

```


tctagtatac agaaacgatg gaaagaactt tctaaggang acttatctcc tgcctttgat 300
cattncacca aacaaaataa tgactgaaaa atacantg 338

<210> 220

<211> 2287

<212> DNA/RNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(2287)

<223> protein tyrosine phosphatase, non -receptor
type 2 (PTPN2) gene.

<400> 220

ggggggcctg agcctctccg ccggcgcagg ctctgctcgc gccagctcgc tcccgcagcc 60
atgccaccca ccctcgagcg ggagttcgaa gaggttggata ctacagctcg ctggcagccg 120
ctgtacttgg aaattcgaaa tgagtcocat gactatcctc atagagtggc caagtttcca 180
gaaaacagaa atcgaaacag atacagagat gtaagcccat atgatcacag tctgtgttaa 240
ctgcaaaatg ctgagaatga ttatattaat gccagtttag ttgacataga agaggcacia 300
aggagttaca tcttaacaca ggttocactt cctaacacat gctgccattt ctggcttatg 360
gtttggcagc agaagaccaa agcagttgtc atgctgaacc gcattgtgga gaaagaatcg 420
gttaaatgtg cacagtactg gccaacag at gaccaagaga tgctgtttaa agaaacagga 480
ttcagtgatga agctcttgtc agaagatgtg aagtcgtatt atacagtaca tctactacaa 540
ttagaaaata tcaatagtgg tgaaccaga acaatatctc actttcatta tactacctgg 600
ccagattttg gaggccctga atcaccagct tcattttctca atttcttgtt taaagtgaga 660
gaatctggct ccttgaaccc tgaccatggg cctgcggtga tocactgtag tgcaggcatt 720
gggcgctctg gcaccttctc tctggtagac acttgtcttg ttttgatgga aaaaggagat 780
gatattaaca taaaacaagt gttactgaac atgagaaaat accgaatggg tcttattcag 840
acccagatc aactgagatt ctacatcatg gctataatag aaggagca aa atgtataaag 900
ggagattcta gtatacagaa acgatggaaa gaactttcta aggaagactt atctcctgcc 960
tttgatcatt caccaaacia aataatgact gaaaaataca atgggaacag aataggtcta 1020
gaagaagaaa aactgacagg tgaccgatgt acaggacttt cctctaaaat gcaagataca 1080
atggaaggaga acagtgtgag tgct ctacgg aaacgtattc gagaggacag aaaggccacc 1140
acagctcaga aggtgcagca gatgaaacag aggttaaagc agaatgaacg aaaaagaaaa 1200
agggtggtat attggcaacc tattctcact aagatggggg ttatgtcagt ctttttggtt 1260
ggcgcttttg ttggctggag actgtttttt cagcaaaatg ccctataaac aattaatatt 1320
gcccagcaag cttctgcact agtaactgac agtgctacat taatcatagg ggtttgtctg 1380
cagcaaacgc ctcatatccc aaaaacgggt cagtagaata gacatcaacc agataagtga 1440
tatttacagt cacaagccca acatctcagg actcttgact gcaggttcct ctgaacccca 1500
aactgtaaat ggctgtctaa aataaagaca ttcatgtt tg ttaaaaactg gtaaatattt 1560
caactgtatt catacatgtc aaacacagta ttacacctga ccaacattga gatatccttt 1620
atcacaggat ttgttttttg aggtatcttg gattttaacc tgcacttgat ataagcaata 1680
aatattgttg ttttatctac gttattggaa agaaaatgac atttaataa tgtgtgtaat 1740
gtataatgta ctattgacat gggcatcaac acttttatct ttaagcattt cagggtaaat 1800
atattttata agtatctatt taatcttttg tagttaactg tactttttta gagctcaatt 1860
tgaaaaatct gttactaaaa aaaaaaattg tatgtcgatt gaattgtact ggatacattt 1920
tccatttttc taaaaagaag tttgatatga gcagttagaa gttggaataa g caattttcta 1980
ctatatattg catttctttt atgtttttaca gttttcccca ttttaaaaag aaaagcaaac 2040
aaagaacaaa aagtttttcc taaaaatc tttgaaggaa aattctcctt actgggatag 2100
tcaggtaaac agttgggtcaa gactttgtta agaaattggt ttctgtaaat cccattattg 2160
atatgtttat ttttcatgaa aatttc aatg tagttggggg agattatgat ttaggaagca 2220
aaagtaagaa gcagcatttt atgattcata atttcagttt actagactga agttttgaag 2280
taaaccc 2287

<210> 221

<211> 296
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<220>
<221> misc_feature
<222> (1)..(296)
<223> 3' terminal sequence. epha2 (EPHA2) gene.

<400> 221
ctcggctggc tcacacaccc gtatggcaaa ggggtgggacc tgatgcagaa catcatgaat 60
gacatgccga tctacatgta ctccgtgtgc aacgtgatg t ctggcgacca gganaactgg 120
ctccgcacca actgggtgta ccgaggagag gctgagcgtg tcttcattga gctcaagttt 180
actgtacgtg actgcaacag cttccctggg tggcgccant tcctggcaag gagactttca 240
acctctacta tgccgagtcg gacctgggac tacggcanca acttncagaa gcgcct 296

<210> 222
<211> 3921
<212> DNA/RNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<220>
<221> misc_feature
<222> (1)..(3921)
<223> epha2 (EPHA2) gene.

<400> 222
cggaagttgc gcgcaggccg gcgggcgggg ggcggacaccg aggccggcgt gcaggcgtgc 60
gggtgtgcgg gagccgggct cggggggatc ggaccgagag cgagaagcgc ggcatggagc 120
tccaggcagc ccgcgcctgc ttgcacctgc tgtggggctg tgcgctggcc gcggccgcgg 180
cggcgagggg caaggaagtg gtactgctgg actttgctgc agctggaggg gagctcggct 240
ggctcacaca ccggtatggc aaaggggtgg acctgatgca gaacatc atg aatgacatgc 300
cgatctacat gtactccgtg tgcaacgtga tgtctggcga ccaggacaac tggctccgca 360
ccaactgggt gtaccgagga gaggtgagc gtaacaactt tgagctcaac ttactgtac 420
gtgactgcaa cagcttccct ggtggcgcca gctcctgcaa ggagactttc aacctctact 480
atgccgagtc ggacctggac tacgg cacca acttcagaa gcgcctgttc accaagattg 540
acaccattgc gcccgatgag atcacctgca gcagcgactt cgaggcacgc cacgtgaagc 600
tgaacgtgga ggagcgctcc gtggggccgc tcaccgcaa aggtttctac ctggccttcc 660
aggatatcgg tgctgtgtg gcgctgctct ccgtccgtgt ctactacaag aagtgcctcc 720
agctgtgca gggcctggcc cacttccctg agaccatgc cggctctgat gcaccttccc 780
tggccactgt ggccggcacc tgtgtggacc atgccgtggt gccaccgggg ggtgaagagc 840
cccgtatgca ctgtgcagt gatggcgagt ggctgggtgc cattgggcag tgctgtgccc 900
aggcaggcta cgagaaggtg gaggatgcct gccaggcctg ctgc ctgga ttttttaagt 960
ttgaggcatc tgagagcccc tgcttgagt gccctgagca cacgtgccca tccctgagg 1020
gtgccacctc ctgcgagtgt gaggaaggct tcttccgggc acctcaggac ccagcgtcga 1080
tgcttgccac acgacccctc tccgcccac actacctcac agccgtgggc atgggtgcc 1140
aggtggagct gcgctggacg cccctcagg acagcggggg ccgcgaggac attgtctaca 1200
gcgtcacctg cgaacagtgc tggcccgagt ctggggaatg cgggccgtgt gaggccagt 1260
tgcgctactc ggagcctcct caggactga ccgcaccag tgtgacagt agcgacctgg 1320
agccccacat gaactacacc ttaccctgg aggcgcgcaa tggcgtctca ggctggtaa 1380
ccagccgcag cttccgtact gccagtgtca gcatcaacca gacagagccc cccaaggtga 1440
ggctggaggg ccgcagcacc acctcgctta gcgtctctg gagcatcccc ccgcccgcagc 1500
agagccgagt gtggaagtac gaggtcactt accgcaagaa gggagactcc aacagctaca 1560
atgtgcgccg caccgaggggt ttctccgtga ccct ggacga cctggcccca gacaccacct 1620

```

acctggtcca ggtgcaggca ctgacgcagg agggccagg ggccggcagc aaggtgcacg 1680
aattccagac gctgtccccg gagggatctg gcaacttggc ggtgattggc ggcgtggctg 1740
tcggtgtggt cctgtctctg gtgctggcag gagttggctt ctttatccac cgcaggagga 1800
agaaccagcg tgcccgccag tcccggagg acgtttactt ctccaagtca gaacaactga 1860
agccctgaa gacatacgtg gacccccaca catatgagga ccccaaccag gctgtgttga 1920
agttcactac cgagatccat ccatcctgtg tcaactcggca gaaggtgatc ggagcaggag 1980
agtttgggga ggtgtacaag ggcatgctga agacatcctc ggggaaga ag gaggtgcccg 2040
tgcccatcaa gacgtgaaa gccggctaca cagagaagca gcgagtggac ttcctcggcg 2100
aggccggcat catggggccag ttcagccacc acaacatcat ccgcctagag ggcgtcatct 2160
ccaaatacaa gcccatgatg atcatcactg agtacatgga gaatggggcc ctggacaagt 2220
tccttcggga gaaggatggc ga gttcagcg tgctgcagct ggtgggcatg ctgcggggca 2280
tcgcagctgg catgaagtac ctggccaaca tgaactatgt gcaccgtgac ctggctgcc 2340
gcaacatcct cgtcaacagc aacctggtct gcaaggtgtc tgactttggc ctgtcccgcg 2400
tgctggagga cgaccccgag gccacctaca ccaccagtgg cggcaagatc cccatccgct 2 460
ggaccgcccc ggaggccatt tcctaccgga agttcacctc tgccagcgac gtgtggagct 2520
ttggcattgt catgtgggag gtgatgacct atggcgagcg gccctactgg gagttgtcca 2580
accacgaggt gatgaaagcc atcaatgatg gcttcgggt cccacacccc atggactgcc 2640
cctccgcat ctaccagctc atgatgcagt gctggc agca ggagcgtgcc cgccgcccc 2700
agttcgctga catcgctcag atcctggaca agctcattcg tgcccctgac tccctcaaga 2760
ccttggtcta ctttgacccc cgcgtgtcta tccggctccc cagcacgagc ggctcggagg 2820
gggtgccctt ccgcacgggt tccgagtggc tggagtccat caagatgcag cagtatacgg 2880
agcacttcat ggccgcccgc taaactgcca tcgagaaggt ggtgcagatg accaacgacg 2940
acatcaagag gattgggggtg cggctgcccg gccaccagaa gcgcctcgcc tacagcctgc 3000
tggtgactcaa ggaccagggtg aacactgttg ggatcccat ctgagcctcg acagggcctg 3060
gagccccatc ggccaagaat acttgaagaa acagagtggc ctccctgctg tgccatgctg 3120
ggccactggg gactttattt atttctagtt ctttctccc cctgcaactt ccgctgaggg 3180
gtctcggatg acaccctggc ctgaactgag gagatgacca gggatgctgg gctgggccct 3240
ctttccctgc gagacgcaca cagctgagca cttagcaggc accgccacgt cccagcatcc 3300
ctggagcagg agccccgcca cagc ctccgg acagacatat aggatattcc caagccgacc 3360
ttccctccgc cttctccac atgaggccat ctcaggagat ggagggcttg gccacgcgc 3420
aagtaaacag ggtacctcaa gcccatttc ctcacactaa gagggcagac tgtgaacttg 3480
actgggtgag acccaaagcg gtccctgtcc ctctagtgcc ttctttagac cctcgggcc 354 0
catcctcatc cctgactggc caaaccttg ctttctcggg cctttgcaag atgcttggtt 3600
gtgttgaggt ttttaaata atattttgta ctttgtggag agaattgtgtg tgtgtggcag 3660
ggggccccgc cagggctggg gacagagggt gtcaaacatt cgtgagctgg ggaactcagg 3720
accggtgctg caggagtgtc ctgccatgc ccagtcg gc cccatctctc atccttttg 3780
ataagtttct attctgtcag tgttaaagat tttgtttgt tggacatttt tttcgaatct 3840
taatttatta tttttttat atttattgtt agaaaatgac ttatttctgc tctggaataa 3900
agttgcagat gattcaaac g 3921

```

<210> 223

<211> 437

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(437)

<223> 3' terminal sequence. tissue inhibitor of metalloproteinase 1 (erythroid potentiating activity, collagenase inhibitor) (TIMP1) gene.

<400> 223

```

ggaacagggt ggacactgtg caggcttcag cttccactcc gggcaggatt caggctatct 60
gggaccgcag gacttgccag gngcacagcc ctggctcccg aggcaggcag gcaaggtgac 120
gggactggaa gcccttttca naggcttga ggagctggnc cgtccacaag caatgagtgc 180
cactctgcag tttgcagggg atggataaac agggaaacac tgtgcattcc tcacagccaa 240

```

147/292

```

cagtntaggt cttggtnaag ccccggcgct gagctaagct caggcttttc caggggagcc 300
acgaaactnc aggtagtgat gtgcaagagt ccatcctgca gttttccagc aatnagaaac 360
tcctcgttng cggttttttg ggaccnttgg aagtntc cg cagacatttt tccatgggcc 420
gggttttaag acgaacc                                     437

```

<210> 224

<211> 466

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(466)

<223> 5' terminal sequence. tissue inhibitor of
metalloproteinase 1 (erythroid potentiating
activity, collagenase inhibitor) (TIMP1) gene.

<400> 224

```

gccncagatc cagcgccag agagacacca gagaaccac catggcccc tttgnagccc 60
ctggcttctg gcacctgtt g ttgctgtg ctgatatgcc ccagcagggc ctgcacctgt 120
gtcccacccc acccacagac ggccttctgc aattccgacc tcgtcatcag ggccaagtgc 180
gtggggacac cagaagtcaa ccagaccacc ttataccagc gttatgagat caagatgacc 240
aagatgtata aagggttcca agccttaggg gatgccgctg acatccggtt cgtctacacc 300
cccgccatgg agagtgtctg cggatacttn cacagggtccc acaaccgnag cgaggagtgt 360
ctcattngct ggaaaactgt aggatggact tcttgacat tnactacctt gcagttttng 420
tgggttcctt gggaacagtc tgaggtttag tttagcggtn ggggtt          466

```

<210> 225

<211> 782

<212> DNA/RNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(782)

<223> tissue inhibitor of metalloproteinase 1
(erythroid potentiating activity, collagenase
inhibitor) (TIMP1) gene.

<400> 225

```

aggggcctta gcgtgccgca tcgccgagat ccagcgccca gagagacacc agagaacca 60
ccatggcccc ctttgagccc ctggttcttg gcacctgtt gttgctgtgg ctgatatgcc 120
ccagcagggc ctgcacctgt gtcccacccc acccacagac ggccttctgc aattccgacc 180
tcgtcatcag ggccaagtgc gtggggacac cagaagtcaa c cagaccacc ttataccagc 240
gttatgagat caagatgacc aagatgtata aagggttcca agccttaggg gatgccgctg 300
acatccggtt cgtctacacc cccgccatgg agagtgtctg cggatacttc cacagggtccc 360
acaaccgcag cgaggagtgt ctcattgctg gaaaactgca ggatggactc ttgcacatca 420
ctacctgcag tttcgtggct ccctggaaca gctgagctt agctcagcgc cggggcttca 480
ccaagaccta cactgttggc tgtgaggaat gcacagtgtt tccctgttta tccatccct 540
gcaaaactgca gattggcact cattgcttgt ggacggacca gctcctccaa ggctctgaaa 600
agggcttcca gtcccgtcac cttgcctgcc tgcctcgga gccagggtctg tgcacctggc 6 60
agtccctgcg gtcccagata gcctgaatcc tgcccggagt ggaactgaag cctgcacagt 720
gtccaccctg tcccactcc catctttctt ccggacaatg aaataaagag ttaccaccca 780

```

gc

782

<210> 226
<211> 353
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<220>
<221> misc_feature
<222> (1)..(353)
<223> 5' terminal sequence. ephrin -a1 (EFNA1)
gene.

<400> 226
acagctacta ctacatctca gccaaaccca tccaccagca tgaagaccgc tgcttgaggt 60
tgaaggtgac tgtcagtggc aaaatcactc acagtcctca ggcccatgtc aatccacagg 120
agaagagact tgcagcagat gaccagagg tgccgggttct acatagcctc ggccacagtg 180
ctgccccacg cctcttccca cttgcctgga ctgtgctgct ccttccactt ctgctgctgc 240
aaaccccggtg aaggtgtatg ccacacctgg ccttaaagag ggaca ggctg aagagaggga 300
caggcactcc aaacctgtct tgggggccac ttccagagcc ccagccctt ggg 353

<210> 227
<211> 1480
<212> DNA/RNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<220>
<221> misc_feature
<222> (1)..(1480)
<223> ephrin-a1 (EFNA1) gene.

<400> 227
gcggagaaag ccagtgggaa ccagaccca taggagaccg gcgtccccgc tcggcctggc 60
caggccccgc gctatggagt tcctctgggc ccctctcttg ggtctgtgct gcagtctggc 120
cgctgctgat cgccacaccg tcttctggaa cagttcaaata ccaagttcc ggaatgagga 180
ctacaccata catgtgcagc tgaatgacta cgtggacatc atctgtccgc actatgaaga 240
tcactctgtg gcagacgctg ccatggagca gtacatactg tacctggtgg agcatgagga 300
gtaccagctg tgccagcccc agtccaagga ccaagtcgcg tggcagtgc accggcccag 360
tgccaagcat ggcccgagga agctgtctga gaagttccag cgcttcacac ctttcacct 420
gggcaaggag ttcaaagaag gacacagcta ctactacatc tccaaaccca tccaccagca 480
tgaagaccgc tgcttgaggt tgaaggtgac tgtcagtggc aaaatcactc acagtcctca 540
ggcccatgtc aatccacagg agaagagact tgcagcagat gaccagagg tgccgggttct 600
acatagcctc ggccacagtg ctgccccg cctcttccca cttgcctgga ctgtgctgct 660
ccttccactt ctgctgctgc aaaccccggtg aaggtgtatg ccacacctgg ccttaaagag 720
ggacaggctg aagagaggga caggcactcc aaacctgtct tggggccact ttccagagcc 780
ccagccctgg gaaccactcc caccacaggc ataagctatc acctagcagc ctcaaacagg 840
gtcagtatta aggttttcaa ccggaaggag gccaaaccagc ccgacagtgc catccccacc 900
ttcacctcgg agggacggag aaagaagtgg agacagtcct ttcccaccat tctgccttt 960
aagccaagaa aacaagctgt gcaggcatgg tcctttaagg cacagtggga gctgagctgg 1020
aagggggccac gtggatgggc aaagcttgct aaagatgccc cctccag gag agagccagga 1080
tgccagatg aactgactga aggaaaagca agaaacagtt tcttgcttgg aagccaggta 1140
caggagaggc agcatgcttg ggctgacca gcatctccca gcaagacctc atctgtggag 1200
ctgccacaga gaagtttgta gccaggtact gcattctctc ccctcctggg gcagcactcc 1260

149/292

```

ccagagctgt gccagcaggg g ggctgtgcc aacctgttct tagagtgtag ctgtaagggc 1320
agtgccatg tgtacattct gcctagagt tagcctaaag ggcagggccc acgtgtatag 1380
tatctgtata taagttgctg tgtgtctgtc ctgatttcta caactggagt ttttttatac 1440
aatgttcttt gtctcaaat aaagcaatgt gttttttcgg 1480

```

<210> 228

<211> 170

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(170)

<223> 3' terminal sequence. endothelin receptor
type a (EDNRA) gene.

<400> 228

```

ttttaagggt tctgtaaact tttattttac acttatgggc cactgcaact cagggccttg 60
gcttctggct catttctaca aagttacttg ttgaaaagat gtagtaaagg tagaaattgg 120
aaatatcct gctagtaaac cacagttact taccagtcca taaataaaat 170

```

<210> 229

<211> 4105

<212> DNA/RNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(4105)

<223> endothelin receptor type a (EDNRA) gene.

<400> 229

```

gaattcgcg g cgcctcttg cgggtcccaga gtggagtga aggtctggag ctttgggagg 60
agacggggag gacagactg g aggcgtgttc ctccggagtt ttctttttcg tgcgagccct 120
cgcgcgcgcg tacagtcac cgcgtggtct gacgattgtg gagaggcggg ggagaggcctt 180
catccatccc acccggtcgt cgccggggat tgggggtccca ggcacacctc cccgggagaa 240
gcagtgccca ggaagttttc tgaagccggg gaagctgtgc agccgaagcc gccgcccgcgc 300
cggagcccgg gacaccggcc accctccgcg ccacccaccc tcgctttctc cggttctctc 360
tggcccaggc gccgcgcgga cccggcagct gtctgcgcac gccgagctcc acggtgaaaa 420
aaaaagtga ggtgtaaaag cagcacaagt gcaataagag atatttcctc aaatttgctt 480
caagatggaa accctttgcc tcaggggcatc cttttggct g gcaactggtg gatgtgtaat 540
cagtataaat cctgagagat acagcacaaa tctaagcaat catgtggatg atttcaccac 600
ttttcgtggc acagagctca gtttcttggt taccactcat caaccacta atttggtcct 660
accagcaat ggtcaatgc acaactattg ccacagcag actaaaatta cttcagcttt 720
caaatacatt aacactg tga tatctgtac tattttcac gtgggaatgg tggggaatgc 780
aactctgtc aggatcattt accagaacaa atgtatgagg aatggcccca acgcgctgat 840
agccagtctt gcccttggag acqttatcta tgttggtcatt gatctcccta tcaatgtatt 900
taagctgctg gctgggcgct ggccttttga tcacaatgac tttggcgat ttctttgca a 960
gctgttcccc tttttgcaga agtctcggg ggggatcacc gtcctcaacc tctgcgctct 1020
tagtgttgac aggtacagag cagttgcctc ctggagtcgt gttcagggaa ttgggattcc 1080
tttggttaact gccattgaaa ttgtctccat ctggatcctg tcctttatcc tggccattcc 1140
tgaagcgatt ggcttcgtca tggatccctt tgaa tatagg ggtgaacagc ataaaacctg 1200
tatgtctaat gccacatcaa aattcatgga gttctaccaa gatgtaaagg actggtggct 1260

```

```

cttcgggttc tatttctgta tgccttgggt gtgcactgcg atcttctaca ccctcatgac 1320
ttgtgagatg ttgaacagaa ggaatggcag cttgagaatt gccctcagtg aacatcttaa 1380
gcagcgtcga gaagtggcaa aaacagtttt ctgcttgggt gtaatttttg ctctttgctg 1440
gttccctctt cacttaagcc gtatatgaa gaaaactgtg tataacgaaa tggacaagaa 1500
ccgatgtgaa ttacttagtt tcttactgct catggattac atcgggtatta acttggaac 1560
catgaattca tgtataaacc ccatagctct gtattttgtg agcaagaa at ttaaaaattg 1620
tttccagtcg tgcctctgct gctgctgtta ccagtcctaaa agtctgatga cctcgggtccc 1680
catgaacgga acaagcatcc agtgggaagaa ccacgatcaa aacaaccaca acacagaccg 1740
gagcagccat aaggacagca tgaactgacc acccttagaa gcactcctcg gtactcccat 1800
aatcctctcg gagaaaaaaa tc acaaggca actgtgactc cggaatctc ttctctgate 1860
cttcttctct aattcactcc cacacccaag aagaaatgct ttccaaaacc gcaaggtaga 1920
ctggtttatc caccacaac atctacgaat cgtacttctt taattgatct aatttacata 1980
ttctgcgtgt tgtattcagc actaaaaaat ggtgggagct gggggagaat gaagactgtt 2 040
aaatgaacac agaggatat ttactacttt tgcagtaaaa tagagcttcc aagtacatgg 2100
ctagctttta tggcagttct ggtgaatggt caatgggaac tggtcacat gaaactttag 2160
agattaacga caagattttc tacttttttt aagtgatttt ttgtccttca gccaaacaca 2220
atatgggctc aggtcacttt tatttgaaat gtcatt tgggt gccagtattt ttttaactgca 2280
taatagccta acatgattat ttgaacttat ttacacatag ttgaaaaaaa aaaagacaaa 2340
aatagtattc aggtgagcaa ttagattagt attttccacg tcaactattta tttttttaa 2400
acacaaattc taaagctaca acaataacta caggccctta aagcacagtc tgatgacaca 2460
tttggcagtt taatagatgt tactcaaaga attttttaag aactgtattt tttttttaa 2520
atgggtgttt attacaaggg acctgaaca tgttttgtat gttaaattca aaagtaatgc 2580
ttcaatcaga tagttctttt tcacaagttc aatactgttt ttcatgtaaa ttttgtatga 2640
aaaatcaatg tcaagtacca aaatgttaat gtatgtgtca ttttaactctg cctgagactt 2700
tcagtgcact gtatatagaa gtctaaaaca cacctaagag aaaaagatcg aatttttcag 2760
atgatccgga aattttcatt cagggtattt taatagtgc atatatatgt atatacatat 2820
cacctcctat tctcttaatt ttgttaaaa tgttaactgg cagtaagtct tttttgatca 2880
ttcccttttc catataggaa acat aatttt gaagtggcca gatgagtta tcatgtcagt 2940
gaaaaataat taccacaaaa tgcaccagt aacttaacga ttcttcaact ottggggttt 3000
tcagtatgaa ctaactccc caccocaaca tctccctccc acattgtcac catttcaaag 3060
ggcccacagt gacttttgcg ggcatttttc ccagatgttt acagactgtg agtacagcag 312 0
aaaatctttt actagtgtgt gtgtgtatat atataaaca ttgtaaattt cttttagccc 3180
atttttctag actgtctctg tggaaatat ttgtgtgtgt gatatatgca tgtgtgtgat 3240
ggtatgtatg gatttaattc aatctaataa ttgtgccccg cagttgtgcc aaagtgcata 3300
gtctgagcta aaatctaggt gattgttcat catgacaa cc tgcctcagtc cattttaacc 3360
tgtagcaacc ttctgcattc ataaatcttg taatcatgtt accattacaa atgggatata 3420
agaggcagcg tgaaagcaga tgagctgtgg actagcaata tagggttttg tttgggttgg 3480
tggtttgata aagcagttat tggggtcata ttgtttcctg tgctggagca aaagtcatta 3540
cactttgaag ttttatattg ttcttatcct caattcaatg tggatgatgaa attgccaggt 3600
tgtctgatat ttctttcaga cttcgccaga cagattgctg ataataaatt aggtgaagata 3660
atgtgttggg ccatatttta ggacaggtaa aataacatca ggttccagtt gcttgaattg 3720
caaggctaag aagtactgcc cttttgtgtg ttagcagtc aatctattat t ccaactggcg 3780
catcatatgc agtgatatat gcctataata taagccatag gttcacacca ttttgtttag 3840
acaattgtct ttttttcaag atgctttgtt tctttcatat gaaaaaaatg cattttataa 3900
attcagaaaag tcatagattt ctgaaggcgt caacgtgcat tttatttatg gactggtaag 3960
taactgtggt ttactagcag gaatat ttcc aatttctacc ttactacat cttttcaaca 4020
agtaactttg tagaaatgag ccagaagcca aggcctgag ttggcagtg cccataagtg 4080
taaaataaaa gtttacagaa acctt 4105

```

<210> 230

<211> 240

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(240)

<223> 3' terminal sequence. growth factor
receptor-bound protein 2 (GRB2) gene.

<400> 230

ggttttcttgt tttttattat tggcgtcagt agngactata cgtggcctta aacgtcatgc 60
actgatggac agaagagaaa aaaggatgaa aaaaaagaca aaggagggga aagaggagca 120
gcagtgaan tttgtaataa aaactcttct taatttatag gtaagttttg gcatttttaa 180
atccaacgcc ccctcccacc ccctaaagt ccaaccaaag tgagaggggc acagggtgac 240

<210> 231

<211> 475

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(475)

<223> 5' terminal sequence. growth factor
receptor-bound protein 2 (GRB2) gene.

<400> 231

cttaatggaa aagacggctt cattcccaag aactacatag aaatga aacc acatccgtgg 60
ttttttggca aaatcccag agccaaggca gaagaaatgc ttagcaaaca gcggcacgat 120
ggggcccttc ttatccgaga gagtgaagac gctcctgggg acttctccct ctctgtcaag 180
tttggaacg atgtgcagca cttcaagggtg ctccgagatg gagccgggaa gtacttcctc 240
tggttggtga agttcaattc ttga atgag ctgggtggatt atcacagatc tacatctgtc 300
tccagaaacc agcagatatt cctgcgggga cattaggaac aggtgccaca gcaggccgac 360
atacgtcca ggggcctttt ttgattttt gattcccag gggggnttgg ngagggtggg 420
ttttccgcg ggggagattt tattccatgt tcntgggttn aatttaggaa ccntt 475

<210> 232

<211> 1109

<212> DNA/RNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(1109)

<223> growth factor receptor -bound protein 2
(GRB2) gene.

<400> 232

gccagtgaat tcggggggtc agccctctc cctcccttcc cctgcttca ggctgctgag 60
cactgagcag cgctcagaat ggaagccatc gccaaatatg acttcaaagc tactgcagac 120
gacgagctga gcttcaaaaag gggggacatc ctcaaggttt tgaacgaaga atgtgatcag 180
aactggtaca aggcagagct taatggaaaa gacggcttca ttccaagaa ctacatagaa 240
atgaaaccac atccgtgggt ttttggcaaa atcccagag ccaaggcaga agaaatgctt 300
agcaaacagc ggcacgatgg ggcctttctt atccgagaga gtgagagcgc tcctggggac 360
ttctccctct ctgtcaagtt tggaacgat gtgcagcact tcaagggtgct ccgagatgga 420
gccgggaagt acttctctg ggtggtgaag ttcaattctt tgaatgagct ggtggattat 480
cacagatcta catctgtctc cagaaaccag cagatatcc tgccggacat agaacagggtg 540
ccacagcagc cgacatacgt ccaggccctc tttagctttg atcccagga ggaaggagag 600
ctgggcttcc gccggggaga ttttatccat gtcattgata actcagaccc caactggtgg 660

152/292

```

aaaggagctt gccacggg ca gaccggcatg tttcccgca attatgtcac ccccgtaac 720
cggaacgtct aagagtcaag aagcaattat ttaaagaaag tgaaaaatgt aaaacacata 780
caaaagaatt aaaccacaa gctgcctctg acagcagcct gtgagggagt gcagaacacc 840
tggccgggtc accctgtgac cctctcactt tggttggaac tttagggggt gggagggggc 900
gttgatttta aaaatgcaa aacttaccta taaattaaga agagttttta ttacaaattt 960
tactgtctgc tcctctttcc cctcctttgt ctttttttcc atcctttttt ctcttctgtc 1020
catcagtgc tgaagttaa ggccacgtat agtcctagct gacgccaata ataaaaaaca 1080
agaaaccaa aaaaaaaac ccgaattca 1109

```

<210> 233

<211> 446

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(446)

<223> 3' terminal sequence. jun d proto -oncogene
(JUND) gene.

<400> 233

```

cgcgctctc ggctgcnng ntgtacaccg cgccgaaag tggggctccg agggggcgca 60
ctcaaaaccc tgcctttcct ttacttttac ttttttttt ttttctttgg aagagagaag 120
aacagagtgt tcgattctgc cctatttatg tttctactcg ggaacaaacg ttggttgtgt 180
gtgtgtgtgt tttcttgtgt tggtttttta a agaaatggg aagaagaaaa aaaaattctc 240
cgccctttc ctgatctcg ctccccctt cggttcttcc gaccgggtcc cccctccctt 300
ttttgttct gttttgtttt gttttgctac gagtccacat tcctgtttgt aatccttggg 360
ttcgnccggt tttctgtttt cagtaaagtc tcgttacggc aaaacctcgt gccgaatttt 420
tggggctcga ggggcaaat ttcca 446

```

<210> 234

<211> 1891

<212> DNA/RNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(1891)

<223> jun d proto -oncogene (JUND) gene.

<400> 234

```

ccgaggctat aagaggggcg acaagtggcg cggcgaggga gccgccgcca gtggaggggc 60
gggcgctgcg gccgcggccg gggcgggcg agggccgagc ggacgggggg gcgcggggcc 120
cccgaggagc cgcggccact ccccccggg ccggcgcggc gggggaggcg gaggatggaa 180
acacccttct acggcgatga ggcgctg agc ggctggggcg gcggcgccag tggcagcggc 240
ggcacgttcg cgtccccggg ccgcttggtc ccggggcggc ccccgacggc cgcggccggc 300
agcatgatga agaaggacgc gctgacgctg agcctgagt agcaggtggc ggcagcgctc 360
aagcctgcgc cgcgcgccgc ctctacccc cctggcgccg acggcgcccc cagcgcgga 420
ccccccgagc gctgctcgc ctctcccgac ctggggctgc tgaagctggc ctccccgag 480
ctcagcgcc tcacatcca gtccaacggg ctggtcacca ccacgccgac gagctcacag 540
ttcctctacc ccaaggtggc ggccagcgag gaggaggagt tcgccgaggg cttcgtcaag 600
gccctggagg atttacacaa gcagaaccag ctggcgcgcg gccgggc cgc tgcgcggcc 660
gccgcgcgc cggggggggc ctggggcacg gccacgggct ccgcgcccc cgcgagctg 720

```

153/292

```

gccccggcgg cggccgcgcc cgaagcgcc gtctacgcga acctgagcag ctacgcgggc 780
ggcgccgggg gcgcgggggg cgccgcgacg gtcgccttcg ctgccgaacc tgtgcccttc 840
ccgccggcgc caccgccagg cgcgt tgggg ccgcgcgcc tggctgcgct caaggacgag 900
ccacagacgg tgcccgacgt gccgagcttc ggcgagagcc cgccgttgct gcccatcgac 960
atggacacgc aggagcgcat caaggcggag cgcaagcggc tgcgcaaccg catcgccgcc 1020
tccaagtgcc gcaagcgcaa gctggagcgc atctcgccgc tgggaagagaa agtgaagacc 1080
ctcaagagtc agaacacgga gctggcgctc acggcgagcc tgctgcgcga gcaggtggcg 1140
cagctcaagc agaaagtcct cagccacgctc aacagcggct gccagctgct gcccagcac 1200
caggtcccg cgtactgagt cgggcatggc ggccacctcc aaggggcggg ctgcggggg 1260
ggtgtctgtg gcgcccgga cttggagagg gtgcggccct ccaccccccc ctcccagat 1320
gtgccagga actcagagag gcgcggcccc ggggattccc ccccgaggtg cccaggactc 1380
ggaagggcg ccccgactc gacaagctgg acccctgct cccggggcg agcgcatgac 1440
cccccgccc tcgcgtgcc tcttcccc gcgcggcgc cccgtgttg acaaaccgc 1500
gcgtctcggc tgccc cttt tacaccgcgc cgcaagggg ctccgaggg gcgcacgtca 1560
aaccctgcct ttcctttact tttactttt tttttcttt ggaagagaga agaacagagt 1620
gttcgattct gccctattta tgtttctact cggggaacaa acgttggtg tgtgtgtgtg 1680
tgttttcttg tgttggttt ttaaagaaat gggaagaaga aaaaaaatt ctcc gccct 1740
ttcctcgatc tcgtcccc ttcggtctt cgaccgtccc cccctccct tttttgttc 1800
tgttttgtt tgttttgcta cgagtccaca ttcctgttg taatccttg ttcgcccggt 1860
tttctgttt cagtaaagtc tcgttacgcc a 1891

```

<210> 235

<211> 421

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(421)

<223> 3' terminal sequence. swi/snf related,
matrix associated, actin dependent regulator of
chromatin, subfamily a, member 2 (SMARCA2) gene.

<400> 235

```

accaaaagtc ttcaagccac gagcggaggg cattcctgca ggccatcttg gagcatgagg 60
aggaaaatga ggaagaagat gaagtaccgg acgatgagac tctgaaccaa atgattgctc 120
gacgagaaga agaatttgac ctttttatgc ggatggacat ggaccggcgg agggaagatg 180
cccggaaccc gaaacggaag ccccgtttaa tggaggagga tgagctgcc tcctggntca 240
ttaaggatga cgctgaagta gaaaggctca cctgtgaaga agaggaggag aaaatatttg 300
ggaggggggc ccgccagcgc cgtgacgtgg actacagtga cgccctcacg gagaagcagt 360
ggctaaaggg ccntcgaaga cggcatttng gaggaattng aagaggaata c ggtaagaa 420
g 421

```

<210> 236

<211> 438

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(438)

<223> 5' terminal sequence. swi/snf related,
matrix associated, actin dependent regulator of

chromatin, subfamily a, member 2 (SMARCA2) gene.

<400> 236

```
tggcaatttt ctgccgggca ctcttaaaca ctgactgtaa gacgatggag tcttcataga 60
tctgggatcc ctccagggtt aacgtctgag cg ttgtgaca gagaagcatg acatccttct 120
ccaggctgcc taggtccggg tacttatgat tacgaatcct ttcctttatt tttttgaaat 180
ccactggctt cctaattaat tcatagtatt ctggtaattc tttccttgaa ggtaactgaa 240
tgaagacttc actgagctgt cgccctgaac tgtttccttc tatttccaac tgagaattac 300
tgggcacctt ctccacgtta cactatctt tgtagtttat cacagtattc gatgattagc 360
gttcatctgg ctttgtcagt ttggggggga tttggtgaca gntttntcag cgggaggggc 420
gcctcttctc ttcttagg                                     438
```

<210> 237

<211> 5257

<212> DNA/RNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(5257)

<223> swi/snf related, matrix associated, actin
dependent regulator of chromatin, subfamily a,
member 2 (SMARCA2) gene.

<400> 237

```
aaaaattttc tgttaccaaa ttttacaact tctaataaga ctactataac tttatgtaaa 60
ctgatgaaga tgtgctgatt aacatattct gtgatatgtt ttacaacttt taatcataat 120
tgtccatgat tttggaatgc tgttatttat cagtaaatgt aaaatatttg aggcatttag 180
ccatacacac actagaactt tttaaaactt tgcctatag tgtaatta ta aactgatgac 240
tattatcttc atacattgag tcttcatgca tcaatgaaat gaaaaatata ggagtagatg 300
tccacgcccc cagaccctgg tgcgatgccc caccagggc cttcgccggg gcctgggcct 360
tcccctgggc caattcttgg gcctagtcca ggaccaggac catccccagg ttccgtccac 420
agcatgatgg ggccaagtcc tggacc tcca agtgtctccc atcctatgcc gacgatgggg 480
tccacagact tccacagga agcatgcat caaatgcata agcccatcga tggatatacat 540
gacaagggga ttgtagaaga catccattgt ggatccatga agggcactgg tatgcgacca 600
cctcacccag gcatggccc tcccagagt ccaatggatc aacacagcca aggttatatg 660
tcaccacacc catctccatt aggagcccca gagcacgtct ccagccctat gtctggagga 720
ggcccaactc cactcagat gccaccaagc cagccggggg cctcatccc aggtgatccg 780
caggccatga gccagcccaa cagaggtecc tcacctttca gtctgtcca gctgcatcag 840
cttcgagctc agatttttag ttataaaatg ctggcccgag gccagc cctt ccccgaaacg 900
ctgcagcttg cagtccaggg gaaaaggacg ttgcctggct tgcagcaaca acagcagcag 960
caacagcagc agcagcagca gcagcagcag cagcagcagc agcaacagca gccgcagcag 1020
cagccgcccg aaccacagac gcagcaacaa cagcagccgg ccttgttaa ctacaacaga 1080
ccatctggcc cggggccgga gc tgagcggc ccgagcacc cgcagaagct gcoggtgcc 1140
gcccggcgcc gcccggccct gcccgccccc cccgcagccg cgcagccgcc cgcggccgca 1200
gtgcccgggc cctcagtgcc gcagccggcc cgggggcagc cctcgccgt cctccagctg 1260
cagcagaagc agagccgcat cagcccatc cagaaaccgc aaggcctgga ccccgaggaa 1 320
attctgcaag agcgggaata cagacttcag gccgcgatag ctcataggat acaagaactg 1380
gaaaatctgc ctggtctttt gccaccagat ttaagaacca aagcaaccgt ggaactaaaa 1440
gcacttcggt tactcaattt ccagcgtcag ctgagagagg aggtggtggc ctgcatgcgc 1500
agggaacaga cctggagac ggctctcaac tccaaa gcat aaaaacggag caagcgccag 1560
actctgagag aagctcgcat gaccgagaag ctggagaagc agcagaagat tgagcaggag 1620
aggaaaagcc gtcagaaaca ccaggaatac ctgaacagta ttttgcaaca tgcaaaagat 1680
tttaaggaat atcatcggtc tgtggccgga aagatccaga agctctcaa agcagtggca 1740
acttggcatg ccaacactga aagagagcag aagaaggaga cagagcggat tgaaaaggag 1800
agaatgcggc gactgatggc tgaagatgag gagagttata gaaaactgat tgatcaaaag 1860
aaagacaggc gtttagctta ccttttgcag cagaccgatg agtatgtagc caatctgacc 1920
```

```

aatctggttt gggagcacia gcaagcccag gcagccaaag agaagaagaa gaggaggagg 1980
aggaagaaga aggtctgagga gaatgcagag ggtggggagt ctgccctggg accggatgga 2040
gagcccatag atgagagcag ccagatgagt gacctccctg tcaaagtac tcacacagaa 2100
accggcaagg ttctgttcgg accagaagca cccaaagcaa gtcagctgga cgcctggctg 2160
gaaatgaatc ctgggttatga agtt gcccct agatctgaca gtgaagagag tgattctgat 2220
tatgaggaag aggatgagga agaagagtcc agtaggcagg aaaccgaaga gaaaatactc 2280
ctggatccaa atagcgaaga agtttctgag aaggatgcta agcagatcat tgagacagct 2340
aagcaagacg tggatgatga atacagcatg cagtacagtg ccaggggctc ccagtcttac 240 0
tacaccgtgg ctcatgccat ctcgagagag gtggagaaac agtctgccct cctaattaat 2460
gggaccctaa agcattacca gctccagggc ctggaatgga tggtttccct gtataataac 2520
aacttgaacg gaatcttagc cgatgaaatg gggcttgaa agaccataca gaccattgca 2580
ctcatcactt atctgatgga gcacaaaaga ctcaatgg cc cctatctcat cattgttccc 2640
ctttcgactc tatctaactg gacatatgaa ttgacaaat gggtccttc tgtggtgaag 2700
atttcttaca aggttactcc tgccatgagt cgctcccttg tccccagct acggagtggc 2760
aaattcaatg tctcttgac tacttatgag tatattataa aagacaagca cattcttgca 2820
aagattcggg ggaatacat gatagtggac gaagcccacc gaatgaagaa tcaccactgc 2880
aagctgactc aggtcttgaa cactcactat gtggcccca gaaggatcct cttgactggg 2940
accccgctgc agaataagct ccctgaactc tgggccctcc tcaacttcct cctccaaca 3000
atthttaaga gctgcagcac atthgaacaa tggttcaatg ctccatttgc c atgactggg 3060
gaaagggagg actthaatga agaagaaact atattgatca tcaggcgtct acataagggtg 3120
ttaagaccat ttttactaag gagactgaag aaagaagttg aatcccagct tccgaaaaa 3180
gtggaatatg tgatcaagtg tgacatgtca gctctgcaga agattctgta tcgccatatg 3240
caagccaagg ggatccttct cacaga tggg tctgagaaag ataagaaggg gaaaggagggt 3300
gctaagacac ttatgaacac tattatgcag ttgagaaaaa tctgcaacca cccatatatg 3360
tttcagcaca ttgaggaatc ctttgcgtgaa cacctaggct attcaaatgg ggtcatcaat 3420
ggggctgaac tgtatcgggc ctgagggaaag tttgagctgc ttgatcgtat tctgcaaaaa 3480
ttgagagcga ctaatcaccg agtgcgtgctt ttctgcaga tgacatctct catgaccatc 3540
atggaggatt atthtgcctt tcggaacttc ctttacctac gccttgatgg caccaccaag 3600
tctgaagatc gtgctgcttt gctgaagaaa ttcaatgaac ctggatccca gtatttcatt 3660
ttcttgctga gcacaagagc tgggtggcctg ggctthaatc ttcaggcagc tcatacagtg 3720
gtcatctttg acagcgactg gaatcctcat caggatctgc agggccaaga ccgagctcac 3780
cgcatcgggc agcagaacga ggtccgggta ctgaggtctt gtaccgtgaa cagcgtggag 3840
gaaaagatcc tcgcgccgcg aaaatacaag ctgaacgtgg atcagaaagt gatccaggcg 3900
ggcatgtttg acca aaagtc ttcaagccac gagcggaggg cattcctgca ggccatcttg 3960
gagcatgaag aggaaaatga ggaagaagat gaagtaccg acgatgagac tctgaaccaa 4020
atgattgctc gacgagaaga agaatttgac ctttttatgc ggatggacat ggaccggcgg 4080
agggaaagatg cccggaaccc gaaacggaag ccccgtttaa tggaggagga tga gctgccc 4140
tcctggatca ttaaggatga cgctgaagta gaaaggctca cctgtgaaga agaggaggag 4200
aaaaatattg ggagggggtc ccgccagcgc cgtgacgtgg actacagtga cgcctcacg 4260
gagaagcagt ggctaagggc catcgaagac ggcaatttgg aggaaatgga agaggaagta 4320
cggcttaaga agcgaaaaag acgaagaa at gtggataaag atcctgcaaa agaagatgtg 4380
gaaaaagcta agaagagaag agggcgccct cccgctgaga aactgtcacc aaatcccccc 4440
aaactgacaa agcagatgaa cgctatcatc gatactgtga taaactacaa agatagttca 4500
ggcgacagc tcagtgaagt cttcattcag ttacctcaa ggaaagaatt accagaatac 4560
tatgaattaa ttagggaagcc agtggaattt aaaaaataa aggaaaggat tcgtaatcat 4620
aagtaccgga gcctaggcga cctggagaag gatgtcatgc ttctctgtca caacgctcag 4680
acgttcaacc tggaggggat ccagatctat gaagactcca tcgtcttaca gtcagtgttt 4740
aagagtgcgc ggcagaaaaat tgccaaagag gaagagagt a ggaatgaa caatgaagag 4800
gaggaagagg aagatgaaga agagtacag tccgaggcaa aatcagtcaa ggtgaaaatt 4860
aagctcaata aaaaagatga caaaggccgg gacaaaggga aaggcaagaa aaggccaaat 4920
cgaggaaaag ccaaacctgt agtgagcgat tttgacagcg atgaggagca ggatgaacgt 4980
gaacagtcag aaggaa gtgg gacggatgat gagtgatcag tatggacctt tttccttgg 5040
agaactgaat tccttctctc cctgtctcat ttctaccag tgagttcatt tgtcatatag 5100
gcactgggtt gttcttatat catcatcgtc tataaactag ctttaggata gtgccagaca 5160
aacatatgat atcatggtgt aaaaacaca cacatacaca aatatttgtg accaa atggg 5220
cctcaaagat tcagattgaa acaaacaaaa agctttt 5257

```

<210> 238

<211> 507

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(507)

<223> 3' terminal sequence. protein phosphatase 2
(formerly 2a), regulatory subunit b (pr 52), gamma
isoform (PPP2R2C) gene.

<400> 238

```
tacatgctca cccgggacta ccttacagtc tatggatggg acctgaacat ggaggcaaga 60
cccatagaga cctaccaggt ccatgactac ctccggagca agctctgttc cctgtacgag 120
aacgactgca ttttcgacaa gtttgaatgt gcctggaacg ggagcgacan tncatcatga 180
ccggggccta caacaacttc ttccgcatgt tcgatcggaa caccaagcgg gacgtgaccc 240
tgaggaggct cgagggaag cagcaagccc cgggctgtgc tcaagccacg gcgcgtgtgc 300
gtgggggggc aagcgccggc gtgnatga ca tcagtgtggg acagcttggg acttcaccaa 360
gaagatcctg cacacggcct ggcaaccggc tgaggaacat catttgccat tcgccgccac 420
caacaacctg ttacatcttt ccaggggcaa ggtaaatttt tgacattgca ttaggtattn 480
tgcaatttcc cggnccttgc caacca 507
```

<210> 239

<211> 521

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(521)

<223> 5' terminal sequence. protein phosphatase 2
(formerly 2a), regulatory subunit b (pr 52), gamma a
isoform (PPP2R2C) gene.

<400> 239

```
taaacagaca attactgcc aacacaattc tggcctagga aagcggggnn gggagggggc 60
ccaaacttcc tgtgtccaca cactgccacc tctgcagctg tctcatcag tgggtgtgact 120
ttcttccct ccttgcatcg cggtcgtgaa ggtcatgtcg gggatgactt gcatgaggct 180
gggtggcagg ggccgggaac tgcacatacc tagtgcattg cagagtttac cttgtcctgg 240
aagatgtaca ggttgttggg ggccggcgat gcaatgatgt tctcagccgg gtgccaggcc 300
gtgtgcagga tcttcttggg gaagtccaag ctgttccaaa atgatgtcat caccggggcc 360
cttgccccc acgnaaangg nccnttggtt tnagcaaagc ccng ggtttg ttgcttttcc 420
ctnagnagcn tncagntca agtnccnttt ggtnttnccc gatcgaacat ncggaagaat 480
tttttttagg ccccntcat gatgaacgtg tncgttccct t 521
```

<210> 240

<211> 350

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(350)

<223> 3' terminal sequence. thrombospondin 3
(THBS3) gene.

<400> 240

```
cagattcatt nnnngganntg cctgtgacaa ttgccccaac gttccaaca atgaccagaa 60
ggacacagat ggcaatgggg aaggagatgc ctgtgacaac gac gtggatg gggatgggtgc 120
aggcctgggg ctgaaggggt ggctggggga cctgtgagaa tttggatcag gtggggatga 180
agcagggaag ctaggaagtc tctgtgaaat agggaggcag gcttntggac gttggcctgg 240
gtgaggagag attacctgca gcagatgtca ataggaatnt gaggtagggc gtagtnttag 300
gcagagtttg gactagaggg t nagacaaga aacaggcaga tttcctggcc 350
```

<210> 241

<211> 2871

<212> DNA/RNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(2871)

<223> thrombospondin 3 (THBS3) gene.

<400> 241

```
atggagacgc aggaacttcg gggggccctg gctcttctcc tcctttgctt tttcacatct 60
gccagtcagg atctgcaggt aattgacctg ctgactgtgg gcgagtctcg gcagatggta 120
gctgtggcag agaagatccg gacagccttg ctcactgtcg gggacatcta cctcttatcc 180
accttccgcc tgcccccaa gcagggtggt gtccctcttg g cctctatcc tgcgaagac 240
aacactcgat ggctggaggc ctctgttgta ggcaagatca acaaagtact ggtgcgatac 300
cagcgggagg atggcaaagt ccacgccgtg aacctacagc aagcgggcct ggctgatggg 360
cgcacacaca cagttctcct gcgactcoga ggtccctcca gaccagccc tgccctacat 420
ctctacgtgg actgcaaaact gggtgaccaaa catgcaggcc ttccagcact ggccccatt 480
cctccagcgg aggtcgatgg gctggagatt aggactggac agaaggcgta tttgaggatg 540
cagggccttg tggaatctat gaaaattatt ctgggtgggt ccatggcccg ggtaggagcc 600
ctgagtgagt gtccattcca aggggacgag tccatccaca gtgcagtac caatgcactg 6 60
cactccattc taggggagca gaccaaggcg ctggtcacc aactcaccct cttcaaccag 720
atcctggttg agctgcggga tgatatacga gaccaggtaa aggaaatgtc cctgatccga 780
aacaccatta tggagtgcga ggtgtgcggc ttccatgagc agcgttccca ctgcagccc 840
aatccctgct tccgaggtgt ggactgcatg gaagtgtacg agtaccagg ctaccgctgt 900
gggccctgcc cccctggcct gcagggaac ggcacccact gcagtacat caatgagtgt 960
gctcacgctg acccctgttt cccgggctcc agctgcatca acaccatgcc cggcttccac 1020
tgtgaggcct gtccctcagg gtacaagggc acacagggtgt ctggtgtggg cattgactat 1080
gcccgggcca gcaaac aggt ctgcaatgac atcgatgaat gcaacgatgg caacaatggt 1140
ggctgtgacc caaactccat ctgcaccaac actgtgggct ctttcaagtg tggctccctgc 1200
cgctgggtt tcttgggcaa ccagagccag ggctgcctcc cagcccggac ctgccacagc 1260
ccagcccaca gcccctgcc catccatgct cactgtctct ttgaacgcaa tgggtg cagtg 1320
tctgccagt gtaacgtggg ctgggctggg aatgggaacg tgtgtgggac tgacacagac 1380
atcgatggct acccagacca agcactgcc tgcatggaca acaacaaaca ctgcaaacag 1440
gacaactgcc ttttgacacc caactctggg caggaagatg ctgataatga tgggtgtggg 1500
gaccagtgtg atgatgatgc tgatggggat gggatcaaga atgttgagga caactgcccg 1560
ctgttcccca acaaagacca gcagaactca gatacagatt catgttggtga tgcctgtgac 1620
aattgcccc aagtttccaa acgtgacacag atggcaatgg ggaaggagat 1680
gcctgtgaca acgacgtgga tggggatggc atccccaatg gattggacaa ttgccctaaa 1740
gtccccaacc cactacagac agacagggat gaggacgggg tgggagatgc ttgcgacagc 1800
tgccctgaaa tgagcaatcc taccagaca gatgcagaca gcgacctggg gggggatgtc 1860
tgtgatacta atgaagacag cgatggggat gggcatcagg acaccaagga caactgccca 1920
cagctgcca atagctccca gctggactct gataacgatg gac ttggaga tgagtgtgat 1980
ggggatgatg acaatgatgg catcccagat tatgtgcctc ctggtcccca taactgccgc 2040
```

158/292

```

ctggtaccca atcccaatca gaaggactca gatggcaatg gcgttggtga tgtgtgtgag 2100
gatgactttg acaatgatgc tgtggtcgac cccctggatg tgtgtcctga aagtgcagag 2160
gtaacgctta cggatttt cg ggcctatcag accgtcgctc tggatcctga gggatgatgct 2220
cagattgacc caaactgggt tgtgtcctcaac cagggcatgg aaatcggtca gaccatgaac 2280
agtgaccctg gcttggcagt tggatacacg gccttcaatg gtgtggactt tgaaggcacc 2340
ttccatgtga acacagtga tgatgatgac tacgcaggct ttctcttcag ttatcaa gac 2400
agtggcggct tctacgtagt catgtggaag cagaccgagc agacctactg gcaggctaca 2460
cccttcggg cggttgccca gcccggtg cagctcaagg cagtgcacac agtgtctggc 2520
ccaggtagac acctccgaaa tgccctgtgg catactggcc acaccctga tcaggtagca 2580
ctcctgtgga cagaccacag aaatgtgggc tggcgggaca agacctccta tcgctggcag 2640
cttctgcacc ggctcaagt tggctacatt cgggtgaagc tctatgaggg accccagctt 2700
gtggcggatt ctggggtgat cattgacaca tccatgcgag gggggcgtct tgggtgtattc 2760
tgcttctccc aagaaaacat aatttggtcc aatctccagt atcgatgcaa tgacacagt 2820
cctgaggact ttgagccatt ccggaggcag ctgctccagg gaagggtgtg a 2871

```

<210> 242

<211> 509

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(509)

<223> 3' terminal sequence. actin, gamma 1 (ACTG1) gene.

<400> 242

```

cacttttatt ttnocttaca caatgacgtg ttgctggggc ctaatgtntc cacataacag 60
tagaaaacca aaatttggtg tcatctcttc aaagantcga ganttcgta caaaaaaac 120
cttacataan ttaagantga ntacatttac aggcgtaaat gcaaaccgnt tccaactcaa 180
agcaagtaac agcccacggt gttctggcca aagacatcag ctaagaaagg aaactggggn 240
cttacggctt gggactttcc aacctggac aggacccgca agncaaaac aactgggttc 300
ttgccagcct ctaggaggaa ttcccgaac actcaggccc tggacangtt taataccagg 360
ggggancagt taactttcan tacaggggnc aaaatcaggc aacagttt tt accantccag 420
tggttggttt cnggttacag gtttcagggt cattttnttt tcggaggggt tnttccggt 480
tcgtgagggt aggtctgagg tttntgctt 509

```

<210> 243

<211> 393

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial S equence:primer

<220>

<221> misc_feature

<222> (1)..(393)

<223> 5' terminal sequence. actin, gamma 1 (ACTG1) gene.

<400> 243

```

gatcaccgcc ctggccccag caccatgaag atcaagatca tcgcaccccc agagcgcaag 60
tactcgggtg ggatcgggtg ctccatctgt gcctcactgt ccaccttc a gcagatgtgg 120
attagcaagc aggagtacga cgagtcgggc ccctccatcg tccaccgcaa atgcttctaa 180
acggactcag cagatgcgta gattttgctg catgggttaa ttgagaatag aaatttgccc 240

```

ctgggaaatt gcacacacct catgctagcc tcacgaaact gggaataagc ctttcgaaaa 300
gaaattgtcc ttgaagcttg tatctgg tat cagcactggg ntgttaggaa nttgttgctg 360
atttttgacc ttgtanttga agtttaactg ttt 393

<210> 244

<211> 1919

<212> DNA/RNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(1919)

<223> actin, gamma 1 (ACTG1) gene.

<400> 244

gtctcagtcg ccgctgccag ctctgcact ctgttcttcc gccgctccgc cgtcgcgttt 60
ctctgccggt cgcaatggaa gaagagatcg ccgctctggt cattgacaat ggctccggca 120
tgtgcaaaagc tggttttgct ggggacgacg ctccccgagc cgtgtttcc t tccatcgtcg 180
ggcgccccag acaccagggc gtcatgggtg gcattgggcca gaaggactcc tacgtgggcg 240
acgaggccca gagcaagcgt ggcatcctga ccctgaagta cccattgag catggcatcg 300
tcaccaactg ggacgacatg gagaagatct ggcaccacac ctctacaac gagctgcgcg 360
tgcccccgga ggagcaccca gtgctgc tga ccgaggcccc cctgaacccc aaggccaaca 420
gagagaagat gactcagatt atgtttgaga ccttcaacac cccggccatg tacgtggcca 480
tccaggccgt gctgtccctc tacgectctg ggcgcaccac tggcattgtc atggactctg 540
gagacgggggt caccacacag gtgcccactc acgagggcta cgccctcccc cagccatcc 600
tgctgtctga cctggctggc cgggacctga ccgactacct catgaagatc ctactgagc 660
gaggctacag cttcaccacc acggccgagc gggaaatcgt gcgcgacatc aaggagaagc 720
tgtgtctacgt cgccctggac ttcgagcagg agatggccac cgccgcatcc tcctcttctc 780
tggaagaagag ctacgagctg ccgatggcc aggtcatcac cattggc aat gagcggttcc 840
ggtgtccgga ggctgtgttc cagccttccct tcctgggtat ggaatcttgc ggcattccacg 900
agaccacctt caactccatc atgaagtgtg acgtggacat ccgcaaagac ctgtacgccca 960
acacggtgct gtcggggcgc accaccatgt acccgggcat tgccgacagg atgcagaagg 1020
agatcacgcg cctggcgccc agca ccatga agatcaagat catcgacccc ccagagcgca 1080
agtactcggg gtggatcggg ggtccatcc tggcctcact gtccaccttc cagcagatgt 1140
ggattagcaa gcaggagtag gacgagtcgg gccctccat cgtccaccgc aaatgcttct 1200
aaacggactc agcagatgag tagcatttgc tgcattgggt aattgagaat agaaatttgc 126 0
ccctggcaaa tgcacacacc tcatgctagc ctacgaaac tgggaataagc cttcgaaaag 1320
aaattgtcct tgaagcttgc atctgatata agcactggat tgtagaactt gttgtgtatt 1380
ttgaccttgc attgaagtta actgttcccc ttgtatttg ttttaataccc tgtacatata 1440
tttgagttca acctttagta cgtgtggctt ggtcactt cg tggctaaggc aagaacgtgc 1500
ttgtggaaga caagtctgtg gcttgggtgag tctgtgtggc cagcagcctc tgatctgtgc 1560
agggatttaa cgtgtcaggg ctgagtgttc tgggatttct ctgaggctg gcaagaacca 1620
gttgttttgt cttgcgggtc tgtcagggtt ggaaagtcca agccgtagga cccagtttcc 1680
tttcttagct gatgtctttg gccagaacac cgtgggctgt tacttgcttt gagttggaag 1740
cggtttgcct ttacgcctgt aaatgtattc attcttaatt tatgtaaggc tttttttgta 1800
cgcaattctc gattctttga agagatgaca acaaattttg gttttctact gttatgtgag 1860
aacattagcc cccagcaaca cgtcattgtg taaggaaaaa taaaagtgc g ccgtaacc 1919

<210> 245

<211> 467

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

160/292

<220>
<221> misc_feature
<222> (1)..(467)
<223> 3' terminal sequence. integrin, alpha 6
(ITGA6) gene.

<400> 245
ccgccgccgg gcagctgtgc ttgctctacc tgtcggcggg gctcctgtcc cggctcggcg 60
cacttncaac ttggacactc gggaggacaa cgtgatccgg aaatatggag accccgggag 120
cctcttcggc ttctcgctgg ccatgcactg gcaactgcag cccgaggaca agcggctgtt 180
gctcgtgggg gccccgccgg agnaagcgct tccactgcag agagccaac a gaacggggagg 240
gctgtacagc ttgcgacatc accgcccggg ggccatgcac ggggatcgag tttnataacg 300
atgcttgacc ccacgtcaga aagcaaggaa gattagttgg atngggggtc aacgtccaga 360
gccaaaggttc agggggcaag gtcgtgacat gtgttnaccc tattgaaaaa aggcagcnn 420
ttattacgna gcangatttc cgagaca ttt ttgggcggtt tttttcc 467

<210> 246
<211> 473
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<220>
<221> misc_feature
<222> (1)..(473)
<223> 5' terminal sequence. integrin, alpha 6
(ITGA6) gene.

<400> 246
gccctctccc atccatatcg tcttcaatcc tgagattctg actcaggaca naacaccgcc 60
caaagatgtc tcgggattcc tgcttcgtat taacatgctg ccttttttca tatcggtgag 120
cacatgtcac gaccttgccc cctggacctt ggctctggac ggtgaccccc atccactgat 180
cttccttgc tcttgacgtg gggtc agcat cgttatcaaa ctcgatccgc gtgcagtggc 240
ccggggcggg ggatgtcgca gctgtacagc cctcccgttc tgttggtct ctgcagtggg 300
aagcgcttct gcccgccggg cccccacgga gcaacagcgc cttgtcctcg ggctgcagtt 360
gccagtgcac gggccagcga gaaagccgaa gaggttcccc ggggtnttcc atattttccg 420
gatcaagttg ttcctnccga gttttccaag ttgaagggt tgcgcaaggc cgt 473

<210> 247
<211> 5611
<212> DNA/RNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<220>
<221> misc_feature
<222> (1)..(5611)
<223> integrin, alpha 6 (IT GA6) gene.

<400> 247
gcgcgaccgt cccgggggtg gggccggggc cagcggcgag aggaggcgaa ggtggctgcg 60
gtagcagcag cgcggcagcc tcggaccag cccggagcgc agggcgggcg ctgcaggtcc 120
ccgctcccct ccccggtgct ccgcccattg ccgcccggcg gcagctgtgc ttgctctacc 180
tgtcggcggg gctcctgtcc cg gctcggcg cagccttcaa cttggacact cgggaggaca 240
acgtgatccg gaaatatgga gaccccgga gcctcttcg cttctcgctg gccatgcact 300

ggcaactgca gcccgaggac aagcggctgt tgctcgtggg ggccccgcgc ggagaagcgc 360
 ttccactgca gagagccaac agaacgggag ggctgtacag ctgcgacatc accgcccggg 420
 ggccatgcac gcggatcgag tttgataacg atgctgaccc cagctcagaa agcaaggaag 480
 atcagtggat ggggggtcacc gtccagagcc aagggtccagg gggcaaggtc gtgacatgtg 540
 ctccaccgata tgaaaaaagg cagcatgtta atacgaagca ggaatcccga gacatctttg 600
 ggcggtgtta tgtcctgagt cagaatctca ggattgaaga cg atatggat gggggagatt 660
 ggagcttttg tgatgggcga ttgagaggcc atgagaaatt tggctcttgc cagcaagggtg 720
 tagcagctac ttttactaaa gactttcatt acattgtatt tggagccccg ggtacttata 780
 actggaaagg gattgttcgt gttagcaaaa agaataacac tttttttgac atgaacatct 840
 ttgaagatgg gccttatgaa gttgggtggag agactgagca tgatgaaagt ctggttcctg 900
 ttctgtctaa cagttactta ggtttttctt tggactcagg gaaagggtatt gtttctaaag 960
 atgagatcac ttttgtatct ggtgtctcca gagccaatca cagtggagcc gtggttttgc 1020
 tgaagagaga catgaagtct gcacatctcc tccctgagca catattcgat ggagaaggtc 1 080
 tggcctcttc atttggctat gatgtggcgg tgggtggacct caacaaggat ggggtggcaag 1140
 atatatgtat tggagcccca cagtattttg atagagatgg agaagttgga ggtgcagtgt 1200
 atgtctacat gaaccagaa ggcatgtgaa ataagtga gccaattcgt cttaattggaa 1260
 ccaaagattc tatgtttggc attgcagtaa aaaata ttgg agatattaat caagatggct 1320
 acccagatat tgcagtggga gctccgtatg atgacttggg aaagggtttt atctatcatg 1380
 gatctgcaaa tggaataaat accaaaccaa cacaggttct caagggtata tcaccttatt 1440
 ttggatatct aattgtctga aacatggacc ttgatcgaaa ttctaccct gatgttgctg 1500
 ttggttcctc ctccagattca gtaactattt tcagatcccg gcctgtgatt aatattcaga 1560
 aaacctcac agtaactcct aacagaattg acctccgcca gaaaacagcg tgtggggcgc 1620
 ctagtgggat atgcctccag gttaaatcct gttttgaata tactgctaac cccgctgggt 1680
 ataactcttc aatatcaatt gtggcacac ttgaagctga aaaagaaaga agaaaatctg 1740
 ggctatcttc aagagttcag tttcgaaacc aaggttctga gcccaaatat actcaagaac 1800
 taactctgaa gaggcagaaa cagaaagtgt gcatggagga aacctgttgg ctacaggata 1860
 atatcagaga taaactgcgt cccattccca taactgcctc agtggagatc caagagccaa 1920
 gctctcgtag gcgagtgaat tcac ttccag aagttcttcc aattctgaat tcagatgaac 1980
 ccaagacagc tcattattgat gttcacttct taaaagaggg atgtggagac gacaatgtat 2040
 gtaacagcaa ccttaaaacta gaatataaat ttgaccccg agaaggaaat caagacaaat 2100
 tttcttattt accaattcaa aaagggtgtac cagaactagt tctaaaagat cagaaggata 216 0
 ttgctttaga aataacagtg acaaacagcc cttccaaccc aaggaatccc acaaaagatg 2220
 gcgatgacgc ccatgaggct aaactgattg caacgtttcc agacacttta acctattctg 2280
 catatagaga actgagggct ttccctgaga aacagttgag ttgtgttgc aaccagaatg 2340
 gctcgaagc tgactgtgag ctccgaaatc cttttaaa ag aaattcaaat gtcacttttt 2400
 atttggtttt aagtacaact caagataaatt tggctccaat tacagctaaa gcaaaagtgg 2460
 agttagaac acaagcaat gaagataaatt tggctccaat tacagctaaa gcaaaagtgg 2520
 ttattgaact gcttttatcg gtctcgggag ttgctaaacc ttccagggtg tattttggag 2580
 gtacagttgt tggcgagcaa gctatgaaat ctgaagatga agtgggaagt ttaatagagt 2640
 atgaattcag gtaataaacc ttaggtaaac ctcttacaac cctcggcaca gcaaccttga 2700
 acattcagtg gccaaaagaa attagcaatg ggaaatggtt gctttatttg gtgaaagtag 2760
 aatccaaagg attggaagg gtaacttgtg agccacaaaa ggagataaac t cctgaacc 2820
 taacggagtc tcacaactca agaaagaatc gggaaattac tgaaaaacag atagatgata 2880
 acagaaaatt ttctttattt gctgaaagaa aataccagac tcttaactgt agcgtgaacg 2940
 tgaactgtgt gaacatcaga tgcccgctgc gggggctgga cagcaaggcg tctcttattt 3000
 tgcgctcgag gttatggaac agcaca ttcc tagaggaata ttccaaactg aactacttgg 3060
 acattctcat gcgagccttc attgatgtga ctgctgctgc cgaaaatata aggctgcca 3120
 atgcaggcac tcaggttcga gtgactgtgt ttccctcaaa gactgtagct cagtattcgg 3180
 gagtaccttg gtggatcatc ctagtggcta ttctcgtgg gatcttgatg cttgctttat 3240
 tagtgtttat actatggaag tgtggtttct tcaagagaaa taagaaagat cattatgatg 3300
 ccacatatca caaggctgag atccatgctc agccatctga taaagagagg cttacttctg 3360
 atgcatagta ttgatctact tctgtaattg tgtggattct ttaaagcgtc taggtacgat 3420
 gacagtgttc cccgatacca tgctgtaagg atccggaaag aagagcgaga gatcaaagat 3480
 gaaaagtata ttgataacct tgaaaaaaa cagtggatca caaagtggaa cagaaatgaa 3540
 agctactcat agcggggggc taiaaaaaaa aaagcttcac agtaccocaa ctgctttttc 3600
 caactcagaa attcaatttg gatttaaaag cctgctcaat ccctgaggac tgatttcaga 3660
 gtgactacac acag tacgaa cctacagttt tattgttacg tagcctaagg 3720
 ctctgtttt gcacagccaa atttaaaact gttggaatgg atttttctt aactgccgta 3780
 atttaacttt ctgggttgcc tttgtttttg gcgtggctga cttacatcat gtgttgggga 3840
 agggcctgcc cagttgcact caggtgacat cctccagata gtgtagctga gga ggcacct 3900
 acactcacct gcactaacag agtggccgct ctaacctcgg gcctgctgcg cagacgtcca 3960

162/292

```

tcacgttagc tgtccacat cacaagacta tgccattggg gtagttgtgt ttcaacggaa 4020
agtgtgtgt taaactaaat gtgcaataga aggtgatgtt gccatcctac cgtcttttcc 4080
tgtttcttag ctgtgtgaat acctgctc ac gtcaaatgca tacaagtttc attctccctt 4140
tactaaaaa cacacaggtg caacagactt gaatgctagt tatacttatt tgtatatggt 4200
atttattttt tcttttcttt acaaaccatt ttgttattga ctaacaggcc aaagagtctc 4260
cagtttacct ttcaggttg ttaatacaat cagaattaga attagagcat gggagggtca 4320
tcactatgac ctaaattatt tactgcaaaa agaaaatctt tataaatgta ccagagagag 4380
ttgttttaat aacttatcta taaactataa cctctccttc atgacagcct ccaccccaca 4440
accctaaagg ttaagaaat agaattataa ctgtaaagat gtttatttca ggcattggat 4500
attttttact ttagaagcct gcataatgtt tctggattta c atactgtaa cattcaggaa 4560
ttcttggaga agatgggttt attcactgaa ctctagtgcg gtttactcac tgctgcaaat 4620
actgtatatt caggacttga aagaaatggt gaatgcctat ggaactagtg gatccaaact 4680
gatccagtat aagactactg aatctgctac caaacagtt aatcagtga tcgagtgttc 4740
tattttttgt ttgttt tctt cccctatctg tattcccaaa aattactttg gggctaattt 4800
aacaagaact ttaaattgtg ttttaattgt aaaaatggca gggggtggaa ttattactct 4860
ataactcaa cagagactga atagatatga aagctgattt tttttaatta ccatgcttca 4920
caatgttaag ttatatggg agcaacagca aacaggtgct aatttgtttt ggata tagta 4980
taagcagtgt ctgtgttttg aaagaataga acacagtttg tagtgccact gttgttttgg 5040
ggggggcttt tttcttttt cgggaaaatc cttaaaccct aagatactaa ggacgttgtt 5100
ttggtgttac ttggaattct tagtcacaaa atatattttg tttacaaaaa tttctgtaaa 5160
acaggttata acagtgttta aagtctcagt ttcttgcttg gggaacttgt gtccctaattg 5220
tgtagattg ctgattgtct aaggagctga tacttgacag ttttttagac ctgtgttact 5280
aaaaaaaaga tgaatgtcgg aaaaagggtg tgaggagggt gtcaacaaag aaacaaagat 5340
gttatggtgt tttagcttat gttgtttaa aatgtcatct caagtcaagt cactggtctg 5400
tttgcatttg atacattttt gtactaacta gcattgtaaa attatttcat gattagaaat 5460
tacctgtgga tattgtata aaagtgtgaa ataaattttt tataaaagtg ttcattgttt 5520
cgtaacacag cattgtatat gtgaagcaaa ctctaaaatt ataatgaca acctgaatta 5580
tctatttcat caaaaaaaaa aaaaaaaaaa a 5611

```

<210> 248

<211> 406

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(406)

<223> 3' terminal sequence. rad9 (s. pombe)
homolog (RAD9) gene.

<400> 248

```

cctttattca agagaccaga tgggttgccc caggatccgg ctgccagacc ctgaggccaa 60
gcacgngtgg agaccacagn acctgggcct gccnttgccc tgagctgcag cctcggtccc 120
aggatcctgn tcacagntca ccgcaggnc gngncaggaa gcagccctgg gggantggaa 180
cgntgtatt gattcattaa aaaaagaaaa gaaan taca ccaaggttcc atntccccg 240
tgacaggtgg gccnagggg tcggggtnac cccccccag natggcagca tgattntnt 300
acaatcaatc catcatntgg gccacagggt ggttttcggg ggtattntnt tggctttggc 360
gaaattncgg gntggggtta tgggtnggcc tccagggtta aggcca 406

```

<210> 249

<211> 2102

<212> DNA/RNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>
 <221> misc_feature
 <222> (1)..(2102)
 <223> rad9 (s. pombe) homolog (RAD9) gene.

<400> 249

```

gcgcgggaag ggaccccgga cccggaggtc gcggagagct gggcagtgtt ggccgctggc 60
ggagcgctgg ggcagcatga agtgcctggt cacgggcggc aacgtgaagg tgctcggcaa 120
ggccgtccac tccctgtccc gcatcgggga cgagctctac ctggaaccct tggaggacgg 180
gctctccctc cggacggtga actcctcccg ctctgcctat gcctgctttc tctttgcccc 240
gctcttcttc cagcaatacc aggcagcca c ccttggtcag gacctgctgc gctgtaagat 300
cctgatgaag tctttcctgt ctgtcttcg ctactggcg atgctggaga agacggtgga 360
aaaatgctgc atctccctga atggccggag cagccgcctg gtggtccagc tgcattgcaa 420
gttcggggtg cggaagactc acaacctgtc cttccaggac tgtgagtccc tgcaggccgt 480
cttcgaccca gctcgtgccc cccacatgct ccgcgcccc gcacgggttc tgggggaggg 540
tgttctgccc ttctctctg cactggtga agtgacgctg ggcattggcc gtggccgag 600
ggtcatcctg cgcagctacc acgaggagga ggcagacagc actgccaaag ccatggtgac 660
tgagatgtgc cttggagagg aggatttcca gcagctgcag gccaggaa g ggggtggccat 720
cactttctgc ctcaaggaaat tccgggggct cctgagcttt gcagagtcag caaactgaa 780
tcttagcatt cattttgatg ctccaggcag gcccgccatc ttcaccatca aggactctt 840
gctggacggc cactttgtct tggccacact ctcagacacc gactcgact cccaggacct 900
gggtcccca gagcgtcacc agccagt gcc tcagctccag gctcacagca caccacccc 960
ggacgacttt gccaatgacg acattgactc ttacatgac gccatggaaa ccactatagg 1020
caatgagggc tcgcgggtgc tgccctccat ttccctttca cctggccccc agcccccaa 1080
gagccccggt cccactccg aggaggaaga tgaggctgag ccagtacag tgcctgggac 1140
tccccacccc aagaagttcc gctcactgtt cttcggtccc atcctggccc ctgtacgctc 1200
ccccagggc cccagccctg tgctggcgga agacagttag ggtgaaggct gaaccaagaa 1260
cctgaagcct gtaccagag gccttgact agacgaagcc ccagccagtg gcagaactgg 1320
gtctctcagc cctggggatc agaaagggtg gcttgctgga g ctgagctgt ttcactgcct 1380
ctcgcaggcc ccagctggt gtactgtaa agctgtccca cagcggtcgg gcctgggccc 1440
ttatctcccc acaaccccca gccaatcagg actttccaga cttggccctg aactactgac 1500
gttctacct cttattttctc attgagcctc aggtataact ccagctggcc aaggctggaa 1560
acctgtctcc ctcaggctca ccttctaag gaaaatgtca tagtaggtgc tgctggcccc 1620
tggtgatcca gttctctgc caatcatgac ctgttctctc ctgaagtcct gggcatgcat 1680
ctgggaaccc cgtggagctg acaagtttct cttgctttcc tgatactctt tggcgctgac 1740
ttggaattct aagagccttg gaccgagtg tgtggtagg gttgccctgg ctggg gcccg 1800
gtgcccagac tcccaagcgg ctctgtgcag aagagctgcc aggcagtgtc ttagatgtga 1860
gacggaggcc atggcgagaa tccagctttg acctttatc aagagaccag atgggttgcc 1920
ccaggatccg gctgccagcc ctgaggccaa gcacggctgg agaccacga cctggcctgc 1980
cgttgccctg agctgcagcc tcggccccag gatcctgctc acagtcaccg cagggtgcagg 2040
caggaaagcag ccctggggga ctggacgctg ctattgattc attaaaaaa gaaaagaaaa 2100
at 2102

```

<210> 250
 <211> 365
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:primer

<220>
 <221> misc_feature
 <222> (1)..(365)
 <223> 3' terminal sequence. activating
 transcription factor 3 (ATF3) gene.

<400> 250

```

tccaatatatt attattctga caggtttaga atactaggat aaataagtaa tatttntct 60

```

164/292

tacagaaaat tgtaatgata ccattgagta caattaaaca ctctgagaat ttcacagaaa 120
 catcagaatt ttaatagaca gtagccagcg tccttgggc cagtgtgagt gacttctcac 180
 agctgcaaac accctgggcc agatttctta aaacagctac atgacaaaaa caatgctatt 240
 gacatccaat aatgctaaag cctgggtacc acccggtcc cactgactgt ggn ttccaaa 300
 catctctcca ctgactgtgg ntttcaaccn caaggnaagg gaaatgggat attccttggg 360
 ctctt 365

<210> 251

<211> 453

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: primer

<220>

<221> misc_feature

<222> (1)..(453)

<223> 5' terminal sequence. activating
transcription factor 3 (ATF3) gene.

<400> 251

cgtggctacc attgtcactc gtaggggatg tggagtgaga acagcattta gtgaagttgt 60
 gcaacggcca gggttgtgct ttctagcaaa tatgctgt ta tgtccagaaa ttgtgtgtgc 120
 aagaaaacta ggcaatgtac tcttcgatg tttgtgtcac acaacactga tgtgactttt 180
 atatgctttt tctcagatct ggtttctaag agttttggcg cggcggggc tgtcaccacg 240
 tgcagtatct caagatattc aggtgggcca gaagagcttg tcagcaagag ggaggacag 300
 aattctccca ggcgtt aaca caaaatccat ggggcagtat ggatgggcag gtocntctgt 360
 tggcaaaactc agttcccaag tcacagggaa gganaggcag gaaagtttca actttcccaa 420
 agggtttagg ggcttttcca cttcaatgtc tta 453

<210> 252

<211> 2056

<212> DNA/RNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: primer

<220>

<221> misc_feature

<222> (1)..(2056)

<223> activating transcription factor 3 (ATF3)
gene.

<400> 252

gcagccaggc gcgcaactgca cagctctctt ctctcgccgc cgcccagagc cacccttcag 60
 cccgcgcgcc ggccgtgagt cctcgtgtgt cgccgcgcgc ccagacaaac agcccgcccg 120
 acccgtccc gaccctggcc gccccagagc gagcctggag caaaatgatg cttcaacacc 180
 caggccaggt ctctgcctcg gaagtgtgtg cttctgccat cgtcccctgc ctgtcccctc 240
 ctgggtcaact ggtgtttgag gatatttcta acctgacgcc ctttgtcaag gaagagc tga 300
 ggtttgccat ccagaacaag cacctctgcc accggatgtc ctctgcgctg gaatcagtca 360
 ctgtcagcga cagaccctc ggggtgtcca tcacaaaagc cgaggtagcc cctgaagaag 420
 atgaaaaggaa aaagaggcga cgagaaagaa ataagattgc agctgcaaag tgccgaaaca 480
 agaagaagga gaagacggag tgccctgcagc ttcag tatta gcagagccac aggccgcctc 540
 tgtggcatca ccagggtttc tctgaagaag agggctgtca ttttcctaaa cccagtgtgtg 600
 ctctcccatc tcccatcttc ctctgcagc ttgatgagcc ccggtgtgtc ccaggagtgc 660
 gagaagctgg aaagtgtgaa tgctgaactg aaggctcaga ttgaggagct caagaacgag 720
 aagcagcatt tga tatacat gctcaacctt catcggccca cgtgtattgt ccgggtcag 780

165/292

```

aatgggagga ctccagaaga tgagagaaac ctctttatcc aacagataaa agaaggaaca 840
ttgcagagct aagcagtcgt ggtatggggg cgactgggga gtccctcattg aatcctcatt 900
ttatacccaa aaccctgaag ccattggaga gctgtcttcc tgtgtacctc tagaa tccca 960
gcagcagaga accatcaagg cgggagggcc tgcagtgatt cagcaggccc ttcccattct 1020
gccccagagt gggctcttga ccagggaag tgcatctttg cctcaactcc aggatttagg 1080
ccttaacaca ctggccattc ttatgttcca gatggccccc agctgggtgtc ctgcccgcct 1140
ttcatctgga ttctacaaaa aaccaggatg cccaccgtta gattcaggca gcagtgtctg 1200
tacctcgggt gggagggatg gggccatctc cttcaccgtg gctaccattg tcactcgtag 1260
gggatgtgga gtgagaacag catttagtga agttgtgcaa cggccagggt tgtgctttct 1320
agcaaatact ctgttatgtc cagaaattgt gtgtgcaaga aaactaggca atgtactctt 1380
ccgatgtttg tgtcacacaa cactgatgtg acttttata gctttttctc agatctggtt 1440
tctaagagtt ttggggggcg gggctgtcac cagctgcagt atctcaagat attcagggtg 1500
ccagaagagc ttgtcagcaa gaggaggaac agaattctcc cagcgttaac acaaaatcca 1560
tgggcagcat gatggcaggt cctctgttgc aaactcagtt ccaa agtcac aggaagaaag 1620
cagaaagttc aacttccaaa gggtaggac tctccactca atgtcttagg tcaggagttg 1680
tgtctaggct ggaagagcca aagaaatatt ccattttcct ttccttgttg ttgaaaccac 1740
agtcagtgga gagatgtttg gaacacagtc agtggagctg gtggtaccag gtttagcatt 1800
attggatgtc aaaagcattt tttttgtcat gtagctgttt taagaaatct ggcccagggt 1860
gtttgcagct gtgagaagtc actcacactg gccacaagga cgctggctac tgtctattaa 1920
aattctgatg tttctgtgaa attctcagag tgtttaattg tactcaatgg tatcattaca 1980
attttctgta agagaaaata ttacttattt atcctagtat tcctaacctg tcagaata at 2040
aatattgtg gtaaaa
2056

```

<210> 253

<211> 502

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(502)

<223> 3' terminal sequence. v-akt murine thymoma
viral oncogene homolog 2 (AKT2) gene.

<400> 253

```

acatcatctc gtacatgacc acaccagcc cantacnntt tccacggccc ggccatagtc 60
attgtcctcc agcacctcag gcgccaggta ctccggggtc ccacagaagg ttttcatggt 120
ggccccgtca ctgatgccct cttgcagag gccaaagtca gtgatcttga tgtggccatc 180
tttgtccagc atgaggtttt ccagcttgat gtgcgggtat accacgtccc gcgagtgcaa 240
gtactcaaga gccgagacaa tctctgcacc ataaaaaccg gcccgctcct ctgtgaagac 300
acgctcccgg ggacagggtg gaagaacagc tcacccccgt tgggcatact ccattcaca 360
aggcacaggc cgggtcgtgg ggtctgggaa gggcattant ttcaggcggc agttgaggga 420
acgggggttc nggggtgtt ctgggaggga cccgggtttt cggttgattn ttttgaggcg 480
attttcatcc nttgggcaat tt
502

```

<210> 254

<211> 1715

<212> DNA/RNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(1715)

<223> v-akt murine thymoma viral oncogene homolog
2 (AKT2) gene.

<400> 254

```

gaattccagc ggcgcgccg ttgccgctgc cgggaaacac aaggaaagg aaccagcgc a 60
gcgtggcgat gggcggggt agagccccc cggagaggct gggcggtgc cggtgacaga 120
ctgtgccctg tccacggtgc ctctgcatg tcctgctgcc ctgagctgtc ccgagctagg 180
tgacagcgta ccacgctgcc accatgaatg aggtgtctgt catcaaagaa ggctggctcc 240
acaagcgtgg tgaatacatc aagacctgga ggccacgg ta ctctctgctg aagagcgacg 300
gctccttcat tgggtacaag gagaggcccg agggccctga tcagactcta ccccccttaa 360
acaacttttc cgtagcagaa tgccagctga tgaagaccga gaggcgcga cccaacacct 420
ttgtcatacg ctgctgcag tggaccacag tcatcgagag gaccttcac gtggattctc 480
cagacgagag ggagga gtgg atgcgggcca tccagatggt cgccaacagc ctcaagcagc 540
gggccccagg cgaggacccc atggactaca agtgtggctc cccagtgac tcctccacga 600
ctgaggagat ggaagtggcg gtcagcaagg caggggctaa agtgaccatg aatgacttcg 660
actatctcaa actccttggc aagggaaacct ttggcaaagt catcctggtg cgggagaa gg 720
ccactggccg ctactacgcc atgaagatcc tgcgaaagga agtcatcatt gccaaaggatg 780
aagtgcctca cacagtcacc gagagccggg tcctccagaa caccaggcac ccgttctca 840
ctgcgtgtaa gtatgccttc cagacccacg accgcctgtg ctttgtgatg gagtatgcca 900
acgggggtga gctgttcttc cacctgtccc gggagc gtgt ctccacagag gagcggggccc 960
ggttttatgg tgacagatt gtctcggtc ttgagtactt gactcgcgg gacgtggtat 1020
accgcgacat caagctggaa aacctcatgc tggccacatc aagatcactg 1080
actttggcct ctgcaaagag ggcatcagt acggggccac catgaaaacc ttctgtggga 1140
ccccggagta cctggcgct gaggtgctgg aggacaatga ctatggccgg gccgtggact 1200
ggtgggggct ggggtgtgtc atgtacgaga tgatgtgcgg ccgcctgcc ttctacaacc 1260
aggaccacga gcgcctcttc gagctcatcc tcatggaaga gatccgcttc ccgcgcacgc 1320
tcagccccga ggccaagtcc ctgcttgctg ggctgcttaa gaaggacccc aagcagaggc 1380
ttggtggggg gccagcgat gccaaaggag tcatggagca caggttcttc ctacgcatca 1440
actgacgaga cgtggtccag aagaagctcc tggcaccctt caaacctcag gtcacgtccg 1500
aggtcgacac aaggtacttc gatgatgaat ttaccgccc gtccatcaca atcacacccc 1560
ctgaccgcta tgacagcctg ggctt actgg agctggacca gcggaccac ttccccagt 1620
tctctactc ggccagcatc cgcgagttag cagtctgcc acgcagagga cgcacgctcg 1680
ctgccatcac cgctgggtgg ttttttacc ctgcc 1715

```

<210> 255

<211> 431

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(431)

<223> 5' terminal sequence. s100 calcium-binding
protein, beta (neural) (S100B) gene.

<400> 255

```

gagaggatgt ctgagctgga gaaggccatg gtggcctcat cgacgttttc caccaatatt 60
ctggaaggga gggagacaag cacaagctga agaaatccga actcaaggag ctcatcaaca 120
atgagctttc ccatttctta gaggaaatca aagagcagga ggttgtggac aaagtcatgg 180
aaacactgga caatgatgga gacggcgaat gtgacttcca gggaattcat ggcctttgtt 240
gccatggtta ctactgcctg ccacgagttc ttgaacat g agtnagatta ggaaagcagc 300
caaacctttt cctgttaaca gaggaagggt catggcaaga naggcaggac aggcaagggg 360
tttgagggt tagttaggga gcttgagggt tttccagccg tntttnttg gttaatttag 420
ggaagggttg a 431

```

<210> 256

<211> 1095
<212> DNA/RNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<220>
<221> misc_feature
<222> (1)..(1095)
<223> s100 calcium-binding protein, beta (neural)
(S100B) gene.

<400> 256
tgccgcccag gaccgcgagc agagacg acg cctgcagcaa ggagaccag aaggggtgag 60
acaaggaaga ggatgtctga gctggagaag gccatggtgg ccctcatcga cgttttccac 120
caatattctg gaagggaggg agacaagcac aagctgaaga aatccgaact caaggagctc 180
atcaacaatg agctttccca tttcttagag gaaatcaaag agcaggagggt tgtggacaaa 240
gtcatggaaa cactggacaa tgatggagac ggcgaatgtg acttccagga attcatggcc 300
tttgttgcca tggttactac tgccctgccac gagttctttg aacatgagtg agattagaaa 360
gcagccaaac ctttctgtga acagagacgg tcatgcaaga aagcagacag caagggcttg 420
cagcctagta ggagctgagc tttccagccg tggtgtagct aattagga ag ctgatttgc 480
tttgtgattg aaaaattgaa aacctcttcc caaaggctgt ttaacggcc tgcatcattc 540
tttctgctat attaggcctg tgtgtaagct gactggcccc agggactctt gttacagta 600
acttaggagt caggctctcag tgataaagcg tgcaccgtgc agcccgccat gccctgtag 660
accctaaccg ggagggaacc ctgact acag aaattacccc ggggcaccct taaaacttcc 720
actaccttta aaaaacaaag ctttatccag cattatttga aaacactgct gttctttaa 780
tgcgcttcctc atccatgcag ataacagctg gttggccggg gtggccctgc aagggcgtgg 840
tggtctcgcc ctgcttcccg ggatgcgcct gatcaccagg tgaacgctca gcgctggcag 900
cgtcctggaa aaagcaactc catcagaact cgcaatccga gccagctctg ggggctccag 960
cgtggcctcc gtgacccatg cgattcaagt cgcggctgca ggatccttgc ctccaacgtg 1020
ctccagcac atgcggcttc cgagggcact accgggggct ctgagccacc gcgagggcct 1080
gcgttcaata aaaa 1095

<210> 257
<211> 542
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<220>
<221> misc_feature
<222> (1)..(542)
<223> 3' terminal sequence. atp-binding cassette,
sub-family b (mdr/tap), member 1 (ABCB1) gene.

<400> 257
ttttaaaatc tactttaatt ctgttataaa atttataatg cagtttaaac tatgatttct 60
ctccacttga tgatgtctct cactctgttc ctttaattac gaagtctctg aagactctga 120
acttgactga ggaaatgtta aacagatacc tcttcataat tctgtaagtgt tttgctttta 180
actttgaata aatgtcatat ctaaacaat attaaaaagt atttaacatc tcatacagtc 240
agagttcact ggcgctttgt tccagcctgg aactgacca ttgaaaaata gatgcctttc 300
tgtgccagca gctgctgatg cgtgccatgc tccttgactc tgccattctg aaacaccact 360
attaagtctg cattctggat ggtggacagg cggtagcaa tcacaatgca ggtgcggcct 420
tctctggcta tgccagggct tcttgacaa ctttttacc tactgtatcc agagctgacg 480
tggctcatcc aaaagcaaaa tantgggctg tctaacaagg gcacgagcta ttgccatgcg 540
tt 542

<210> 258
<211> 4643
<212> DNA/RNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<220>
<221> misc_feature
<222> (1)..(4643)
<223> atp-binding cassette, sub-family b
(mdr/tap), member 1 (ABCB1) gene.

<400> 258
cctactctat tcagatattc tccagatt cc taaagattag agatcatttc tcattctcct 60
aggagtactc acttcaggaa gcaaccagat aaaagagagg tgcaacggaa gccagaacat 120
tcctcctgga aattcaacct gtttcgcagt ttctcgagga atcagcattc agtcaatccg 180
ggcggggagc agtcatctgt ggtgaggctg attggctggg caggaaacagc gccggggcgt 240
gggctgagca cagcgcttcg ctctctttgc cacaggaagc ctgagctcat tcgagtagcg 300
gctcttccaa gctcaaaagaa gcagaggccg ctgttcgttt cctttaggtc tttccactaa 360
agtcggagta tcttcttcca agatttcacg tcttggtggc cgttccaagg agcgcgagg 420
cgggatggat cttgaagggg accgcaatgg aggagcaaag aagaagaac t tttttaact 480
gaacaataaa agtgaaaaag ataagaagga aaagaaacca actgtcagtg tattttcaat 540
gtttcgctat tcaaattggc ttgacaagtt gtatatggtg gtgggaactt tggctgccat 600
catccatggg gctggacttc ctctcatgat gctggtggtt ggagaaatga cagatatctt 660
tgcaaatgca ggaaatttag aagatct gat gtcacacatc actaatagaa gtgatatcaa 720
tgatacaggg ttcttcatga atctggagga agacatgacc aggtatgcct attattacag 780
tggaattggt gctggggtgc tgggtgctgc ttacattcag gtttcatttt ggtgcctggc 840
agctggaaga caaatcacaca aaattagaaa acagttttt catgctataa tgcgacagga 900
gataggctgg tttgatgtgc acgatgttg ggagcttaac acccgactta cagatgatgt 960
ctccaagatt aatgaaggaa ttggtgacaa aattggaatg ttctttcagt caatggcaac 1020
atthttcact ggttttatag taggatttac acgtggttgg aagctaacc ttgtgatttt 1080
ggccatcagt cgtgttcttg gactgtcagc tgctgtctgg gcaaa gatac tatcttcatt 1140
tactgataaa gaactcttag cgtatgcaaa agctggagca gtagctgaag aggtcttggc 1200
agcaattaga actgtgattg catttgagg acaaaagaaa gaacttgaaa ggtacaacaa 1260
aaatttagaa gaagctaaaa gaattgggat aaagaaagct attacagcca atatttctat 1320
aggtgctgct ttctgtctga tctatgcac ttatgctctg gccttctggt atgggaccac 1380
cttggctctc tcaggggaa atctatttg acaagtactc actgtatttt ctgtattaat 1440
tgggctgttt agtcttgagc aggcattctc aagcattgaa gcatttgcaa atgcaagagg 1500
agcagcttat gaaatcttca agataattga taataagcca agtattgaca gctattcga a 1560
gagtgggcac aaaccagata atattaagg aaatttgaa ttcagaaatg ttcacttcag 1620
ttaccatct cgaaaagaag ttaagatctt gaagggtctg aacctgaagg tgcagagtgg 1680
gcagacggtg gccctggtt gaaacagtgg ctgtgggaag agcacaacag tccagctgat 1740
gcagaggctc tatgacccca cagaggggat ggt cagtgtt gatggacagg atattaggac 1800
cataaatgta aggtttctac gggaaatcat tgggtgtggt agtcaggaac ctgtattgtt 1860
tgccaccacg atagctgaaa acattcgcta tggcctgaa aatgtacca tggatgagat 1920
tgagaaagct gtcaaggaag ccaatgccta tgactttatc atgaaactgc ctcataaatt 1980
tgacacctg gttggagaga gaggggcca gttgagtgtt gggcagaagc agaggatcgc 2040
cattgcacgt gccctggtt gcaaccccaa gatcctctg ctggatgagg ccacgtcagc 2100
cttggacaca gaaagcgaag cagtgttca ggtggctctg gataaggcca gaaaaggctc 2160
gaccaccatt gtgatagctc atcgtttgtc tacagttcgt aatgctg acg tcatcgctgg 2220
tttcatgat ggagtcttg tggagaaagg aaatcatga gaactcatga aagagaaagg 2280
catttacttc aaacttgtca caatgcagc agcaggaaat gaagtgaat tagaaaatgc 2340
agctgatgaa tccaaaagt gaaattgatgc cttggaaatg tcttcaaatg attcaagatc 2400
cagtctaata agaaaaagat caactcgtg gagtgtccgt ggatcacaag cccaagacag 2460
aaagcttagt accaaagagg ctctggatga aagtatacct ccagtttct tttggaggat 2520
tatgaagcta aatttaactg aatggcctta tttgtgtgtt ggtgtatttt gtgccattat 2580
aatggaggc ctgcaaccag catttgcaat aatattttca aagattatag gggtttttac 2640
aagaattgat gatcctgaaa caaacgcaca gaatagtaac ttgttttcac tattgtttct 2700

```

agccottgga attatttctt ttattacatt tttccttcag ggtttcacat ttggcaaagc 2760
tggagagatc ctcaccaagc ggctccgata catggttttc cgatccatgc tcagacagga 2820
tgtgagttgg tttgatgacc ctaaaaacac cactg gagca ttgactacca ggctcgccaa 2880
tgatgctgct caagttaaag gggctatagg ttccaggctt gctgtaatta cccagaatat 2940
agcaaattctt gggacaggaa taattatata cttcatctat ggttggcaac taacactgtt 3000
actcttagca attgtaccca tcattgcaat agcaggagtt gttgaaatga aaatgttgtc 3060
tggacaagca ctgaaagata agaaagaact agaagggtgt gggaagatcg ctactgaagc 3120
aatagaaaac ttccgaaccg ttgtttcttt gactcaggag cagaagtgtt aacatatgta 3180
tgctcagagt ttgcagggtac catacagaaa ctctttgagg aaagcacaca tctttggaat 3240
tacattttcc ttcacccagg caatgatgta tttttcctat gctggatgt t tccggtttgg 3300
agcctacttg gtggcacata aactcatgag ctttgaggat gttctgttag tattttcagc 3360
tgtttgtctt ggtgccatgg ccgtggggca agtcagttca tttgctcctg actatgccaa 3420
agccaaaata tcagcagccc acatcatcat gatcattgaa aaaacccctt tgattgacag 3480
ctacagcacg gaaggcctaa tgc cgaacac attggaagga aatgtcacat ttggtgaagt 3540
tgtattcaac tatcccacc gaccggacat ccagtgctt cagggactga gctggagggt 3600
gaagaagggc cagacgctgg ctctgggtgg cagcagtggt tgtgggaaga gcacagtgtt 3660
ccagctcctg gagcggttct acgacccctt ggcagggaaa gtgctgcttg atggcaaaga 37 20
aataaagcga ctgaatgttc agtggctccg agcacacctg ggcacgtgtt cccaggagcc 3780
catcctgttt gactgcagca ttgctgagaa cattgcctat ggagacaaca gccgggtgtt 3840
gtcacaggaa gagattgtga gggcagcaaa ggaggccaac atacatgcct tcctcgagtc 3900
actgcctaat aaatatagca ctaaagtagg agacaaa gga actcagctct ctggtggcca 3960
gaaacaacgc attgccatag ctctgtccct tgtagacag cctcatattt tgcttttga 4020
tgaagccacg tcagctctgg atacagaaag tgaagggtt gtccaagaag ccctggacaa 4080
agccagagaa ggccgcacct gcattgtgat tgctaccgc ctgtccacca tccagaatgc 4140
agacttaata gtggtgtttc agaatggcag agtcaaggag catggcacgc atcagcagct 4200
gctggcacag aaaggcatct atttttcaat ggtcagtgct caggctggaa caaagcgcca 4260
gtgaactctg actgtatgag atgttaaata ctttttaata tttgtttaga tatgacattt 4320
attcaaaagt aaaagcaaac acttacagaa ttatgaagag gtatctgttt aacatttcct 4380
cagtcaagtt cagagtcttc agagacttcg taattaaagg aacagagtga gagacatcat 4440
caagtggaga gaaatcatag tttaaactgc attataaatt ttataacaga attaaagtag 4500
attttaaaag ataaaatgtg taattttgtt tataatttcc catttggtact gtaactgact 4560
gccttgctaa aagattatag aagta gcaaa agtattgaa atgtttgcat aaagtgtcta 4620
taataaaaact aaactttcat gtc

```

4643

<210> 259

<211> 486

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(486)

<223> 3' terminal sequence. selectin e
(endothelial adhesion molecule 1) (SELE) gene.

<400> 259

```

caacctttat agtgttatgt caaatagggtc tgacataagc ttaaataaat atatacttta 60
aaaattataa aatatttttaa gttataattht aaaattctca ataaaactca aacacaaacc 1 20
acactgggat ttcacacagc taattttctaa tgcagtttac ataaatattt acaacactta 180
aacaatttca aagaaaataa cactgtattc catacatagc ctgatcacag tagttgttct 240
ctcttatttc ccagagttttt tctgccctt taaaaggaaac ctctggctgt tctgancctt 300
atcacatctc tgttttgact gttgggcttt ggttgggtgc cagtgggttc gccaggaaact 360
tctctgggaa actttttttt tcaacactgg ctagggtang gggngttag gggggnggt 420
ttggtttcnt cacantccct cagggtnggg ggcgggttng ggnattacc ggcgggggt 480
tttttc

```

486

<210> 260
<211> 478
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<220>
<221> misc_feature
<222> (1)..(478)
<223> 5' terminal sequence. selectin e
(endothelial adhesion molecule 1) (SELE) gene.

<400> 260
gcctactatg ccagatgcct ttatggctga aaccgcaaca cccatcacca cttcaataga 60
tcaaagtcca gcaggcaagg acggccttca actgaaaaga ctgagtgttc cctttcctac 120
tctcaggatc aagaaagtgt tggctaata agggaaagga tattttcttc caagcaaagg 180
tgaagagacc aagactctga aatctcagaa ttccttttct aactctccct tgctcg ctgt 240
aaaatcttgg cacagaaaca caatattttg tggctttctt tcttttgccc ttcacagtgt 300
ttcgacagct gattacacag ttcctgtcat aaggaatgaa taattaatta tccagagttt 360
agaggaaaaa aatgactaaa aatattatta acttaaaaaa tggacagggtg ttggatgccc 420
acaggcaaat gcatgggggg gttgtttaat gggg gcaaat ccctacttga atgctctt 478

<210> 261
<211> 3834
<212> DNA/RNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<220>
<221> misc_feature
<222> (1)..(3834)
<223> selectin e (endothelial adhesion molecule 1)
(SELE) gene.

<400> 261
cctgagacag aggcagcagt gataccacc tgagagatcc tgtgtttgaa caactgcttc 60
ccaaaacgga aagtatttca agcctaaacc tttgggtgaa aagaactcct gaagtcata 120
ttgcttcaca gtttctctca gctctcactt tgggtgctct cattaagag agtggagcct 180
ggtcttaca cacctccacg gaa gctatga cttatgatga ggccagtgc tattgtcagc 240
aaaggtagac acacctggtt gcaattcaaa acaaagaaga gattgagtag ctaaaactcca 300
tattgagcta ttcaccaagt tattactgga ttggaatcag aaaagtcaac aatgtgtggg 360
tctgggtagg aaccagaaaa cctctgacag aagaagccaa gaactgggct ccaggtgaac 420
ccaacaatag gcaaaaagat gaggactgcg tggagatcta catcaagaga gaaaaagatg 480
tgggcatgtg gaatgatgag aggtgcagca agaagaagct tgccctatgc tacacagctg 540
cctgtaccaa tacatcctgc agtggccacg gtgaatgtgt agagaccatc aataattaca 600
cttgcaagtg tgacctggc ttcagtggac tcaagtgtga gca aattgtg aactgtacag 660
ccctggaatc ccctgagcat ggaagcctgg tttgcagtca cccactggga aacttcagct 720
acaattcttc ctgctctatc agctgtgata ggggttacct gccagcagc atggagacca 780
tgcaagtgtat gtcctctgga gaatggagtg ctctattcc agcctgcaat gtggttgagt 840
gtgatgctgt gacaaatcca gccaatgggt tcgtggaatg tttccaaaac cctggaagct 900
tcccatggaa cacaacctgt acatttgact gtgaagaagg atttgaacta atgggagccc 960
agagccttca gtgtacctca tctgggaatt gggacaacga gaagccaacg tgtaaagctg 1020
tgacatgcag ggccgtccgc cagcctcaga atggctctgt gaggtgcagc cattcccctg 1080
ctggagagtt caccttcaaa tcatcctgca acttcacctg tgaggaggc ttcattgttc 1140
agggaccagc ccaggttgaa tgcaccactc aagggcagtg gacacagcaa atcccagttt 1200
gtgaagcttt ccagtgcaca gccttgtcca accccagcgg aggtacatg aattgtcttc 1260

```

ctagtgtcttc tggcagtttc cgttatgggt ccagctg tga gttctcctgt gagcaggggt 1320
ttgtgttgaa gggatccaaa aggtcccaat gtggcccccac aggggagtg gacaacgaga 1380
agccacatg tgaagctgtg agatgcgatg ctgtccacca gccccgaag ggtttggtga 1440
gggtgtctca ttcccctatt ggagaattca cctacaagtc ctctgtgtgc ttcagctgtg 1500
aggagggatt tgaattatat ggatcaactc aacttgagtg cacatctcag ggacaatgga 1560
cagaagaggt tccttcctgc caagtgttaa aatgttcaag cctggcagtt ccgggaaaga 1620
tcaacatgag ctgcagtggt gagccctgtg ttggcactgt gtgcaagttc gcctgtcctg 1680
aaggatggac gctcaatggc tctgcagctc ggacatgtgg agccacagga cactgggtctg 1740
gcctgtctacc tacctgtgaa gctcccactg agtccaacat tcccttggtg gctggacttt 1800
ctgtgtctgg actctccctc ctgacattag caccatttct cctctggctt cggaaatgct 1860
tacggaaagc aaagaaattt gttcctgcca gcagctgcca aagccttgaa tcagacggaa 1920
gctacccaaa gccttcttac atcct ttaag ttcaaaagaa tcagaaacag gtgcatctgg 1980
ggaactagag ggatacactg aagttaacag agacagataa ctctcctcgg gtctctggcc 2040
cttcttgctt actatgccag atgcctttat ggctgaaacc gcaacacca tcaccacttc 2100
aatagatcaa agtccagcag gcaaggacgg ccttcaactg aaaagactca gtgttccctt 2160
tcctactctc aggatcaaga aagtgttggc taatgaaggg aaaggatatt ttcttccaag 2220
caaaggtgaa gagaccaaga ctctgaaatc tcagaattcc ttttctaact ctcccttgct 2280
cgctgtaaaa tcttggcaca gaaacacaat atttgtggc tttctttctt ttgcccttca 2340
cagtgtttcg acagctgatt acacagttgc tgtcataag a atgaataata attatccaga 2400
gtttagagga aaaaaatgac taaaaatatt ataacttaa aaaaatgacag atgttgaatg 2460
cccacaggca aatgcatgga ggggtgttaa tgggtgaaat cctactgaat gctctgtgcg 2520
agggttacta tgcacaattt aatcacttcc atccctatgg gattcagtg tctttaaaga 2580
gttcttaagg attgtgatat ttttacttgc attgaatata ttataatctt ccatacttct 2640
tcattcaata caagtgtggt agggacttaa aaaacttgta aatgctgtca actatgatat 2700
ggtaaaaagt acttattcta gattaccctc tcattgttta ttaacaaatt atgttacatc 2760
tgttttaaat ttatttcaaa aagggaaact attgtcccct agcaaggcat ga tgttaacc 2820
agaataaagt tctgagtgtt tttactacag ttgttttttg aaaacatggg agaattggag 2880
agtataaact gaatggaagg tttgtatatt gtcagatatt ttttcagaaa tatgtgggtt 2940
ccacgatgaa aaacttccat gaggccaaac gttttgaact aataaaagca taaatgcaaa 3000
cacacaaagg tataatttta tgaatgt ctt tgttggaaaa gaatacagaa agatggatgt 3060
gctttgcatt cctacaaaga tgtttgtcag atgtgatatg taacataat tcttgtatat 3120
tatggaagat tttaaattca caatagaaac tcaccatgta aaagagtcac ctggtagatt 3180
tttaacgaat gaagatgtct aatagttatt cctatttgt tttcttctgt atgttagggg 3240
gctctggaag agaggaatgc ctgtgtgagc aagcatttat gtttatttat aagcagattt 3300
aacaattcca aaggaatctc cagttttcag ttgatcactg gcaatgaaaa attctcagtc 3360
agtaattgcc aaagctgtct tagccttgag gagtgtgaga atcaaaactc tcctacactt 3420
ccattaactt agcatgtgtt gaaaaaaaaa gtttcagaga agttctggct gaacactggc 3480
aacgacaaag ccaacagtca aaacagagat gtgataagga tcagaacagc agaggttctt 3540
ttaaaggggc agaaaaactc tgggaaataa gagagaacaa ctactgtgat caggctatgt 3600
atggaataca gtgttatttt ctttgaaatt gttaaagtgt tgtaaatatt tatgtaaaact 3660
gcattagaaa tttagcgtgt gaaataccag tgtggtttgt gtttgagttt tattgagaat 3720
tttaaattat aacttaaaat attttataat ttttaaagta tatatttatt taagcttatg 3780
tcagacctat ttgacataac actataaagg ttgacaataa atgtgcttat gttt 3834

```

<210> 262

<211> 267

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(267)

<223> 3' terminal sequence. epidermal growth factor (beta-urogastrone) (EGF) gene.

<400> 262

gtttatgttt ttggtgattt tatttaaata attagaagaa attcatcgtt gt ctataatg 60

172/292

```

aaaacaaatc aggcaattta cttacaatct tgtaactgaa aatacatata aattctgtgc 120
aatcacacca agagggaaaa ttctgtaggg gaaaaggaca gtaatgacta agaaactccg 180
aagcctcctg tgtaatatct taaaatanaa tgttttcatt caaatatttt aaaaaataag 240
natctaactc gaaaaaatca gtttcta                                267

```

<210> 263

<211> 383

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(383)

<223> 5' terminal sequence. protein kinase c
substrate 80 k-h (PRKCSH) gene.

<400> 263

```

ggagtccgag gtgcaggggg agcagcccaa gccggccagc cctgctgagn gaagacaaaa 60
tncggcccta cgacgagcag acgcaggcct tcatogatgc tgcccaggag gcccgcaaca 120
agttcgagga ggccgagcgg tcgctgaagg acatggagga gtccatcagg aacctggnag 180
caaganatct cttttgactt tggccccaac ggnagttttg cttacctgta cagccagtgc 240
tacgagctca ccaccaacga atacgtctac cgcctctncc ccttcaagct tgtnttcgna 300
gaaacccaaa ctccgggggt ctcccaccag ccttggcacc tgggggcttc atgggattgg 360
gcccgacca cnacaatttc agt                                383

```

<210> 264

<211> 2056

<212> DNA/RNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(2056)

<223> protein kinase c substrate 80k -h (PRKCSH)
gene.

<400> 264

```

ggaaccgcgg ctgctggaca agaggggtgc ggtggatact gacctttgct ccggcctcgt 60
cgtgaagaca cagcgcatct cccgcgtgta ggctttctcc acagaaccgg ttctgggcct 120
cagagcgtct ggtgagatgc tgttgccgct gctgctgctg ctacctatgt gctgggcctg 180
ggaggtcaag agggcccggg gcgtctccct caccaatcat cacttctacg atgag tccaa 240
gcctttcacc tgctggagcg gtctggccac catoccatct gatcaggtca acgatgacta 300
ttgcgactgc aaagatggct ctgacgagcc aggcacggct gcctgtccta atggcagctt 360
ccactgcacc aacactggct ataagcccct gtatatcccc tccaaccggg tcaacgatgg 420
tgtttgtgac tgctgcatg gaacagacga gta caacagc ggcgtcatct gtgagaacac 480
ctgcaaaagag aaggggccgta aggagagaga gtccctgcag cagatggccg aggtcaccgg 540
cgaagggttc cgtctgaaga agatccttat tgaggactgg aagaaggcac gggaggagaa 600
gcagaaaaag ctcatgagc tacaggctgg gaagaagtct ctggaagacc aggtggagat 660
gctgcggaca gtgaaggagg aagctgagaa gccagagaga gaggccaaag agcagcacca 720
gaagctgtgg gaagagcagc tggctgctgc caaggcccaa caggagcagg agctggcggc 780
tgatgccttc aaggagctgg atgatgacat ggacgggacg gtctcggtga ctgagctgca 840
gactcaccgg gagctggaca cagatgggga tggggcggtg tcagaagcgg aag ctcaggc 900
cctcctcagt ggggacacac agacagacgc cacctctttc tacgaccgcg tctgggccgc 960

```

```

catcagggac aagtaccggt ccgaggcact gcccacogac cttccagcac cttctgcccc 1020
tgacttgacg gagcccaagg aggagcagcc gccagtgcc tcgtcgcca cagaggagga 1080
ggaggagag gaggaggagg aagaagaggc tgaagaagag gaggaggagg aggattccga 1140
ggaggcccca ccgccactgt caccgccgca gccggccagc cctgctgagg aagacaaaat 1200
gccgccctac gacgagcaga cgcaggcctt catcgatgct gcccaggagg cccgcaacaa 1260
gttcgaggag gccgagcggg cgctgaagga catggaggag tccatcagga acctggagca 1320
agagatttct tttgactttg gcccacaacg ggagtttgct tacctgtaca gccagtgcta 1380
cgagctcacc accaacgaat acgtctaccg cctctgcccc ttcaagcttg tctcgcagaa 1440
acccaaactc gggggctctc ccaccagcct tggcacctgg ggtcatgga ttggccccga 1500
ccacgacaag ttcagtgcc tgaagtatga gcaaggcacg ggc tgctggc agggcccca 1560
ccgtccacc accgtgcgc tcctgtgcgg gaaagagacc atggtgacca gcaccacaga 1620
gcccagtcgc tgcgagtacc tcatggagct gatgaogcca gccgcctgcc cggagccacc 1680
gcctgaagca cccaccgaag acgaccatga cgagctctag ctggatgggc gcagagaacc 1740
tcaagaaggc atgaagcc ag cccctgcagt gccgtccacc cgcctctctg ggctgcctg 1800
tggtctgtt gccctcctct gtggcggcag gacctttgtg gggcttcgtg ccctgctctg 1860
gggcccagc ggggctggtc cacattccca ggccccaaca gcctccaaag atgggtaaag 1920
gagcttgccc tccctggggc cccaccttg gtgactgcc ccaccacccc cagccct gtc 1980
cctgccccc ctctagtgg ggactagtga atgacttgac ctgtgacctc aatacaataa 2040
atgtgatccc ccaccc 2056

```

<210> 265

<211> 379

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence :primer

<220>

<221> misc_feature

<222> (1)..(379)

<223> 5' terminal sequence. diphtheria toxin
receptor (heparin-binding epidermal growth
factor-like growth factor) (DTR) gene.

<400> 265

```

ggttctgtga ccatctgta gtaatttatt gtctgtctac atttctgc ag atcttcctg 60
gtcagagtgc cactgcggga ntctgtatgg tcaggatgta ggggttaact tggtcagagc 120
cactctatga gttggacttc agtcttgccct aggcgatttt gtctaccatt tgtgttttga 180
aagcccaagg tgctgatgtc aaagtgtaac agatatcagt gtctccccgt gtctctctcc 240
tgccaagtct cagaagaggt tgggctt cca tgctgtagc ttctctggtc cctcaccccc 300
atggccccag gccacagcg tggagactnc actttncct tgtgtcaaga catttctctn 360
aactcctgnc attcttctg 379

```

<210> 266

<211> 2360

<212> DNA/RNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(2360)

<223> diphtheria toxin receptor (heparin-binding
epidermal growth factor-like growth factor) (DTR)
gene.

<400> 266

```

gctacgcggg ccacgctgct ggctggcctg accta ggcgc gcggggctcg gcggccgcgc 60
gggcgggctg agtgagcaag acaagacact caagaagagc gagctgcgcc tgggtcccgg 120
ccaggcttgc acgcagaggc gggcggcaga cgggtgcccgc cggaatctcc tgagctccgc 180
cgcccagctc tggtgccagc gcccagtggc cgcgccttcg aaagtgaactg gtgcctcgcc 240
gcctcctctc ggtgcgggac catgaagctg ctgccgtcgc tgggtgctgaa gctctttctg 300
gctgcagttc tctcggcact ggtgactggc gagagcctgg agcggcttcg gagagggcta 360
gctgctggaa ccagcaaccc ggacctccc actgtatcca cggaccagct gctacccta 420
ggaggcggcc gggaccggaa agtccgtgac ttgcaagagg cagatctgga cctttt gaga 480
gtcactttat cctccaagcc acaagcactg gccacaccaa acaaggagga gcacgggaaa 540
agaaagaaga aaggcaaggg gctaggggag aagagggacc catgtcttcg gaaatacaag 600
gacttctgca tccatggaga atgcaaatat gtgaaggagc tccgggctcc ctccctgcac 660
tgccacccgc gttaccatgg agagagggtg catg ggctga gcctcccagt ggaaaatcgc 720
ttatatacct atgaccacac aaccatcctg gccgtggtgg ctgtggtgct gtcactctgc 780
tgtctgctgg ccactgtggg gcttctcatg tttaggtacc ataggagagg aggttatgat 840
gtgaaaaaat aagagaaagt gaagtgggc atgactaatt cccactgaga gagacttggtg 900
ctcaaggaat cggctgggga ctgctacctc tgagaagaca caaggtgatt tcagactgca 960
gaggggaaag acttccatct agtcacaaag actccttcgt cccagttgc cgtctaggat 1020
tgggcctccc ataattgctt tgccaaaata ccagagcctt caagtgccaa acagagtatg 1080
tccgatggta tctgggtaag aagaaagcaa aagcaaggga ccttcatgcc ct tctgattc 1140
ccctccacca aaccccaactt cccctcataa gtttgtttaa acacttatct tctggattag 1200
aatcccggtt aaattccata tgctccagga tctttgactg aaaaaaaaaa agaagaagaa 1260
gaaggagagc aagaaggaaa gatttgtgaa ctggaagaaa gcaacaaaga ttgagaagcc 1320
atgtactcaa gtaccaccaa gggatct gcc attgggaccc tccagtgtg gatttgatga 1380
gttaactgtg aaataaccaca agcctgagaa ctgaattttg ggacttctac ccagatggaa 1440
aaataacaac tatttttgtt gttgtgtgtt gtaaatgcct cttaaattat atatttattt 1500
tattctatgt atgttaattt atttagtttt taacaatcta acaataatat ttcaagtgcc 1560
tagactgtta ctttgccaat ttcttgccc tccactctc atccccaca tctggcttag 1620
tgccacccac ctttgccaca aagctaggat ggttctgtga occatctgta gtaatttatt 1680
gtctgtctac atttctgcag atcttccgtg gtcagagtgc cactgcggga gctctgtatg 1740
gtcaggatgt aggggttaac ttggtcagag ccactctatg agttggactt cagtcttgcc 1800
taggcgattt tgtctaccat ttgtgttttg aaagcccaag gtgctgatgt caaagtgtaa 1860
cagatatcag tgtctcccg tgctctctcc ctgccaaagtc tcagaagagg ttgggcttcc 1920
atgcctgtag ctttctgtgt ccctcaccce catggcccca ggccacagcg tgggaactca 1980
ctttcccttg tgca agaca tttctctaac tctgcccatt cttctggtgc tactccatgc 2040
aggggtcagt gcagcagagg acagtctgga gaaggtatta gcaaagcaaa aggctgagaa 2100
ggaacaggga acattggagc tgactgttct tggttaactga ttacctgcca attgctaccg 2160
agaaggttg aggtggggaa ggctttgtat aatcccacc acctcaccaa aacg atgaag 2220
gtatgctgtc atggtccttt ctggaagttt ctggtgccat ttctgaactg ttacaacttg 2280
tatttccaaa cctggttcat atttatactt tgcaatccaa ataaagataa cccttattcc 2340
ataaaaaaaaa aaaaaaaaaa 2360

```

<210> 267

<211> 435

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(435)

<223> 5' terminal sequence. integrin, beta 2

(antigen cd18 (p95), lymphocyte

function-associated antigen 1; macrophage antigen

1 (mac-1) beta subunit) (ITGB2) gene.

<400> 267

```

aggagtcccc cggctgcccc tcacctgtg gcaagtacat ctctgcgcc gactgcctga 60

```

```

agttcgaaaa gggccctnt ggaagaactg cagcgcgggc tgtccgggcc tgcagctgtc 120
gaacaacccc gtgaagggca ggacctgcaa ggagaggac tcagag ggct gctgggtggc 180
ctacacgctg gacgagcagg acgggatgga ccgctacctc atctatgttg atgagagccg 240
agagtgtgtg gcaggcccca acatcgccgc catcgctggg ggcaccgtgg gcaggcatcg 300
tgctgatcgg cattctcctg ctggtcactc gggaaggctc tgatccacct gagcgacctc 360
cgggagttac aggcgttttg agna ggagaa gctcaagtc cagtnggaac aatgattatt 420
ccctttttca agagc

```

435

<210> 268

<211> 2776

<212> DNA/RNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(2776)

<223> integrin, beta 2 (antigen cd18 (p95),
 lymphocyte function-associated antigen 1;
 macrophage antigen 1 (mac-1) beta subunit) (ITGB2)
 gene.

<400> 268

```

cagggcagac tggtagcaaa gccccacgc ccagccagga gcaccgccgc ggact ccagc 60
acaccgaggc acatgctggg cctgcgccc cactgctcg cctgggtggg gctgctctcc 120
ctcgggtgcg tctctctca ggagtgcacg aagttcaagg tcagcagctg ccgggaatgc 180
atcgagtcgg ggcgggctg cactggtgc cagaagctga acttcacagg gccgggggat 240
cctgactcca ttgctgcga caccggcca cagc tgctca tgaggggctg tgcggtgac 300
gacatcatgg accccacaag cctcgtgaa acccaggaag accacaatgg gggccagaag 360
cagctgtccc caaaaaagt gacgctttac ctgcgaccag gccaggcagc agcggtcaac 420
gtgaccttcc ggcgggccaa gggctacccc atcgacctgt actatctgat ggacctctcc 480
tactccatgc ttgatgacct caggaatgtc aagaagctag gtggcgacct gctccgggcc 540
ctcaacgaga tcaccgagtc cggccgcat ggcttcgggt ccttcgtgga caagaccgtg 600
ctgccgttcg tgaacacgca ccctgataag ctgcgaaacc catgccccaa caaggagaaa 660
gagtgccagc ccccgtttgc cttcaggcac gtgctgaagc tgaccaacaa ctcc aaccag 720
tttcagaccg aggtcgggaa gcagctgatt tccggaaacc tggatgcacc cgagggtggg 780
ctggacgcca tgatgcagg cgccgcctgc ccggaggaaa tcggctggcg caacgtcacg 840
cggctgctgg tgtttgccac tgatgacggc ttccatttcg cggcgacgg aaagctgggc 900
gccatcctga ccccaacga cggccgctgt ca cctggagg acaacttga caagaggagc 960
aacgaattcg actaccatc ggtgggccag ctggcgaca agctggctga aaacaacatc 1020
cagcccatct tcgcggtgac cagtaggatg gtgaagacct acgagaaact caccgagatc 1080
atccccagt cagccgtggg ggagctgtct gaggactcca gcaatgtggt ccattctatt 1140
aagaatgctt acaataaact ctctccagg gtcttcttg atcacaacgc cctccccgac 1200
accctgaaag tcacctacga ctcttctgc agcaatggag tgacgcacag gaaccagccc 1260
agaggtgact gtgatggcgt gcagatcaat gtcccgatca ccttcagggt gaaggtcacg 1320
gccacagagt gcatccagga gcagtcgttt gtcacccggg cgtggg ctt cacggacata 1380
gtgaccgtgc aggttcttcc ccagtgtgag tgccggtgcc gggaccagag cagagaccgc 1440
agcctctgcc atggcaagg cttcttgagg tgccgcatct gcagggtgta cactggctac 1500
attgggaaaa actgtgagtg ccagacacag ggccggagca gccaggagct ggaagggaagc 1560
tgccggaagg acaacaactc c atcatctgc tcagggtctg gggactgtgt ctgcgggcag 1620
tgccgtgccc acaccagca cgtccccggc aagctgatat acgggcagta ctgcgagtgt 1680
gacaccatca actgtgagcg ctacaacggc caggtctgcg gcggcccggg gagggggctc 1740
tgcttctgcg ggaagtgcg ctgccaccg ggctttgagg gctcagcgtg ccagtgcag 1800
aggaccactg agggctgcct gaaccgcgg cgtgttgagt gtagtggtcg tggccggtgc 1860
cgtgcaacg tatgcgagtg ccattcaggc taccagctgc ctctgtgcca ggagtcccc 1920
ggctgcccc caccctgttg caagtacatc tcctgcgcc agtgccgtgaa gttcgaaaag 1980
ggccctttg ggaagaactg cagcgcgggc tgtcc gggcc tcagctgtc gaacaacccc 2040
gtgaagggca ggacctgcaa ggagaggac tcagagggt gctgggtggc ctacacgctg 2100

```


176/292

```

gagcagcagg acgggatgga ccgctacctc atctatgtgg atgagagccg agagtgtgtg 2160
gcaggcccca acatcgccgc catcgctggg gccaccgtgg caggcatcgt gctgatcggc 2220
attctcctgc tggatcatctg gaaggctctg atccacctga gcgacctccg ggagtacagg 2280
cgctttgaga aggagaagct caagtcccag tggacaatg ataatcccct tttcaagagc 2340
gccaccacga cggatcatgaa cccaagttt gctgagagtt aggagcactt ggtgaagaca 2400
aggccgtcag gaccacccat gtctgcccc tccgcggcc gagacatgg c ttggccacag 2460
ctcttgagga tgtcaccaat taaccagaaa tccagttatt ttccgccctc aaaatgacag 2520
ccatggccgg ccggtgcttc tgggggctcg tcggggggac agctccactc tgactggcac 2580
agtctttgca tggagacttg aggagggtt gaggttggtg aggttaggtg cgtgtttcct 2640
gtgcaagtca ggacatcagt ctg attaaag gtggtgcaa tttatttaca tttaaacttg 2700
tcagggtata aaatgacatc ccattaatta tattgttaat caatcacgtg tatagaaaaa 2760
aaaataaaac ttcaat 2776

```

<210> 269

<211> 449

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(449)

<223> 5' terminal sequence. neogenin (chicken)
homolog 1 (NEO1) gene.

<400> 269

```

ccaggaccct gaaggtgcta ccagctcctc ttacttgccc agctcccaag aggaagattc 60
aggccagagt cttcccaactg cccatgttcg cccttcccac ccattgaaga gcttcgccgt 120
gccagcaatc ccgctccag gacctccac ctatgatcct gcattgcaa gcacaccatt 180
actgtcccag caagctctga accatcacat tcaactcagt aagacagcct ccacgggac 240
tctaggggaag ggagccggcc tcctatgcca gtggttggtc ccagtgcctc t gaagtgcag 300
ggagaccaca aggtgtgttg gaaggattnc gagagtaggt attgaaccag ntgaggttga 360
ncaaagagtt gggccatngg gggagggatt aattgaangg gaccttaac gtttttnac 420
aacagcttga cggactttta acggggggc 449

```

<210> 270

<211> 5297

<212> DNA/RNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(5297)

<223> neogenin (chicken) homolog 1 (NEO1) gene.

<400> 270

```

gggcccggcc gggctgggct ggagcagcgg cgcccgggag ccgagcttgc agcaggggac 60
cggctgaggc gcgcgggagg gaaggaggca agggctccgc ggcgctgtcg cgctgccgt 120
cactctcggg gaagagatgg cggcggagcg gggagcccgg cgactcctca gcacccctc 180
cttctggctc tactgcctgc tgcgtctcgg gcgcgggccc ccgggcgcgg cggcgccag 240
gagcggtccc gcgcgcagc cccaggagc cagcattcga acgttccact cattttattt 300
tctggtggag ccggtggata cactctcagt tagaggctct tctgttatat taaactgttc 360
agcatattct gagccttctc caaaaattga atggaaaaa gatggaactt ttttaaactt 420
agtatcagat gatcgacgcc agcttctccc ggatggatct ttatttatca gcaatgtggt 480

```

gcattccaaa	cacaataa ac	ctgatgaagg	ttattatcag	tgtgtggcca	ctgttgagag	540
tcttggaaact	attatcagta	gaacagcgaa	gtccatagta	gcaggcttct	caagatttac	600
cagccaacca	gaaccttct	cagtttatgc	tgggaacgga	gcaattctga	atttgtgaagt	660
taatgcagat	ttggtcccat	tttgtagggtg	ggaacagaac	agacaacccc	ttcttctgga	720
tgatagagtt	atcaaaacttc	caagtggaaat	gctggttatc	agcaatgcaa	ctgaaggaga	780
tggcgggctt	tatcgctgcg	tagtggaag	tgggtggcca	ccaaagtata	gtgatgaagt	840
tgaattgaag	gtttctccag	atcctgagggt	gataatcagac	ttggtatitt	tgaacacggc	900
ttctccotta	gtcagagatca	ttgtgcagg	tgtagtgt tg	ccatgtgttg	cttcaggact	960
tcctactcca	accattaaat	ggaatgaaaa	tggaggagca	cttgacacag	aaagctctga	1020
aagattggta	ttgctggcag	gtggtagcct	ggagatcagt	gatgttactg	aggatgatgc	1080
tgggacttat	ttttgtatag	ctgataatgg	aaatgagaca	attgaagctc	aagcagagct	1140
tacagtgcaa	gct caacctg	aattcctgaa	gcagcctact	aatatatatg	ctcacgaatc	1200
tatgatatat	gtatttgaat	gtgaagtgc	tggaaaacca	actccaactg	tgaagtgggt	1260
caaaaatggg	gatattggta	tcccaagtga	ttatttttaag	attgtaaagg	aacataatct	1320
tcaagttttg	ggctctggta	atccagatga	agggtttctat	cagtgcatgt	ct gaaaatga	1380
tgttggaat	gcacaagctg	gagcccaact	gataatcctt	gaacatgcac	cagccacaac	1440
gggaccactg	ccttcagctc	ctcgggatgt	cgtggcctcc	ctggtctcta	cccgttctat	1500
caaattgacg	tggcggacac	ctgcatcaga	tcctcacgga	gacaacctta	cctactctgt	1560
gttctacacc	aaggaaggga	ttgctag gga	acgtgttgag	aataccagtc	acccaggaga	1620
tgatgaagta	accattcaaa	acctaattgc	agcgacctg	tacatcttta	gagttatggc	1680
ctcaaaaatg	catggctcag	gagagagttc	agctccactg	cgagttagaaa	cacaacctga	1740
ggttcagctc	cctggcccag	cacctaacct	tcgtgcatac	gcagcttcgc	ctacctctat	1800
cactgttacg	tgggaaacac	cagtgtctgg	caatggggaa	attcagaatt	ataagttgta	1860
ctacatggaa	aaggggactg	ataaagaaca	ggatgttgat	gtttcaagtc	actcttacac	1920
cattaatggg	tgaaaaaat	atacagagta	tagtttccga	gtggtggcct	acaataaaca	1980
tggtcctggg	gtttccacac	cagatgttgc	tgttcgaaca	ttgtcagatg	ttcccagtg	2040
tgtcctcag	aatctgtcct	tgaagtgcg	aaattcaaag	agtattatga	ttcactggca	2100
gccacctgct	cagccacac	aaaattggga	gattactggc	tacaagattc	gctaccgaa	2160
ggcctccga	aagagtgatg	tcactgagac	cttgtaagc	gggacacagc	tgtctcagat	2220
gattgaaggt	ctga tcggg	ggactgagta	taatttccga	gtggctgctc	taacaatcaa	2280
tgttacaggc	ccggcaactg	actggctgtc	tgtgaaact	tttgaaagtg	acctagatga	2340
aactcgtgtt	cctgaagtgc	ctagctctct	tcactgacgc	ccgctcgta	ctagcatcgt	2400
atgtagcttg	actcctccag	agaatcagaa	cattgtggtc	agaggttacg	ccat tggta	2460
tggcattggc	agccctcatg	cccagaccat	caaagtggac	tataaacagc	gctattaccg	2520
cattgaaaat	ctggatccca	gctctcacta	tgtgattacc	ctgaaagcat	tttaaacagt	2580
gggtgaaggc	atccccctgt	atgagagtgc	tgtgaccagg	cctcacacag	acacttctga	2640
agttgattta	tttgttatta	atgctccat a	cactccagtg	ccagatccca	ctcccatgat	2700
gccaccagtg	ggagttcagg	cttcattct	gagtcatgac	accatcagca	ttacgtgggc	2760
agacaaactg	ctgcccacac	accagaagat	tacagactcc	cgatactaga	ccgtccgatg	2820
gaaaaccaac	atccagcaa	accacaaagta	caagaatgca	aatgcaacca	ctttgagta	2880
tttggtgact	ggtttaaagc	cgaatacact	ctatgaattc	tctgtgatgg	tgaccaaaag	2940
tcgaagatca	agtacatgga	gtatgacagc	ccatgggacc	acctttgaat	tagttccgac	3000
ttctccaccc	aaggatgtga	ctgttgtgag	taaagagggg	aaacctaa	ccataattgt	3060
gaattggcag	cctccctctg	aagccaatgg	caaaattaca	gg ttacatca	tatattacag	3120
tacagatgtg	aatgcagaga	tacatgactg	ggttattgag	cctgttgtgg	gaaacagact	3180
gactcaccag	atacaagat	taactcttga	cacaccatc	tacttcaaaa	tccaggcacg	3240
gaactcaaa	ggcatgggac	ccatgtctga	agctgtccaa	ttcagaacac	ctaaaggcga	3300
ctcctctgat	aaaatgc cta	atgatcaagc	ctcagggct	ggaggggaaag	gaagccggct	3360
gccagaccta	ggatccgact	acaaactcc	aatgagcggc	agtaacagcc	ctcatgggag	3420
ccccacctct	cctctggaca	gtaatatgct	gctggtcata	attgtttctg	ttggcgtcat	3480
caccatcgtg	gtggttgta	ttatcgtctg	cttttgtacc	cgctgtacca	cctctc acca	3540
gaaaagaaga	cgagctgcct	gcaaatcagt	gaatggctct	cataagtaca	aagggaattc	3600
caagatgtg	aaacctccag	atctctggat	cccatctag	agacttgcgc	tgaaaacctat	3660
tgataagtct	ccagacccaa	accccatcat	gactgatact	ccaattctgc	gcaactctca	3720
agatatcaca	ccagttgaca	actccatgga	cagcaatata	catcaaaggc	gaaattcata	3780
cagagggcat	gagtcagagg	acagcatgtc	tacatggct	ggaaggcgag	gaatgagacc	3840
aaaaatgatg	atgccctttg	actcccagcc	accccagcct	gtgattagtg	cccatcccat	3900
ccattccctc	gataaccctc	accatcattt	ccactccagc	agcctcgctt	ctccagctcg	396

```

cttggccagc tccaagagg aagattcagg ccagagtctt ccca ctgccc atgttcgccc 4200
ttcccaccca ttgaagagct tcgccgtgcc agcaatcccg cctccaggac ctcccaccta 4260
tgatcctgca ttgccaagca caccattact gtcccagcaa gctctgaacc atcacattca 4320
ctcagtgaag acagcctcca tcgggactct aggaaggagc cggcctccta tgccagtggg 4380
tgttcccagt gccctgaa g tgcaggagac cacaaggatg ttggaagact ccgagagtag 4440
ctatgaacca gatgagctga ccaaagagat ggcccacctg gaaggactaa tgaaggacct 4500
aaacgctatc acaacagcat gacgaccttc accaggacct gacttcaaac ctgagtctgg 4560
aagtcttgga acttaaccct tgaacaacag gaattgtaca gactacgaga ggacagca ct 4620
tgagaacaca gaatgagcca gcagactggc cagcgctct gtgtagggct ggctccaggc 4680
atggccacct gccttcccct ggtcagcctg gaagaagcct gtgtcgaggc agcttccctt 4740
tgctgctga tattctgcag gactgggcac catgggcca aattttgtgt ccagggaaga 4800
ggcgagaagt gcaacctgca ttctactttg tg gtcaggcc gtgtctttgt gctgtgactg 4860
catcaccttt atggagtgtg gacattggca tttatgtaca attttatttg tgtcttattt 4920
tattttacct tcaaaaacaa aaacgccatc caaaaccaag gaagtccttg gtgttctcca 4980
caagtgttg acatttgact gcttgttcca attatgtatg gaaagtcctt gacagtgtgg 5040
gtcgttccg gggttggctt gttttttggt ttcatTTTTA ttttttaatt ctgagtcatt 5100
gcacctctca ccagctgtta atccatcact ctgaggggga ggaaatgttg cattgctgtt 5160
tgtaagcttt ttttattatt tttttattat aattattaaa ggcctgactc tttcctctca 5220
tcactgtgag attacagatc tatttgaatt gaatgaaatg taacat tgaa aaaaaaaaaa 5280
aaaaaaaaaa aaaaaaa 5297

```

<210> 271

<211> 389

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(389)

<223> 3' terminal sequence. pou domain, class 2,
transcription factor 2 (POU2F2) gene.

<400> 271

```

cagggaattn nttcatnatg gaaaagaca actgaatgcc ctcaactgaa tgtcttcac 60
ccctcttgcc tgaaatttcc accttcccat aggctgggga gggagtcagt tccagagcag 120
aggagggtga cagggttg ag gagggacttg tgagagctag aacttgga aatggcctag 180
cccacccttc aaaggggaaa agaggggagga acaggggatg aaaagtntc cgcagccttc 240
ccttgaaactc tccctgctg ggggagggag gaggttaaag caagaccccc tgcccagggtg 300
gggagagctg ggggccaggg gagaagggga caaatggtag ggacacattc tgtttgagca 360
caatgctaaa aattctgtac atcctttgg 389

```

<210> 272

<211> 2048

<212> DNA/RNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(2048)

<223> pou domain, class 2, transcription factor 2
(POU2F2) gene.

<400> 272

```

cgtcaacatg agttggggcct ggggcagatg aggctggctg gcggggcggg cagcatggtt 60
cactccagca tgggggctcc agaaataaga atgtctaagc ccctggaggc cgagaagcaa 120
ggctctggact ccccatcaga gcacacagac accgaaagaa atggacca ga cactaatcat 180
cagaaccccc aaaataagac ctccccattc tccgtgtccc caactggccc cagtacaaag 240
atcaaggctg aagacccagc tggcgattca gcccagcag caccctgcc ccctcagccg 300
gcccagcctc atctgcccc aggccaaactc atgttgacgg gcagccagct agctggggac 360
atacagcagc tcctccagct ccagca gctg gtgcttgtgc caggccacca cctccagcca 420
cctgctcagt tcctgctacc gcaggcccag cagagccagc caggcctgct accgacacca 480
aatctatttc agctacctca gcaaaccagc ggagctcttc tgacctcca gcccggggcc 540
gggcttcccc cacagcccc caaatgcttg gagccaccat cccacccga ggagcccagt 600
gatctggagg agctggagca attcgccgc accttcaagc aacgccgat caagctgggc 660
ttcacgcagg gtgatgtggg cctggccatg ggcaagctct acggcaacga cttcagccag 720
acgaccattt cccgcttcga ggccctcaac ctgagcttca agaactgtg caaactcaag 780
cccctcctgg agaagtggct caacgatgca gagactatgt ctgtgg actc aagcctgcc 840
agccccaacc agctgagcag cccagcctg ggtttcgacg gcctgcccgg ccggagacgc 900
aagaagagga ccagcatcga gacaaacgct cgcttcgct tagagaagag ttttctagcg 960
aaccagaagc ctacctcaga ggagatcctg ctgatcgccg agcagctgca catggagaag 1020
gaagtgatcc gcgtctggtt ctg caaccgg cgccagaagg agaaacgcat caaccctgc 1080
agtggggccc ccatgctgcc cagcccaggg aagccggcca gctacagccc ccatatggtc 1140
acacccaagc ggggcgcggg gaccttaccg ttgtccaag cttccagcag tctgagcaca 1200
acagttacta cttatcctc agctgtgggg acgtccacc ccagccggac agctggaggg 12 60
gggtggggcg ggggcggggc tgcgcccccc ctcaattcca tcccctctgt cactcccca 1320
ccccggcca ccaccaacag cacaacccc agccctcaag gcagccactc ggctatcggc 1380
ttgtcaggcc tgaaccccag caggggccct ggctctggt ggaaccctgc ccctaccag 1440
ccttgatggc agcgggaatc tgggtgtggg ggcagcc ggt gcagcccg ggagccctgg 1500
cctggtgacc tcgcccctct tcttgaatca tgctgggctg cccctgctca gcacccgcc 1560
tggtgtgggc ctggtctcag cagcggctgc ggctgtggca gcctccatct ccagcaagtc 1620
tcctggcctc tcctcctcat cctcttcac ctcactctcc tcctcctcca cttgcagcga 1680
gacggcagca cagaccctg gaggtccagg ggggcccag gcagggtcca aacctgagtg 1740
agggccagcc atgcctccc tccattcct ctggtccctg ccttggctcc ttgcctggga 1800
agaggggcag gaggccagtg gtggggacgc agagggctct cagagcagga gtgacaaggg 1860
aggaaagacc aaaaaaaca ccaacaaaa aaaaaaaa aaaaggaaa aaactaacca 1920
acaaaagaga aaacaaaaa taatcacaa agaaaccagc tgcccaaaag gaaccagagg 1980
tgaaaaacaa aaaaaaaa caaaaaaca accaaaaaa aaaaaaacc tctacccct 2040
ctagagcc 2048

```

<210> 273

<211> 472

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(472)

<223> 3' terminal sequence. baculoviral iap
repeat-containing 4 (BIRC4) gene.

<400> 273

```

ttttctatct ttccaccagc atggaaca at tgattccttt ttcacacaaa acaaattatg 60
tgattgggga gattaactct aatctccaca tttatataca gaaagctcca ttgtttaagc 120
ctatctgaaa agaataaaaa atccagatga ttaattcact tacacttaga aattaaatca 180
gtatactatg aatacacatt gtgttcagtt atagtatgat gcttcttatt cttagtctat 240
ggtttcaatt aaataacagt aaaaaaaatg gataatacag ctaataccct gaaaaatcaa 300
gaaattcaaa gatttatatt ccaactaaaa cactgccatg tacatttttt ttctacttg 360
gtagcaaatg ctaatggaat tcaatcctga ttacttaaag tcagttcaca tcacacattc 420
aatcagggta ataagaacaa cataacatgc ctaccataga gttagatta a ga 472

```

<210> 274
<211> 2540
<212> DNA/RNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<220>
<221> misc_feature
<222> (1)..(2540)
<223> baculoviral iap repeat -containing 4 (BIRC4)
gene.

<400> 274
gaaaagggtg acaagtccta ttttcaagag aagatgactt ttaacagttt tgaaggatct 60
aaaacttggt tacctgcaga catcaataag gaagaagaat ttgtagaaga gtttaataga 120
ttaaaaactt ttgctaattt tccaagtggg agtcctgttt cagcatcaac actggcacga 180
gcagggtttc ttatactggg tgaaggagat accgtgcggg gcttt agttg tcatgcagct 240
gtagatagat ggcaatatgg agactcagca gttggaagac acaggaaagt atccccaaat 300
tgcagattta tcaacggcctt ttatcttgaa aatagtgcga cgcagtctac aaattctggt 360
atccagaatg gtcagtacaa agttgaaaac tatctgggaa gcagagatca ttttgcctta 420
gacaggccat ctgagacaca tgc agactat cttttgagaa ctgggcaggt tgtagatata 480
tcagacacca tatacccgag gaacctgcc atgtattgtg aagaagctag attaaagtc 540
tttcagaact ggccagacta tgctcaccta accccaagag agttagcaag tgctggactc 600
tactacacag gtattggtga ccaagtgcag tgcttttgtt gtggtggaaa actgaaaaat 660
tggaacacct gtgatcgtgc ctggtcagaa cacaggcgac actttcctaa ttgcttcttt 720
gttttgggcc ggaatcttaa tattcgaagt gaatctgat ctgtgagttc tgataggaat 780
ttccaaat tccaaatct tccaagaaat ccatccatgg cagattatga agcacggatc 840
tttactttt ggacatggat atactcagtt aacaaggagc agc ttgcaag agctggattt 900
tatgcttttag gtgaagggtga taaagtaaag tgctttcact gtggaggagg gctaactgat 960
tggaagccca gtgaagacc ttgggaacaa catgctaaat ggtatccagg gtgcaaatat 1020
ctgttagaac agaagggaca agaatatata aacaatattc atttaactca ttcacttgag 1080
gagtgtctgg taagaactac tgagaaaaca ccatcactaa ctagaagaat tgatgatacc 1140
atcttccaaa atcctatggg acaagaagct atacgaatgg ggttcagttt caaggacatt 1200
aagaaaataa tggaggaaaa aattcagata tctgggagca actataaato acttgagggt 1260
ctggttcag atctagtga tgctcagaaa gacagtatgc aagatgagtc aagtcagac t 1320
tcattacaga aagagattag tactgaagag cagctaaggc gcctgcaaga ggagaagctt 1380
tgcaaaatct gtatggatag aaatattgct atcgttttt ttccttggg acatctagtc 1440
acttgtaaac aatgtgctga agcagttgac aagtgtccca tgtgctacac agtcattact 1500
ttcaagcaaa aaatttttat gtcttaactc aac tctatag taggcatgtt atgttgttct 1560
tattaccctg attgaatgtg tgatgtgaac tgactttaag taatcaggat tgaattccat 1620
tagcatttgc taccagtag gaaaaaaaat gtacatggca gtgttttagt tggcaatata 1680
atctttgaat ttcttgattt ttcagggtat tagctgtatt atccattttt tttactgtta 1740
tttaattgaa accatagact aagaataaga agcatcatac tataactgaa cacaatgtgt 1800
attcatagta tactgattta atttctaagt gtaagtgaat taatcatctg gattttttat 1860
tcttttcaga taggcttaac aaatggagct ttctgtatat aaatgtggag attagagtta 1920
atctcccaa tcacataatt tgttttgtgt gaaaaaggaa taaattg ttc catgctggtg 1980
gaaagataga gattgttttt agaggttggg tgttgtgttt taggattctg tccattttct 2040
tgtaaaaggga taaacacgga cgtgtgcgaa atatgtttgt aaagtattt gccattgttg 2100
aaagcgtatt taatgataga atactatcga gccaacatgt actgacatgg aaagatgtca 2160
gagatatgtt aagtgtaaaa t gcaagtggc gggacactat gtatagtctg agccagatca 2220
aagtatgtat gttgttaata tgcatagaac gagagatttg gaaagatata caccaaactg 2280
ttaaatgtgg tttctcttcg gggagggggg gattggggga ggggccccag aggggtttta 2340
gaggggcctt ttcacttttc acttttttca ttttgttctg ttcggatttt ttataagtat 2400
gtagaccccg aagggtttta tgggaactaa catcagtaac ctaaccccgc tgactatcct 2460
gtgctcttcc tagggagctg tgttgtttcc caccaccac ccttccctct gaacaaatgc 2520
ctgagtgtcg gggcactttg 2540

181/292

<210> 275
<211> 842
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<220>
<221> misc_feature
<222> (1)..(842)
<223> 3' terminal sequence. death associated
protein 3 (DAP3) gene.

<400> 275
tagaaagata ttttattttt taggaaaaga gccataatta tcttaaa tgt gaaaaaccac 60
atccaataaa ctgatataaa gtttaggaa caagggaata tcttattgtc acgcattcac 120
agtgaacccc attttaatgc aggtccagag ccaactgcag tccgtgccaa tcccataggt 180
acaaggccct ggctcctctt cctgtgtact gcccgacttc ctcattctac tgggtccagc 240
ataaagcaga tgtccactgt ctctct caca tgctgtgatc ttggcttaga ggtaggcaca 300
gtgccgctcc agcagcgagg ggttcgctt acttaggaac agcagctctt tttcccttc 360
ttctgtagga gctntctcat gttgaagcca attgttttcc aaataatact gaatacaact 420
ttcaaattcc tttaggttat agttggaac caggatggga ataaagggaat ccagggcac 480
aaatccttcc ttccacaga actcctgcg cagataggct ttccggggct taaagagaga 540
cccagctctg ctcagagccg acacaatggc gcctccatgc caatcatnct tcatcatttt 600
cctcagttgt gaacaagtgc taattccctc ggggcaatcg ggctttatct tctgttttca 660
gagggttctt cccaangag cattgatgcc accacggcca cctatg ggtg aaacataccc 720
caatgaactt tgctctttag ctctttcagc acaatttcaa actgatctgg tgcgtccctc 780
aaccgtgtta tgccctgtca aaccacttct ccagaagac tccctttctt aggtttttct 840
ct 842

<210> 276
<211> 1608
<212> DNA/RNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<220>
<221> misc_feature
<222> (1)..(1608)
<223> death associated protein 3 (DAP3) gene.

<400> 276
gaattccgcc ggcccaggc agcgtgtgtc ggtcgcctag gctggagaac tagtcct cga 60
ctcacgtgca aggatgatgc tgaaaggaat aacaaggctt atctctagga tccataagtt 120
ggaccctggg cgttttttac acatggggac ccaggctcgc caaagcattg ctgctcacct 180
agataaccag gttccagttg agagtccgag agctatttcc cgcaccaatg agaatgacct 240
ggccaagcat ggggatcagc acgagggtca gcacta caac atctccccc aggatttga 300
gactgtattt ccccatggcc ttctctctcg ctttgtgatg cagggtgaaga cattcagtga 360
agcttgctg atggttaagga aaccagccct agaacttctg cattacctga aaaacaccag 420
tttgcttat ccagctatac gatatttct gtatggagag aagggaacag gaaaaaccct 480
aagtctttgc catgttattc atttctgtgc aaaacaggac tggctgatac tacatattcc 540
agatgctcat ctttgggtga aaaattgtcg ggatcttctg cagtccagct acaacaaaca 600
gcgctttgat caacctttag aggtttcaac ctggctgaag aatttcaaaa ctacaaatga 660
gcgcttctcg aaccagataa aagttcaaga gaagtatgtc tgaataaga gagaaa gcac 720
tgagaaaggg agtctcttg gagaaaggt tgaacagggc ataacacggg tgaggaacgc 780
cacagatgca gttggaattg tgctgaaaga gctaaagagg caaagttctt tgggtatgtt 840
tcacctcta gtggccgtgg atggaatcaa tgctctttgg ggaagaacca ctctgaaaag 900

182/292

```

agaagataaa agccccgattg cccccgagga atta gcactt gttcacaact tgaggaaaat 960
gatgaaaaat gattggcatg gaggcgccat tgtgtcggct ttgagccaga ctgggtctct 1020
ctttaagccc cggaagcct atctgccccca ggagttgctg ggaaaggaag gatttgatgc 1080
cctggatccc tttattocca tcctggtttc caactataac ccaaaggaat ttgaaagttg 1140
tattcagtat tatttggaat acaattggct tcaacatgag aaagctccta cagaagaagg 1200
gaaaaaagag ctgctgttcc taagtaacgc gaaccctcgc ctgctggagc ggcactgtgc 1260
ctacctctaa gccaaagatca cagcatgtga ggaagacagt ggacatctgc tttatgctgg 1320
accagtaag atgaggaagt cgggcagtac acaggaagag gagccaggc c cttgtaccta 1380
tgggattgga caggactgca gttggctctg gacctgcatt aaaatgggtt tcactgtgaa 1440
tgcgtgacaa taagatatcc ccttgttcct aaaactttat atcagtttat tggatgtggt 1500
ttttcacatt taagataatt atggctcttt tcctaaaaaa taaaatatct ttctaaaaaa 1560
aaaaaaaaaa aaaaaaaaaa aaa aaaaaaa aaaaaaaaaa aaaaaaaa 1608

```

<210> 277

<211> 361

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(361)

<223> 5' terminal sequence. gonadotropin -releasing hormone 1 (leutinizng -releasing hormone). (GNRH1) gene.

<400> 277

```

ttagattgca tgetattgta tgtctacagg gcatttgaca gcccaggnt aaatccagg 60
gggacggtat ctaatgatgt cctgtccttc actgtccttg ccacaccag ccacagagat 120
ccaggctttg gggactocca cagcttatcg accag tgttt gatttagttt ttagcctctt 180
tcccatcaaa tgaaaattaa cttggagaca catttcatta gaaaattaga ggcccccttg 240
gctaggaagg catctggtct ggggactaac tactttgaac agtgttgagt cctctctccc 300
acagatgggt cagccagcag taatgctnag ggaagactga agggatcaaa taganaaatg 360
t 361

```

<210> 278

<211> 470

<212> DNA/RNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(470)

<223> gonadotropin-releasing hormone 1 (leutinizng -releasing hormone) (GNRH1) gene.

<400> 278

```

gggatctttt tggctctctg cctctaaaca gaatgaagcc aattcaaaaa ctctagctg 60
gccttattct actgacttgg tgcgtggaag gctgtccag ccagcactgg tcctatggac 120
tgcgccctgg aggaagaga gatgccgaaa atttgattga ttctttcca a gagatagtca 180
aagaggttgg tcaactggca gaaacccaac gcttcgaatg caccacgcac cagccacgtt 240
ctccccctcg agacctgaaa ggagctctgg aaagtctgat tgaagaggaa actgggcaga 300
agaagattta aatccattgg gccagaagga atgaccatta ctaacatgac ttaagtataa 360
ttctgacatt gaaaatttat aacccat taa atacctgtaa atggtatgaa tttcagaaat 420

```

ccttacacca agttgcacat attccataat aaagtgtgtg gttgtgaatg

470

<210> 279

<211> 320

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(320)

<223> 3' terminal sequence. interleukin 2
receptor, gamma (severe combined immunodeficiency)
(IL2RG) gene.

<400> 279

ntctaaatat caacagaaaac tttatttctc atcggttcag gaacaatcgg agggtagatg 60
gaaagaggaa gggagggaaa gagggaggga ggaagaatcc tgcgaaaagg aagggccaga 120
ctgaggggaga agaaaaacat gttcggggca aaagggtaat tctcaagtgg ggaatgccaa 180
atgaaggggt gcttacatgg gggcacaaaa ttccaaatca gccacagtgg ggtgaggtga 240
gtatgagacg caggtgggggt tgaatgaagg aaagttagta ccncttaggg ctacaggacc 300
ctgggggttct tctttcag ag 320

<210> 280

<211> 407

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(407)

<223> 5' terminal sequence. interleukin 2
receptor, gamma (severe combined immunodeficiency)
(IL2RG) gene.

<400> 280

attcggcaca gggaactttt cggcctggag tgggtgtgtt aagggactgg ctgagagtct 60
gcagccagac tacagtgaac gactctgcct cgtcagttag attccccaa aaggaggggc 120
ccttggggag gggcctgggc tncctcatgc aaccagcata gccctactg ggcccccca 180
tggtacacc taaagcctga aacctgaacc ccantactct gacagaagaa cccaggggtc 240
ctgtagccct aagtgggtact aactttcctt cattcaaccc acctgcgtct tatactcanc 300
tcanccact gttggctgat tttggatttt tgtggcccca tgtaaggaac cctttaattt 360
ggcattnccc aattgagaat taaccttttt gnccgaaca tgttttt 407

<210> 281

<211> 1451

<212> DNA/RNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature
<222> (1)..(1451)
<223> interleukin 2 receptor, gamma (severe
combined immunodeficiency) (IL2RG) gene.

<400> 281
gaagagcaag cgccatgttg aagccatcat taccattcac atccctctta ttccctgcagc 60
tgccctgct gggagtggg ctgaacacga caattctgac gcccaatggg aatgaagaca 120
ccacagctga ttcttctctg accactatgc ccactgactc cc tcaagtgt tccactctgc 180
ccctcccaga gggtcagtgt ttgtgttca atgtcgagta catgaattgc acttgaaca 240
gcagctctga gcccagcct accaacctca ctctgcatta ttggtacaag aactcggata 300
atgataaagt ccagaagtgc agccactatc tattctctga agaaatcaact tctggctgtc 360
agttgcaaaa aaaggagatc cacctctacc aaacatttgt tgttcagctc caggaccac 420
gggaacccag gagacaggcc acacagatgc taaaactgca gaatctggtg atccctggg 480
ctccagagaa cctaacactt cacaaactga gtgaatcca gctagaactg aactggaaca 540
acagattctt gaaccactgt ttggagcact tgggtcagta cgggactgac tgggaccaca 60 0
gctggactga acaatcagtg gattatagac ataagttctc cttgcctagt gtggatggg 660
agaaacgcta cacgtttcgt gtccggagcc gctttaacc cctctgtgga agtgcctcagc 720
attggagtga atggagccac ccaatccact gggggagcaa tacttcaaaa gagaatcctt 780
tcctgtttgc attggaagcc gtggttatct ctgttggtc catgggattg attatcagcc 840
ttctctgtgt gtatttcttg ctggaacgga cgtgccccg aattcccacc ctgaagaacc 900
tagaggatct tgttactgaa taccacggga acttttcggc ctggagtggg gtgtctaagg 960
gactggctga gagtctgcag ccagactaca gtgaacgact ctgcctcgtc agtgagattc 1020
ccccaaaagg agggccc tt ggggaggggc ctggggcctc cccatgcaac cagcatagcc 1080
cctactgggc cccccatgt tacaccctaa agcctgaaac ctgaaccca atcctctgac 1140
agaagaaccc cagggtcctg tagccctaag tggtaactaac ttctctcat tcaaccacc 1200
tgcgctctcat actcaacctca cccactgtg gctgatttg aattttgtgc cccatg taa 1260
gcaccccttc atttggcatt cccacttga gaattaccct ttgccccga acatgtttt 1320
cttctccctc agtctggccc ttcttttctg caggattctt cctccctccc tctttccctc 1380
ccttctctt tccaactacc ctccgattgt toctgaaccg atgagaaata aagtttctgt 1440
tgataatcat c 1451

<210> 282
<211> 317
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<220>
<221> misc_feature
<222> (1)..(317)
<223> 3' terminal sequence. death associated
protein 3 (DAP3) gene.

<400> 282
atctaacaca acactttaga aagatatattt attttttagg aaaagagcca taattatctt 60
aaatgtgaaa aaccacatcc aataaactga tataaagttt taggnacaag ggaatatctt 120
attgtcacgc attcacagt aaacccattt taatgcaggt ccagagccaa ctgcagtcct 180
gtccaatccc ataggttaca agggcctggg ctctcttcc tgtgtactgc ccgacttcc 240
catcttactg gggccagca taaagcagga tgcactgt ctctctcaca tgcgtganc 300
ttggncttag gagtag 317

<210> 283
<211> 358
<212> DNA
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(358)

<223> 5' terminal sequence. death associated protein 3 (DAP3) gene.

<400> 283

aggacgggcg ctttggagcc ggccccaggc agcgtgtgtc ggtcgccctag tctggagaac 60
tagtcctcga ct cactgtga aggatgatgc tgaaaggaat aacaaggctt atctctagga 120
tccataagtt ggaccttggg cgttttttac acatggggac ccaggctcgn caaagcattg 180
ctgctcacct agataaccga ggttcccagt tgagagtccc gagagctatt ttcccgcaac 240
caatgagaat gaccccggcc caagcatggg ggatcancaa ggagggtcaa gcaa tnacaa 300
canttttccc cccaggattt tgggagaatt gtaattttcc ccatnggcct ttncttcc 358

<210> 284

<211> 416

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(416)

<223> 5' terminal sequence. ptk2 protein tyrosine kinase 2 (PTK2) gene.

<400> 284

gcacagaagc tattgaactc tgacctgggt gagctcatca acaagatgaa actggcccag 60
cagtatgtca tgaccagcct ccagcaagag tacaaaaagc aaatgctgac tgctgctcac 120
gccctggctg tggatgcaa aaacttactc gatgtcattg a ccaagcaag actgaaaatg 180
cttgggcaga cgagaccaca ctgagcctcc cctaggagca cgtcttgcta ccctcttttg 240
aagatgttct ctagccttcc accagcagcg agganttaac cctgtgtcct cagtncgcca 300
gcacttacag ctccaacttt tttgaatgac catctggttg aaaaatcttt ctcatataag 360
tttnaaccac atttggattt ggggttcatt ttttgtttg ttttttttc aatcat 416

<210> 285

<211> 3052

<212> DNA/RNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(3052)

<223> ptk2 protein tyrosine kinase 2 (PTK2) gene.

<400> 285

ccggtgtgaa ggccatgagt gattactggg ttgttggaaa gaagtctaac tatgaagtat 60
tagaaaaaga ttttggttta aagcgatttt ttcttaagag ttactggat tctgtcaagg 120
ccaaaacact aagaaaactg atccaacaaa catttagaca atttgccaac cttaatagag 180
aagaaagtat tctgaaattc tttgagat cc tgtctccagt ctacagattt gataaggaa 240
gcttcaagtg tgctcttggg tcaagctgga ttatttcagt ggaactggca atcggccag 300

186/292

```

aagaaggaat cagttaccta acggacaagg gctgcaatcc cacacatctt gctgacttca 360
ctcaagtgcga aaccattcag tattcaaaaca gtgaagacaa ggacagaaaa ggaatgctac 420
aactaaaaat agcaggtgca cccgagcctc tgacagtgcg ggcaccatcc ctaaccattg 480
cggagaatat ggctgaccta atagatgggt actgccggct ggtgaatgga acctcgagct 540
catttatcat cagacctcag aaagaagggt aacgggcttt gccatcaata ccaaagttgg 600
ccaacagcga aaagcaaggc atgcggaacac acgccgtctc tgtgtcag aa acagatgatt 660
atgtcgagat tatagatgaa gaagatactt acaccatgcc ctcaaccagg gattatgaga 720
ttcaaaagaga aagaatagaa cttggacgat gtattggaga aggccaattt ggagatgtac 780
atcaaggcat ttatatgagt ccagagaatc cagctttggc ggttgcaatt aaaacatgta 840
aaaactgtac ttcggaacgc gtgaga gaga aatttcttca agaagcctgc cattacacat 900
ctttgcactg gaattgggtgc agatatataa gtgacctaag tgttgatgcc tgcccagacc 960
ccaggaatgc agagttaaca atgcgctcag ttgaccatcc tcatattgtg aagctgattg 1020
gagtcacac agagaatcct gtctggataa tcatggagct gtgcacactt ggagagctga 1080
ggtcattttt gcaagtaagg aaatacagtt tggatctagc atctttgatc ctgtatgcct 1140
atcagcttag tacagctctt gcatacttag agagcaaaag atttgtacac agggacattg 1200
ctgctcgga tttctggtg tctcaaatg atttgttaa attaggagac tttggattat 1260
ccgatatat ggaagatagt acttactaca aagcttccaa a ggaatttg cctattaaat 1320
ggatggctcc agagtcaatc aattttcgac gttttacctc agctagtgc gtatggatgt 1380
ttggtgtgtg tatgtgggag atactgatgc atggtgtgaa gccttttcaa ggagtgaaga 1440
acaatgatgt aatcggtcga attgaaaatg gggaaagatt accaatgcct ccaaattgtc 1500
ctctaccct ctacag cctt atgacgaaat gctgggccta tgacccagc agggggccca 1560
ggtttactga acttaaagct cagctcagca caatcctgga ggaagagaag gctcagcaag 1620
aagagcgcat aggatggag tccagaagac aggccacagt gtcctgggac tccggagggt 1680
ctgtgaagc accgccaag cccagcagac cgggttatcc cagtccagg tccag cgaag 1740
gattttatcc cagcccacag cacatggtac aaaccaatca ttaccaggtt tctggctacc 1800
ctggttcaca tggaaacaca gccatggctg gcagcatcta tccaggctag gcactcttt 1860
tggacaaaac agattcatgg aatcatagat ctcaggagat agcaatgtgg cagcccaatg 1920
tggaggactc tacagtattg gacctgcgag ggattgggca agtgttgcca acccatctga 1980
tgaagagcg tctaattcga cagcaacagg aaatggaaga agatcagcgc tggctggaaa 2040
aagaggaaa atttctgatt ggaaaccaac atatatatca gcctgtgggt aaaccagatc 2100
ctgcagctcc accaaagaaa ccgcctcgcc ctggagctcc cggctcatctg ggaagccttg 2160
ccagcctcag cagcctgct gacagctaca acgaggggtg caagcttcag cccaggaaa 2220
tcagccccc tctactgcc aacctggacc ggtcgaatga taagggtgac gagaatgtga 2280
cgggcctggg gaaagctgtc atcgagatgt ccagtaaaat ccagccagcc ccaccagagg 2340
agtatgtccc tatgggtgaag gaagtcggct tggccctgag gac attattg gccactgtgg 2400
atgagaccat tcccctccta ccagccagca cccaccgaga gattgagatg gcacagaagc 2460
tattgaactc tgacctgggt gagctcatca acaagatgaa actggcccag cagtatgtca 2520
tgaccagcct ccagcaagag taaaaaagc aaatgctgac tgccgctcac gccctggctg 2580
tggatgccaa aaacttac tc gatgtcattg accaagcaag actgaaaatg cttgggcaga 2640
cgagaccaca ctgagcctcc cctaggagca cgtcttgcta ccctcttttg aagatgttct 2700
ctagccttcc accagcagcg aggaattaac cctgtgtcct cagtcgccag cactcacagc 2760
tcaaactttt ttgaatgacc atctggttga aaatcttct tcatataagt ttaacca cac 2820
tttgatttg gttcattttt tgttttgtt ttttcaatca tgatattcag aaaaatccag 2880
gatccaaaat gtggcgtttt tctaagaatg aaaattatat gtaagctttt aagcatcatg 2940
aagaacaatt tatgttcaca ttaagatacg ttctaaagg ggaatggcaa ggggtgacat 3000
cttaattcct aaactacctt agctgcatag t ggaagagga gagccggaat tc 3052

```

<210> 286

<211> 377

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(377)

<223> 3' terminal sequence. cyclin-dependent
kinase 4 (CDK4) gene.

<400> 286

gnataaaaaa ggaccccaaa tataaaggna gggaaaggga caagagggaa catacccctt 60
agtgtagaga aatgggaagg agaaggagaa gcctcaaaag gaggtgggag gggaatgtca 120
ttaaggcagc aaagtaatct ctgtagaaag atggaggagg accctocata gcctcagaga 180
taaaggcaaa gattgccctc tc agtgtcca gaagggaat gggcagcttt tcttcctcc 240
atgggcagcc actccattgc tcactccggn ttaccttcat ccttatgtag gataagagtn 300
ctgcagagct tcgaaaggcg agagattcgc ttgtgtgggg ttaaaagtca gcatttccan 360
cagcagcttt tgcttcc 377

<210> 287

<211> 363

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(363)

<223> 5' terminal sequence. cyclin -dependent
kinase 4 (CDK4) gene.

<400> 287

catatctgga caaggcaccc ccaccaggct tgcagccgaa acgatcaagg atctgatgcg 60
ccagtttcta agaggcctag atttccttca tgccaattgc atcggtcacc gagatctgaa 120
gccagagaac attctggtga caagtggtna aacagtcaag ctggctgact ttngcctggc 180
cagaatctac agctaccaga tggcacttac acccgtggtt gttacactct ggtacc gagg 240
tcccgaagtt cttctngcag tccacatatg caacacctgt gggacatgtg ggagtgttgg 300
ctgtatcttt gcagagatgt ttcgtcgaaa ncctctcttt ctgtggnaaa ctctgtaagg 360
ccg 363

<210> 288

<211> 1443

<212> DNA/RNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(1443)

<223> cyclin-dependent kinase 4 (CDK4) gene.

<400> 288

gccctcccag tttccgcgcg cctctttggc agctggtcac atggtgaggg tgggggtgag 60
ggggcctctc tagcttgccg cctgtgtcta tggctgggcc ctctgcgtcc agctgctccg 120
gaccgagctc ggggtgatgg ggccgtagga accggtccg gggccccgat aacggggccg 180
ccccacagca ccccgggctg gcgtgagggt ctcccttgat ctgagaatgg ctacctctcg 240
atatgagcca gtggctgaaa ttgggtgcgg tgcctatggg acagtgt aca agggccgtga 300
tcccacaggt ggccactttg tggccctcaa gagtgtgaga gtccccaatg gaggaggagg 360
tggaggaggc cttcccatca gcacagttcg tgagggtgct ttactgaggc gactggaggc 420
ttttgagcat cccaatggtg tccggctgat ggacgtctgt gccacatccc gaactgaccg 480
ggagatcaag gtaaccctgg tgttt gagca tgtagaccag gacctaaagg catatctgga 540
caaggcaccc ccaccaggct tgccagccga aacgatcaag gatctgatgc gccagtttct 600
aagaggccta gatttccttc atgccaattg catcgttcac cgagatctga agccagagaa 660
cattctggtg acaagtgggt gaacagtcaa gctggctgac tttggcctgg ccagaatcta 720

188/292

```

cagctaccag atggcactta cacccggtgt gtgtacactc tggtagcgag ctcccgaagt 780
tcttctgcag tccacatatg caacacctgt ggacatgtgg agtggtggct gtatctttgc 840
agagatgttt cgtcgaaagc ctctcttctg tggaaactct gaagccgacc agttgggcaa 900
aatctttgac ctgattgggc tgcctccaga ggatgactgg cctcg agatg tatccctgcc 960
ccgtggagcc tttcccccca gagggccccg cccagtgcag tgggtggtac ctgagatgga 1020
ggagtcggga gcacagctgc tgctggaaat gctgactttt aaccacaca agcgaatctc 1080
tgcttttoga gctctgcagc actcttatct acataaggat gaaggtaatc cggagtgcgc 1140
aatggagtggt ctgccatgga aggaagaaaa gctgccattt cccttctgga cactgagagg 1200
gcaatctttg cctttatctc tgaggctatg gagggtcctc ctccatcttt ctacagagat 1260
tactttgtcg ccttaatgac attccccctc cacctctcct tttgaggctt ctcttctcc 1320
ttccatttc tctacactaa ggggtatgtt ccctcttctc cctttcccta cctttatatt 1380
tggggtcctt ttttatacag gaaaaacaaa accaaaagaa awaatggccc tttttttttt 1440
ttt 1443

```

<210> 289

<211> 394

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(394)

<223> 3' terminal sequence. basic transcription
factor 3 (BTF3) gene.

<400> 289

```

ccgcggtgtg tgcgcctaan ctgagngngn ccacccgaga ccccttgagc accaaccccta 60
gtcccccgcg cggccctna ttcgctccga caagatgaaa gaaaca atca tgaaccaggg 120
aaaactcgcc aaactgcagg cacaagtgcg cattggtggg aaaggaactg ctgcagaaaa 180
gaagaagggtg gttcatagaa cagccacagc agatgacaaa aaacttcagt tctccttaaa 240
gangttagggt gtaaacataa tctctggnat tgaagagggt aatatgttta caaacagggt 300
aacagtgatc cactttaaca acc tnaagt tcagggcatc tctgggcagc ggacactttc 360
accattacng gccttgctga gncaagcag ctgg 394

```

<210> 290

<211> 477

<212> DNA/RNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(477)

<223> basic transcription factor 3 (BTF3) gene.

<400> 290

```

atgcgacgga caggcgcacc cgctcaggct gactctcggg ggcgaggctg agccaggggc 60
ggctgccctg gggcgaggc gacgctgtct caacctccac ctgcggcgag aaccgagga 120
gaggagcctc agatgaaaga aacaatcatg aaccag gaaa aactcgccaa actgcaggca 180
caagtgcgca ttggtgggaa agtgaatatg tttaaaacc aaggaacagt gatccacttt 240
aacaacccta agtttcaggc atctctggca ggaacactt tcaccattac aggccatgct 300
gagacaaaag agctgcagaa aatgctaccc agcatcttaa accagcttgg tgcggatagt 360
ctgactagtt taaggagact ggccgaagct ctgccaaac aatctgtgga tggaaaagca 420
ccacttgcta ctggagagga tgatgatgat gaagttccag gaggttcca agaata 477

```

<210> 291
<211> 388
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<220>
<221> misc_feature
<222> (1)..(388)
<223> 3' terminal sequence. colony stimulating
factor 1 receptor, formerly mcdonough feline
sarcoma viral (v-fms) oncogene homolog (CSF1R)
gene.

<400> 291
tgctgttagt ttaatgtgga cagagacatc ccacggcgtg actgttagt t aggatgagtc 60
agcttggggg agtttgtgct tcctgcttgg ngtgggccagc cacatgccaa ggtcccctgc 120
cttctagccc agaatgacgg gactgggcag aacacccccca acttttagct gccacttggc 180
tcattacagc agtaccagta tgggggtggg aggggtgagg cnttggagtg aaggcggcgt 240
atagggcaga gactaagagg gtcctgtg ag attcttagag gagccatcct gntccaaggg 300
gcctgagctg agtntgggtc tgtgagcatc tgctgctcct ctcagagagg ggagatctca 360
ctctctgcc a gtcgtgctag ccccaaag 388

<210> 292
<211> 3992
<212> DNA/RNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<220>
<221> misc_feature
<222> (1)..(3992)
<223> colony stimulating factor 1 receptor,
formerly mcdonough feline sarcoma viral (v -fms)
oncogene homolog (CSF1R) gene.

<400> 292
ggcttcagga agggcagaca gagtgtccaa aagcgtgaga gcacgaagtg aggagaaggt 60
ggagaagaga gaagaggaag aggaagagga agagaggaag cggaggggaac tgcggccagg 120
ctaaaagggg aagaagagga tcagcccaag gaggaggaag aggaaaacaa gacaaacagc 180
cagtgcagag gagaggaacg tgtgtccagt gtcccgatcc ctgaggagct agtagctgag 24 0
agctctgtgc cctgggcacc ttgcagccct gcacctgcct gccacttccc caccgaggcc 300
atgggcccag gagttctgct gtcctgtctg gtggccacag cttggcatgg tcagggaatc 360
ccagtgatag agcccagtggt ccccgagctg gtcgtgaagc caggagcaac ggtgaccttg 420
cgatgtgtgg gcaatggcag cgtggaatgg gatggccccg catcacctca ctggaccctg 480
tactctgatg gtcacagcag catcctcagc accaacaacg ctaccttcca aaacacgggg 540
acctatcgct gcactgagcc tggagacccc ctgggaggca gcgcgcgcat ccacctctat 600
gtcaaagacc ctgcccggcc ctggaacgtg ctagcacagg aggtgggtcgt gttcgaggac 660
caggacgcac tactgccct g tctgctcaca gaccgggtgc tggaagcagg cgtctcgctg 720
gtgcgtgtgc gtggccggcc cctcatgcgc cacaccaact actccttctc gccctggcat 780
ggcttcacca tccacagggc caagttcatt cagagccagg actatcaatg cagtgccttg 840
atgggtggca ggaaggtgat gtccatcagc atccggctga aagtgcagaa agtcatccca 900
gggccccag ccttgacact ggtgcctgca gagctggtgc ggattcgagg ggaggctgcc 960
cagatcgtgt gtcagccag cagcgttgat gttactttg atgtcttctt ccaacacaac 1020

190/292

```

aacactaagc tcgcaatccc tcaacaatct gactttcata ataaccgtta ccaaaaagtc 1080
ctgaccctca acctcgatca agtagatttc caacatg ccg gcaactactc ctgcgtggcc 1140
agcaacgtgc agggcaagca ctccacctcc atgttcttcc gggtagtaga gaggctctac 1200
ttgaacttga gctctgagca gaacctcacc caggaggtga ccgtggggga ggggctcaac 1260
ctcaaagtca tggtaggagg ctacccaggc ctgcaagggt ttaactggac ctacctggga 1320
cccttttctg accaccagcc tgagcccaag cttgctaattg ctaccacca ggacacatac 1380
aggcacacct tcacctctct tctgccccgc ctgaagccct ctgaggettg ccgctactcc 1440
ttcctggcca gaaacccagg aggtctggaga gctctgacgt ttgagctcac ccttcgatac 1500
ccccagagg taagcgtcat atggacattc atcaacggct ctggcacccct tttgtgtgct 1560
gcctctgggt acccccagcc caacgtgaca tggctgcagt gcagtggcca cactgatagg 1620
tgtgatgagg cccaagtgtc gcaggtctgg gatgacccat accctgaggt cctgagccag 1680
gagcccttcc acaaggtgac ggtgcagagc ctgctgactg ttgagacctt agagcacaac 1740
caaacctacg agtgcagggc ccaca acagc gtggggagtg gctcctgggc cttcataccc 1800
atctctgcag gagccacac gcacccccgc gatgagttcc tcttcacacc agtgggtggc 1860
gcctgcagt ccacatggc cttgctgctg ctgctgctcc tgctgctatt gtacaagtat 1920
aagcagaagc ccaagtacca ggtccgctgg aagatcatcg agagctatga gggcaacagt 1980
tatactttca tcgacccacc gcagctgcct tacaacgaga agtgggaggt ccccggaac 2040
aacctgcagt ttggaagac cctcggagct ggagcctttg ggaaggtggg ggaggccacg 2100
gcctttggtc tgggcaagga gtagtctgtc ctgaaggtgg ctgtgaagat gctgaagtcc 2160
acggcccatg ctgatgagaa ggaggccctc atgtccgag c tgaagatcat gagccacctg 2220
ggccagcacg agaacatcgt caacctcttg ggagcctgta cccatggagg ccctgtactg 2280
gtcatcacgg agtactgttg ctatggcgac ctgtcaact tcttgcaag gaaggctgag 2340
gccatgctgg gacccagcct gagccccggc caggaccccg agggaggcgt cgactataag 2400
aacatccacc tcgagaagaa atatgtccgc agggacagtg gcttctccag ccagggtgtg 2460
gacacctatg tggagatgag gcctgtctcc acttcttcaa atgactcctt ctctgagcaa 2520
gacctggaca aggaggtagg acggccctg gagctccggg acctgttca cttctccagc 2580
caagtagccc agggcatggc cttctctgct tccaagaatt gcacccaccg gg acgtggca 2640
gcgcgtaacg tgctgttgac caatggatc gtggccaaga ttggggactt cgggctggct 2700
agggacatca tgaatgactc caactacatt gtcaaggcca atgcccgcct gcctgtgaag 2760
tggatggccc cagagagcat ctttgactgt gtctacacgg ttcagagcga cgtctggtcc 2820
tatggcatcc tctctggga gatcttc tca cttgggctga atccctacc tgccatcctg 2880
gtgaacagca agttctataa actggtgaag gatggatacc aaatggcca gcctgcattt 2940
gccccaaaga atatatagc catcatgcag gcctgctggg ccttgagcc caccacaga 3000
cccaccttcc agcagatctg ctcttctctt caggagcagg cccaagagga caggagagag 3060
cgggactata ccaatctgcc gagcagcagc agaagcgggt gcagcggcag cagcagcagt 3120
gagctggagg aggagagctc tagtgagcac ctgacctgct gcgagcaagg ggatatcgcc 3180
cagcccttgc tcgagcccaa caactatcag ttctgtgag gagttgacga caggagtagc 3240
cactctcccc tctccaaaac ttcaactcct ccatggatgg ggcgacacgg ggagaacata 3300
caaactctgc cttcggtcat ttcaactcaac agctcggccc agctctgaaa cttgggaagg 3360
tgagggatcc aggggaggtc agaggatccc acttctgag catgggcat cactgccagt 3420
caggggctgg gggctgagcc ctaccccccc gcctccccta ctgttctcat ggtgttggcc 3480
tcgtgtttgc tatgc caact agtagaacct tctttcctaa tccccttacc ttcattgaaa 3540
tgactgact ttatgcctat gaagtcccca ggagctacac tgatactgag aaaaccaggc 3600
tctttggggc tagacagact ggcagagagt gagatctccc tctctgagag gagcagcaga 3660
tgctcacaga ccacactcag ctacggcccc ttggagcagg atggctcctc taag aatctc 3720
acaggacctc ttagtctctg ccctatacgc cgccttact ccacagcctc acccctccca 3780
ccccatact ggtactgctg taatgagcca agtggcagct aaaagttggg ggtgttctgc 3840
ccagtcccgt cattctgggc tagaaggcag gggaccttgg cattggctgg ccacaccaag 3900
caggaagcac aaactcccc aagctgact c atcctaacta acagtcacgc cgtgggatgt 3960
ctctgtccac attaaactaa cagcattaat gc 3992

```

<210> 293

<211> 356

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: primer

<220>

<221> misc_feature
<222> (1)..(356)
<223> 3' terminal sequence. friend leukemia virus
integration 1 (FLI1) gene.

<400> 293
tttatttagt caaattattt tacaacatgg ncttctttga cagttgtcag cttaacactt 60
aatatagtta aaaaagtcaa caattacctg caaaattata tataatntnaa tgtctaaaaa 120
tatgtngctt atatatagca ggaaaatccc tctctccac aagggaagt ttcgttggtt 180
tncccagagc tgtgattatn gcagtactgt tacacgcatt tccaaagcat taaagancta 240
aatgggatta tctttncctt gcttgtgtat gcctgtnaaa taactgtacc agtggctttg 300
ctttctcata ggtcagtgac ttaaacagcc ctgtttcctt ttcggtata g ggcatt 356

<210> 294
<211> 465
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<220>
<221> misc_feature
<222> (1)..(465)
<223> 5' terminal sequence. friend leukemia virus
integration 1 (FLI1) gene.

<400> 294
gaccaaagca gtttcttgtc aatacacggg gttcagtatg acacagaatc atggacttaa 60
cccgctcatgt tctggtttga gatttagtga caaatagagg tgggaagctt ataactaat 120
tttaggagga ccaaattcag tggatggcaa ctggaacatt gattgtaagg ccagtgaagt 180
tttcacccaa ctggaatttg atggaagaa ggtt tgtgtg tttaagacgc caagggcatt 240
gcagaatccc tctcagtgga cagtatgcac tcagctgacc actctctcta gccaatagtc 300
aagatatgga actaaggaaa ttttaatgcc aaattacata cattcctgaa agacggggga 360
attaaattna ctaattttnt tttttttttt ttaaattgatn gacagtggnt ccccggaact 420
tgggaaangt tgtaggggnt ttctaaaccc aagncgattc gcant 465

<210> 295
<211> 2957
<212> DNA/RNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<220>
<221> misc_feature
<222> (1)..(2957)
<223> friend leukemia virus integrati on 1 (FLI1)
gene.

<400> 295
gaattcccaa acgtgcacag gggagtgagg gcagggcgct cgcagggggc acgcagggag 60
ggcccagggc gccagggagg ccgcgccggg ctaatccgaa ggggctgcga ggtcaggctg 120
taaccgggtc aatgtgtgga atattggggg gctcggctgc agacttggcc aaatggacgg 180
gactattaag gaggctctgt cggtggtgag cgacgaccag tccctcttg actcagcgta 240
cggagcggca gccatctcc ccaaggccga catgactgcc tcggggagtc ctgactacgg 300
gcagcccccac aagatcaacc ccctcccacc acagcaggag tggatcaatc agccagttag 360
ggtcaacgctc aagcgggagt atgaccacat gaatggatcc agggagtctc c ggtggactg 420

192/292

```

cagcgttagc aaatgcagca agctgggtggg cggaggcgag tccaaccca tgaactacaa 480
cagctatatg gacgagaaga atggccccc tctcccaac atgaccacca acgagaggag 540
agtcacgtgc cccgcagacc ccacactgtg gacacaggag catgtgaggc aatggctgga 600
gtggggccata aaggagtaca gcttgatgga gatcgacaca tcctttttcc agaacatgga 660
tggcaaggaa ctgtgtaaaa tgaacaagga ggacttcctc cgcgccacca ccctctacaa 720
cacggaagtg ctgtgtgcac acctcagtta cctcaggga agttcactgc tggcctataa 780
tacaacctcc cacaccgacc aatcctcacg attgagtgtc aaagaagacc cttcttatga 840
cctcgtcaga agaggagctt ggggcaataa catgaattct ggctcaaca aaagtctctc 900
ccttggaggg gcacaaacga tcagtaagaa tacagagcaa cggccccagc cagatccgta 960
tcagatcctg ggcccgacca gcagtgcct agccaacct ggaagcgggc agatccagct 1020
gtggcaattc ctcttgagc tgctctccga cagcgccaac gccagctgt a tcacctgga 1080
ggggaccaac ggggagttca aaatgacgga cccgatgag gtggccaggc gctggggcga 1140
gcggaagc aagccaaca tgaattacga caagctgagc cgggccctcc gttattacta 1200
tgataaaaac attatgacca aagtgcacgg caaaagatat gcttacaat ttgacttcca 1260
cggcattgac caggctctgc agc cacatcc gaccgagtcg tccatgtaca agtacccttc 1320
tgacatctcc tacatgcctt cctaccatgc ccaccagcag aaggtgaact ttgtccctcc 1380
ccatccatcc tccatgcctg tcaactctcc cagcttcttt ggagcgcgcat cacaatactg 1440
gacctcccc acggggggaa tctaccccaa cccaacgtc ccccgccatc ctaacaccca 15 00
cgtgccttca cacttaggca gctactacta gaagcttctt ctagtgaag cccatcctgc 1560
acacttactg gatgcttttg actcaacagg acatatgtgg ccttgaaggg aagacaaaac 1620
tgatgttct tcttgttg atagaacctt tgtatttgtt ctttaaaaac atttttttta 1680
atgttggtaa ctttgcctc ctctacctga acaaaga gat gaataattcc atgggccagt 1740
atgccagttt gaattctcag tctcctagca tcttgtgagt tgcataatga gattactgga 1800
atggttaagt catggttctg agaaagaagc tgtacgtttt ctttatgttt ttatgaccaa 1860
agcagtttct tgtcaatata cggggttcag tatgacacag aatcatggac ttaaccogtc 1920
atgttctggt ttgagattta gtgacaaata gagtgaggaa gcttataatc taattttagg 1980
aggaccaa atcagcggatg gcaactggaa cattgattgt aaggccagtg aagttttcac 2040
ccaactggaa ttgatggaa agaaggtttg tgtgtttaag acgccaaggg cattgcagaa 2100
tccctctcag tggacagtat gcactcagct gaccactctc tctagaaata gtcaagatat 2160
gaactaagaa attttaatgc aaatacatac attcctgaaa gacggggaat taaattacta 2220
attttttttt tttaaatgat gacagtggc ccagaacttg gaaaagtgt agggatttct 2280
aaactcaagc agattcgaa gtgctgtgcg cttgtcagac catcagacca gggccaacca 2340
atcagaaggc aacttactgt ataaa ttatg cagagtattt ttcctatatc tcacagtatt 2400
aaaaaataaa taattaaaaa ttaagaataa ataaacgagt tgacctcgtt cacaagaagca 2460
gttttactat cgaatcaatc gctgttattt ttttttaag taatttgtac atcttttttc 2520
aatctgtaca tttgggctgt cttgtatgtt tttatgctcc tttttaaaaa gcataatatg 2580
cctatagctg aaaaggaagc agggctgttt aagtactga cttatgagaa agcaaagcac 2640
tggtacagtt atttaacagg catacacaa cagggaagaa ataatccatt tagatcttta 2700
atgctttgga aatgcgtgta acagtactgc aataatcaca gctctgggaa aaacaacgaa 2760
actttccctt gtggagagga gggattttcc tgctctata t aagcaacata tttttagaca 2820
ttaaaatata tataattttg caggtaattg ttgacttttt taactatatt aagtgttaag 2880
ctgacaactg tcaagaaga ccatgttgta aaataatttg actaaataaa tggttccttc 2940
tctcaaaaaa aaaaaaa 2957

```

<210> 296

<211> 400

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(400)

<223> 3' terminal sequence. ests, highly similar
to tvhume hepatocyte growth factor receptor
precursor [h.sapiens] (EST R97218) gene.

<400> 296

193/292

```
caccccttct cttcacagat cacgaagatc ccattgaatg gcttgggctg cagacatttc 60
cagtcctgca gtcaatgcct ctctgcccc ccctttgttc agtgtggctg gtgcaganca 120
aatgtgtgcg atcggaggaa tgcctgagcg ggacatggac tcaacagatc tgtctgcctg 180
caatctacaa ggtaggaatc tctaacagct ggcatacatg tttttgtttg gtgttttttt 240
tttttttttg gtttggtttg gtttgttttt tgttttttta gatacaaatc ccactaatga 300
aaaaaattta aaaatcaatt tactcattta ggctgtgagg tcatcaggct aaagcaccat 360
ctctctcttg ggctttatcc ctggggcagg ggagggggg 400
```

<210> 297

<211> 464

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(464)

<223> 5' terminal sequence. ests, highly similar
to tvhume hepatocyte growth factor receptor
precursor [h.sapiens] (EST R97218) gene.

<400> 297

```
cgtggtagat tttcatagt cgaatatat gcttaagcaa ataaggcaac acagtttagca 60
tggctgcgat gtttagccaat gtccattgcc agaaactgag ttctctatca gcaagagatg 120
tgctcatctt gttctggact atatctctc a gggactaga gggcagcctg ctaaatggta 180
tgcactcaat aaatatTTTT ggaatgaatt aaagagtggc atggccttaca gaagtataga 240
tgtagtata gtcatccgtt gagcctttgc ttttttttct gggaacactg aaggaagact 300
cacagccacc catgggtgtt tgaccctcca ctgaccttgc ccacctcacc ccgggaaata 360
atcttcagtc tcatctgttg aacagacaag gccacctct atggccttcgg nacaggtagn 420
aaaactgtcc tgtgtggccc cgctnggcag ggatcaccag tttg 464
```

<210> 298

<211> 378

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(378)

<223> 3' terminal sequence. ets variant gene 5
(ets-related molecule) (ETV5) gene.

<400> 298

```
aaataccaaa actacaaaaa tcagtttata aactgttttt ccaaaacaac caccaaaaca 60
aaacaatccc ccaaatcagg gcaaaacaaa atactgtcaa aagtgttaat cgcccttctc 120
ctaaataaaa agtcatccac actcagccac gtgattggga agagaaaggg ggcttgctct 180
acttggcgac cacatggccg ggtggttccc aagagtagcc atggtttatg attttgagaa 240
ccacggaggg ggnaaacagc tgttctgact gcccccctt ttctagacaa ggggtaatat 300
ttcagattca gctagaagag ctttccaat g ttttaagatgt atttttaanc cttaatgggt 360
tnaggcctcc ccaacttt 378
```

<210> 299

<211> 317

194/292

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(317)

<223> 5' terminal sequence. ets variant gene 5
(ets-related molecule) (ETV5) gene.

<400> 299

```
actggaagag gttgctcggc gctggggcat ccagaagaac cggccagcca tgaactatga 60
caagctgagc cgctctctcc gctattacta tgaaaagggc atcatgcaga aggtggctgg 120
agagcgatac gtctacaaat ttgtctgtga cccagatgcc ctcttctcca tggctttccc 180
ggataaccag cgtcggttcc tgaaggcaga gtccgagtgc cacctcagcg aggaggacac 240
cctgccgctg acccaactttg aagacagccc cgcttacctc ctggacatgg accgctgcag 300
cagcctcccc tatgccg                                     317
```

<210> 300

<211> 4071

<212> DNA/RNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(4071)

<223> ets variant gene 5 (ets -related molecule)
(ETV5) gene.

<400> 300

```
gagtcagacc gctggtgcgc ggagcgggtc accgtcttcg gagcgggttcg gccagaccctt 60
tcgccagacc gccagggccc gctgcgcgcg tgcgtgagcg cgcctgcgcc gccagggccg 120
tgcaagggg aggagagcgg ccgcctcagg aggatccctt ttccccaga aattactcaa 180
tgctgaaacc tctcaaagtg gtattagaga cgctgaaagc accatggacg ggttttatga 240
tcagcaagtc ctttttatgg tcccagggaa atctcgatct gaggaatgca gaggcgccg 300
tgtgattgac agaaagagga agtttttga cacagatctg gctcacgatt ctgaagagct 360
atttcaggat ctcaagtcaac ttcaagaggc ttgggttagct gaagcacaag ttcctgatga 420
tgaacagttt gtccagatt ttcaagtctga taacctgggtg ctcatgccc cacctccaac 480
caagatcaaa cgggagctgc acagcccctc ctctgagctg tcgtcttgta gccatgagca 540
ggctcttggt gctaactatg gagaaaagtg cctctacaac tattgtgcct atgataggaa 600
gcctccctct gggttcaagc cattaacccc tccctacaacc cccctctcac ccacccatca 660
gaatcccta tttccccac ctcaggcaac tctgccacc tcagggcagc cccctgcagc 720
tgccccagtt caaggtgtgg gcccgcgcc cgcccccat tcgcttcag agcctggacc 780
acagcagcaa acatttgcg tccccgacc accacatcag cccctgcaga tgccaaagat 840
gatgcctgaa aaccagtatc catcagaaca gagatttc ag agacaactgt ctgaaccctg 900
ccaccccttc cctcctcagc caggagttcc tggagataat cgccccagtt accatcgcca 960
aatgtcagaa cctattgtcc ctgcagctcc ccgccccct cagggtatca aacaagaata 1020
ccatgaccca ctcctatgaa atgggggtccc gggcccccag cacacgggtt 1080
ccagtcacca atgggaatca agcaggagcc tcgggattac tgcgtcgatt cagaagtgcc 1140
taactgccag tcatcctaca tgagaggggg ttatttctcc agcagccatg aaggtttttc 1200
atatgaaaaa gatccccgat tatactttga cgacacttgt gttgtgcctg agagactgga 1260
aggcaagtc aaacaggagc ctacatgta tcgagagggg ccccttacc aga ggcgagg 1320
ttcccttcag ctgtggcagt tcctggtcac cttcttctg gaccagcca atgccactt 1380
cattgcctgg acaggtcgag gcatggagtt caagctgata gaaccggaag aggttgctcg 1440
gcgctggggc atccagaaga accggccagc catgaactat gacaagctga gccgctctct 1500
```

195/292

```

ccgctattac tatgaaaagg gcatcatg ca gaaggtggct ggagagcgat acgtctacaa 1560
atttgtctgt gaccagatg ccctctctc catggcttcc ccggataacc agcgtccgtt 1620
cctgaaggca gaggccgagt gccacctcag cgaggaggac accctgccgc tgaccactt 1680
tgaagacagc cccgcttacc tcctggacat ggaccgctgc agcagcctcc cctatgccga 1740
aggctttgct tactaagttt ctgagtggcg gagtggccaa accctagagc tagcagttcc 1800
cattcaggca aacaagggca gtggttttgt ttgtgttttt ggttgttccct aaagcttgcc 1860
ctttgagtat tatctggaga acccaagctg tctctggatt ggcaccctta aagacagata 1920
cattggctgg ggagtgggaa cagggagggg cagaaaacca c caaaaggcc agtgccctcaa 1980
ctcttgattc tgatgaggtt tctgggaaga gatcaaatg gagtctcctt accatggaca 2040
atacatgcaa agcaatatct tgttcagggt agtaccgcga aaacgggaca tgatgtgaca 2100
atctcgatcg atcatggact actaaatggc cttacatag aagggctctg atttgacaaa 2160
tttgttgaaa aatcac aaac ccatagaaaa gtgagttagc taagtgggg aggctcaaac 2220
cattaagggt taaaaatata tcttaaacat tggaaagctc ttctagctga atctgaaata 2280
ttaccccttg tctagaaaaa ggggggcagt cagaacagct gttccccact ccgtgttctc 2340
aaaatcataa accatggcta ctcttggaa caccgccgcc atgtggtcgc caagt agagc 2400
aagccccctt tctctccca atcacgtggc tgagtgtgga tgacttttat tttaggagaa 2460
gggagattaa cacttttgac agtattttgt tttgccctga tttgggggat tgttttgtt 2520
tgggtggtgt tttggaaaaa cagtttataa actgattttt gtagtttttg tatttaaagc 2580
aaaaaaacga aaaaacaaaa acaaaaacaa accttttggg aatgtgcact gtgtcttttag 2640
ccagggccgt gaaacttatg aagacactgc agcttgagag gggctttgct gaggttccc 2700
cttgcccatg tgaagcccg ccttgttgcc tgctttgtgc ttctgcacc agacaacctg 2760
atggaacatt tgcacctgag ttgtacattt ttgaagtgtg cagggcagcc tggacacaag 2820
cttagattct ctatgtatag ttcccgtgt tcaactaat gccctctctg gaaagcata 2880
gtatataaca tgtgtcatgt cctttggaaa cctggtcacc tggtgaaaac cctggggatt 2940
cttcctggg catgactgat gacaatttcc atttcatcag tttgttttgt tttccttttt 3000
ctttaaactc tggactttta accctacctg tgtgattcag tag ggtttga gacttagctg 3060
tgatactgac aggtaagcaa cagtgttagc attctagatt cctgcctttt tttaaaaaga 3120
aattattctc attgctgtat tatattggaa aagttttaaa caaccaagct aaagctatgt 3180
gaaagttgag ctcaaagtag aggaaaagt actggtggta ccttgcctgc tgcctctgct 3240
gtagaattct gtgctccc cg tgacacttag tacattaaga atgactacac tgttccctgt 3300
atgtgaagga ggcagtgtct actccgtgag tgtgagacac gtgctttgaa ctgcttttct 3360
attcatggag cactccatag tctcaactg tcccccttat gaccaacagc acatttgtga 3420
agagggttcg agggataagg ggtgcactt atagctatgg aaacatgaga ttctcct cta 3480
ttggaagcta attagccac aaaggtggt aacctgtaga ttgggcctta attagcattg 3540
tactctaate aaaggactct ttctaaacca tttttatagc tttcttaacc tacacatagt 3600
ctatacatag atgcatattt tacccccagc tggctagaga tttatttgtt gtaaattgctg 3660
tatagatttg gttttccttt ctttacttac c ctggttttg attttttttt ttttttttt 3720
tgaatggatt tatgctgtct tagcaatatg acaataatcc tctgtagctt gagctacccc 3780
tcccctgctg taacttactg gacctgtgct gtcactgggc ataggacagc ggcattcacgg 3840
ttgcattccc attggactca tgcacctccc ggatggtttt tgtttttttc ggggggttctt 3900
tgggggtttgt ttgtttgctt cttttccaga gtgtggaaaag tctacagtgc agaaaggctt 3960
gaacctgccg gctgatttga aatactttca cctgcgcag ggcgctatgc atcctgccaa 4020
gtgcggttat attctgtact gtgtacaata aagaagtttg cttttcgttt a 4071

```

<210> 301

<211> 407

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(407)

<223> 3' terminal sequence. cyclin -dependent
kinase 4 (CDK4) gene.

<400> 301

```

nccngtataa aaaaggaccc caaatataaa ggtagggaaa gggacaagag ggaacata cc 60

```

196/292

ccttagtgta gagaaatggg aaggagaagg agaagcctca aaaggngagg tgggagggga 120
atgtcattaa ggcagcaaag taatctctgt agaaagatgg aggaggaccc tccatagcct 180
cagagnataa ggcaaagntt gccctctcag tntccngaag ggaaatggca gcttttcttc 240
cttccatggg cagccactcc attgctcact ccggatt acc ttcattcctta tgtaggataa 300
gggtgctgca gagctcgaaa gggcagagat tcgcttntgt ggggttaaaa gtcagccttt 360
ncccgacgca gctttgcttc cccgactcct nccttttcag gnacccc 407

<210> 302

<211> 405

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(405)

<223> 5' terminal sequence. cyclin -dependent
kinase 4 (CDK4) gene.

<400> 302

attcgnaca gaggaggagg tggaggaggc cttcccatca gcacagttcg tgaggtggct 60
ttactgaggc gactggaggc ttttgagca t cccaatgttg tccggctgat ggacgtctgt 120
gccacatccc gaactgaccg ggagatcaag gtaaccctgg tgtttgagca tgtagaccag 180
gacctaagga catatctgga caaggcacc ccaccaggct tgccagccga aacgatcaag 240
gatctgatgc gccagtttct aagaggccta gatttccttc atgccaatg catcgttcac 300
cgaggatctg aagccagaga acattctggg tgacaagtgg ttggancagt caagctggct 360
ggactttggg cctgggcagn aatctancag cttaccagat gggca 405

<210> 303

<211> 420

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(420)

<223> 3' terminal sequence. v -yes-1 yamaguchi
sarcoma viral oncogene homolog 1 (YES1) gene.

<400> 303

caatgagaac tttttatttc aattatccac aaaacaatat tacaatactt tataaaaaata 60
ttaagttag gctaccatta ttcatttaaa aaagtgtgct agaaggctgt ttttgccaac 120
ttcctttttt ggtaagggtt aacttccaca ttaagacact gaagacgaaa agctgttggt 180
aaaatatctc caaatattaca aagttgtttt tcttgggcaa tttaaaaata caggancaat 240
ttaaantgaa tacacattaa ggtaggtgt tttatcccta ctatacaatt gttattatat 300
agggaaactgc tcccttcn gg ttaaanccct aatggaatac ccatcaactt ttcccggccc 360
ntactttccc nggattgggg tttagggtac ctaaacggga aatttaggtc nccccnttg 420

<210> 304

<211> 4517

<212> DNA/RNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(4517)

<223> v-yes-1 yamaguchi sarcoma viral oncogene
homolog 1 (YES1) gene.

<400> 304

```
gcgagagccaa ggcacacggg tctgaccctt gggccggccc ggagcaagtg acacggaccg 60
gtcgctatc ctgaccacag caaagcggcc cggagcccgc ggaggggacc tgacgggggc 120
gtaggcgccg gaaggctggg gggcccgag ccggcccgag gtggcccgag ttccggtgag 180
cggacggcgg cgccgcgaga tttgataatg ggctgcatta aaagtaaaga aaacaaaagt 240
ccagccatta aatacagacc tgaaaatact ccagagcctg tcagtacaag tgtgagccat 300
tatggagcag aacccactac agtgtcacca tgtccgtcat ctt cagcaaa gggaacagca 360
gttaatttca gcagtctttc catgacacca tttggaggat cctcaggggt aacgcctttt 420
ggaggtgcat cttcctcatt ttcagtgtg ccaagttcat atcctgctgg tttacaggt 480
ggtgttacta ttttgtggc cttatatgat tatgaagcta gaactacaga agacctttca 540
tttaagaagg gtgaaagatt t caaataatt aacaatacgg aaggagattg gtgggaagca 600
agatcaatcg ctacaggaag gaatggttat atcccgagca attatgtagc gcctgcagat 660
tcatttcagg cagaagaatg gtattttggc aaaatgggga gaaaagatgc tgaaagatta 720
cttttgaatc ctggaaatca acgaggtatt ttcttagtaa gagagagtga aacaactaaa 780
ggtgcttatt ccttttctat tcgtgattgg gatgagataa ggggtgacaa tgtgaaacac 840
tacaaaatta ggaaacttga caatggtgga tactatatca caaccagagc acaatttgat 900
actctgcaga aattggtgaa acactacaca gaacatgctg atggtttatg ccacaagttg 960
acaactgtgt gtccaactgt gaaacctcag actcaaggtc t agcaaaaaga tgcttgggaa 1020
atccctcgag aatcttttgc actagagggt aaactaggac aaggatgttt cggcgaagtg 1080
tggtatggaa catggaatgg aaccacgaaa gtagcaatca aaacactaaa accaggtaca 1140
atgatgccag aagctttcct tcaagaagct cagataatga aaaaattaag acatgataaa 1200
cttggtccac tatatgctgt tgtttctgaa gaaccaattt acattgtcac tgaatttatg 1260
tcaaaaaggaa gcttattaga tttccttaag gaaggagatg gaaagtattt gaagcttcca 1320
cagctggttg atatggctgc tcagattgct gatggtatgg catatattga aagaatgaac 1380
tatattcacc gagatcttcg ggctgctaatt attctttag tagaaaaatct tgtgt gcaaa 1440
atagcagact ttggttttag aaggttaatt gaagacaatg aatacacagc aagacaaggt 1500
gcaaaatttc caatcaaatg gacagctcct gaagctgcac tgtatggtcg gtttacaata 1560
aagtctgatg tctggtcatt tggaattctg caaacagaac tagtaacaaa gggccgagtg 1620
ccatatccag gtatggtgaa ccgtgaagta ctagaacaag tggagcgagg atacaggatg 1680
ccgtgccctc agggctgtcc agaatccctc catgaattga tgaatctgtg ttggaagaag 1740
gaccctgatg aaagaccaac atttgaatat attcagtcct tcttggaaga ctacttcact 1800
gctacagagc cacagtacca gccaggagaa aatttataat tcaagtagcc tattttatat 1860
gcacaaatct gccaaaatat aaagaacttg ttagattttt ctacaggaat caaaagaaga 1920
aaatcttctt tactctgcat gtttttaatt gttaaactgga atcccagata tggttgcaca 1980
aaaccacttt tttttcccca agtattaaac tctaattgtac caatgatgaa tttatcagcg 2040
tatttcaggg tccaaacaaa atagagctaa gatactgatg aca gtgtggg tgacagcatg 2100
gtaatgaagg acagtgaggg tctgtcttat ttataaatca tttcctttct ttttttccc 2160
aaagtcagaa ttgctcaaag aaaattattt attgttacag ataaaaactg agagataaaa 2220
agctatacca taataaaatc taaaattaag gaatatcatg ggaccaaata attccattcc 2280
agttttttaa agtttcttgc atttattatt ctcaaaagtt ttttctaagt taaacagtca 2340
gtatgcaatc ttaatatatg ctttcttttg catggacatg ggccagggtt ttcaaaagga 2400
atataaacag gatctcaaac ttgattaaat gtttagaccac agaagtggaa tttgaaagta 2460
taatgcagta catataatatt catgttcacg gaactgaaag aataagaact ttttcac ttc 2520
agtccttttc tgaagagttt gacttagaat aatgaaggta actagaaagt gagttaatct 2580
tgtatgaggt tgcattgatt ttttaaggca atatataatt gaaactactg tccaatcaaa 2640
ggggaaatgt tttgatcttt agatagcatg caaagtaaga ccagcattt taaaagccct 2700
tttttaaaaa ctagacttgc tactgtgagt a ttgcttata tgtccttatg gggatgggtg 2760
ccacaaatag aaaatatgac cagatcaggg acttgaatgc acttttgctc atggtgaata 2820
tagatgaaca gagaggaaaa tgtattttaa agaaatacga gaaaagaaaa tgtgaaagtt 2880
ttacaagtta gagggatgga aggtaatgtt taatgttgat gtcatggagt gacagaatgg 2940
ctttgctggc actcagagct cctcacttag ctatatctg agactttgaa gagtataaa 3000
gtataactat aaaactaatt tttcttacac actaaatggg tatttgttca aaataatgaa 3060
```

198/292

```

gttatggctt cacatcoatt gcagtgggat atgggttttta tgtaaaacat ttttagaact 3120
ccagtttttca aatcatgttt gaattctacat tcactttttt ttgtt ttctt ttttgagacg 3180
gagtcctcgt ctgccgccca ggctggagtg cagtggcgcg atctcggctc actgcaagct 3240
ctgcctccca ggttcacacc attctcctgc ctcagcctcc cgagtagctg ggactacagg 3300
tgcccaccac cagcctgggc tagttttttt tttttttagt agagacgcag tttcaccgtg 3360
ttagccagga tggctcctgat ctcttgacct tgtgatctgc ccgctcggc ctcccaaagt 3420
gctgggatta caggtgtgag ccaccgcgcc cagcctacat tcacttctaa agtctatgta 3480
atgggtggta ttttttccct tttagaatac attaaatggt tgatttgagg aggaaaactt 3540
attctgtaata ttaacgggtg tgaaaagggg acagttttta ccctaaagt caaaagtga a 3600
acatacaaaa taagactaat ttttaagagt aactcagtaa tttcaaaata cagatttgaa 3660
tagcagcatt agtggtttga gtgtctagca aaggaaaaat tgatgaataa aatgaaggtc 3720
tggtgtatat gttttaaaat actctcatat agtcacactt taaattaagc cttatattag 3780
gcccctctat tttcaggata taattottaa cta tcattat ttacctgatt ttaatcatca 3840
gattcgaaat tctgtgccat ggcttatatg ttcaaattca aaccattttt aaaatgtgaa 3900
gatggacttc atgcaagttg gcagtgggtc tggtaactaa aattgtggtt gttttttctg 3960
tttactgaac ctgcttagta ttgacactct ctaccaagag ggtcttccta agaagagtgc 4020
tgtcattatt tcctcttctc aacaacttgt gacatgagat tttttaaggg ctttatgtga 4080
actatgatat tgtaattttt ctaagcatat tcaaaagggt gacaaaatta cgtttatgta 4140
ctaaatctaa tcaggaaagt aaggcaggaa aagttgatgg tattcattag gttttaactg 4200
aatggagcag ttctttatat aataacaatt gtatagtagg gataaaa cac taacaatgtg 4260
tattcatatt aaattgttct gtatttttaa attgccaaga aaaacaactt tgtaaatgtg 4320
gagatatttt ccaacagctt ttctgttcta gtgtcttaat tggaagtta acccttacca 4380
aaaaaggaag ttggcaaaaa cagccttcta gcacactttt ttaaataaat aatggtagcc 4440
taaacttaat atttttataa a gtattgtaa tattgttttg tggataattg aaataaaaag 4500
ttctcattga atgcacc 4517

```

<210> 305

<211> 459

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(459)

<223> 3' terminal sequence. interferon -induced protein 75, 52kd (IFI75) gene.

<400> 305

```

ncttgtctga aggtgtgctg gacacctcct ggggtctctc tgggtcattt ggttctggag 60
aattatctct tatctctggc atagagccca agggagagtg gggcatctct tgagggtctt 120
ctttatctct tatttggggg atcagggttg cactggccac ttgcacagtg ctagtgagga 180
ggctgggcat ctctcttgag tcttctttcg cattcatttt ggangttaac ttgtcattgg 240
tcactgaagt gcttcttctt tcctgggatg agtgcaggga gaggcaggac agggtcagat 300
gggctgggcy actcaactcag gatctcatcg ctttctgagg agg atgttcc agggctcact 360
gactcttggg cgcacaaggt gaaacagctt ggtttgaagg gggttnttgg tngggggcaa 420
gcncaatngg gtatggaagg aagcttccct ctaanaagg 459

```

<210> 306

<211> 370

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

199/292

<221> misc_feature
<222> (1)..(370)
<223> 5' terminal sequence. interferon -induced
protein 75, 52kd (IFI75) gene.

<400> 306
tgcgtttgtc aaagcacaga ctctctgttt tgcctgctag catctccctg taactctccc 60
aatcttgagg agtgatccct gtccc agccc ctggaaaggg anggaaacga caaactcaaa 120
gtccaggatg ttaccatga caagagccat ggaagaggct ctttttcagc acttcatgca 180
ccagaagctg gggatcgcc atgcatata caagccatit cccttctttg aaggcctcct 240
agacaactcc atcatcata agagaatgta catggaatct ctggaagcct gtagaaattt 300
gatccctgta tccagagtgg tgcacaacat tctcaccaa ctgggagagg actttttaac 360
ctgtctctt 370

<210> 307
<211> 1541
<212> DNA/RNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<220>
<221> misc_feature
<222> (1)..(1541)
<223> interferon -induced protein 75, 52kd (IFI75)
gene.

<400> 307
aattccggca tcgctttgct gggaggatgt tccaggctca ctgactcttg gcgcacaggg 60
tgaacagctt ggttgagtcg cccagcccat ctgacctgt cctgcctctc cctgcactca 120
tccaggaagg agaagcact tcagtgaaca atgacaagtt aacatccaaa atgaatgcgg 180
aagaagactc agaagagatg cccagcctcc tcactagcac tgtgcaagtg gccagtga 240
acctgatccc ccaataaga gataaagaag accctcaaga gatgccccac tctcccttgg 300
gctctatgcc agagataaga gataattctc cagaaccaa t gacccagaa gagccccagg 360
aggtgtccag cacaccttca gacaagaaag gaaagaaaag aaaaagatgt atctgttcaa 420
ctccaaaaag gagacataag aaaaaagcc tcccaagagg gacagcctca tctagacacg 480
gaatccaaa gaagctcaa aggttgatc aggttctctc aaagaaagat gactcaactt 540
gtaactccac ggtagagaca agggcccaa aggcgagaa tgaatgtgcc cgaaagtcga 600
gatcagagga gatcattgat ggcacttcag aaatgaatga aggaaagagg tcccagaaga 660
cgcctagtac accacgaagg gtcacacaag ggcagcctc acctgggcat ggcattccaag 720
agaagctcca agtggtgat aagtgactc aaaggaaaga cgactcaacc tggaactcag 7 80
aggtcatgat gagggtccaa aaggcaagaa ctaaatgtgc ccgaaagtcc agatcgaaag 840
aaaagaaaa ggagaaagat atctgttcaa gctcaaaaag gagatttcag aaaaatattc 900
accgaagagg aaaacccaaa agtgacactg tggattttca ctgttctaag ctccccgtga 960
cctgtggtga ggcgaaaggg attttatata agaagaaaat gaaacacgga tcctcagtga 1020
agtgcattcg gaatgaggat ggaacttggg taacaccaa tgaatttgaa gtcgaaggaa 1080
aaggaaaggaa cgaaagaac tggaaacgga atatacgttg tgaaggaaatg acctaggag 1140
agctgctgaa gcgaaaaaac tcggatgaat gcgaggtgtg ctgtcaaggg ggacaacttc 1200
tctgctgcgg tacttgtcca cgagtcttcc atgaggactg tcacatcccc cctgtggaag 1260
ccaagaggat gctgtggagt tgcaccttct gcaggatgaa gaggtcttca ggaagccaac 1320
agtgcacata tgtatctaag accctggaga ggcagatgca gcctcaggac cagctgaatg 1380
tgagttcttc cctttgaagg cctactgtca tccacaaagc tcctttttta cgg gcatccc 1440
atttaatat cgagattacg gtgagccttt caggaaagca tgtggttggg cctggttaag 1500
ggaaaggctg attacggaaa tgtacacggt ggcccggaat t 1541

<210> 308
<211> 416
<212> DNA

200/292

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(416)

<223> 3' terminal sequence. v-myb avian
myeloblastosis viral oncogene homolog -like 2
(MYBL2) gene.

<400> 308

```
gttannncnan tnnatttttt aagagagagg caatttttatt cttccaaaaa aatgcaccag 60
agagggtgag cacaggagca cccctggcca catcccccat cctaagcagg gtctgagatg 120
aggccaggnc tgacgtgggc ttgggagaag ctgacggagc tccctgtggc cttggggagg 180
gaaccaggca gacctgggaa gtggaacttt gttgttagca ccaggagccg cccacagctg 240
ggcttcggca acagggcagc acatggccct gtcccttcca cctgagagt c tggggagggg 300
ctgggtggcag aaggctccct gcaggagggt cacctgaatg actctcagat tcacagaccc 360
cctnttgccc ccacaacccc tgtaaacatg agaatggggc tcgtgacacc ctnaac 416
```

<210> 309

<211> 426

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(426)

<223> 5' terminal sequence. v-myb avian
myeloblastosis viral oncogene homolog -like 2
(MYBL2) gene.

<400> 309

```
gaactcatc tcgaggacga catcaggccc gagaagcaga agaggaagcc tgggctgcgg 60
cggaccatt caagaaagtc cggaaagtctc tggtcttga cattgtggat gaggatatga 120
agctgatgat gtccacactg cccaagtctc tatccttgcc gacaactgcc ccttcaaact 180
cttccagcct caccctgtca ggtatcaaag aagacaacag cttgctcaac cagggttct 240
tgcaggccaa gcccagaaag gcagcagtgg ccagaagcc ccgaagc cac ttcacgacac 300
ctgcccctat gtccagtgcc tgggaagacg gtggcctgcg gggggaccag gggaccagct 360
tttcatggca ggagaaagcc cggcagcttc tggggccgct tgaagcccag ccacactttt 420
cgggac 426
```

<210> 310

<211> 2627

<212> DNA/RNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(2627)

<223> v-myb avian myeloblastosis viral oncogene
homolog-like 2 (MYBL2) gene.

<400> 310

```
gctgacgcct tgcagcgcgg ccc ggggccc ggagcggccg gagcagcccg ggtcctgacc 60
cgggcccggc tcccgcctccg ggctctgccg gcgggcccggc gagcgcggcg cggcccgggc 120
cgggggggatg tctcggcgga cgcgctgcga ggatctggat gagctgcact accaggacac 180
agattcagat gtgccggagc agaggggatag caagtgcag gtcaaattga cccatgagga 240
ggacgagcag ctgaagggtcc tggtaggca gtttgacag caggactgga agttcctggc 300
cagccacttc cctaaccgca ctgaccagca atgccagtac aggtggctga gagttttgaa 360
tccagacctt gtcaaggggc catggaccaa agaggaagac caaaaagtca tcgagctggt 420
taagaagtat ggcacaaagc agtggacact gattgccaa cacc tgaagg gccggtggg 480
gaagcagtgc cgtgaacgct ggcacaacca cctcaaccct gaggtgaaga agtcttgctg 540
gaccgaggag gaggaccgca tcatctgcga ggcccacaag gtgctgggca accgctgggc 600
cgagatcgcc aagatgttgc cagggaggac agacaatgct gtgaagaatc actggaactc 660
taccatcaaa aggaagggtg ac acaggagg ctcttgagc gagtccaaag actgcaagcc 720
cccagtgtac ttgctgctgg agctcgagga caaggacggc ctccagagt cccagcccac 780
ggaaggccag ggaagtcttc tgaccaactg gccctccgct cctcctacca taaaggagga 840
ggaaaacagt gaggaggaac ttgcagcagc caccacatcg aaggaacagg agcccatcg 900
tacagatctg gacgcagtgc gaacaccaga gcccttgag gaattcccga agcgtgagga 960
ccaggaaggc tccccaccag aaacgagcct gccttacaag tgggtgggtg aggcagctaa 1020
cctcctcatc cccgctgtgg gttctagcct ctctgaagcc ctggacttga tcgagtcgga 1080
cctgatgct tgggtgtgacc tgagtaaatt tgacctccct gaggaacct ctgcagagga 1140
cagtatcaac aacagcctag tgcagctgca agcgtcacat cagcagcaag tctgccacc 1200
ccgccagcct tccgccctgg tgcccagtgt gaccgagtac cgcctggatg gccacaccat 1260
ctcagacctg agccggagca gccggggcga gctgatcccc atctcccca gactgaagt 1320
cgggggctct ggcat tggca caccgccctc tgtgctcaag cggcagagga agaggcgtgt 1380
ggctctgtcc cctgtcactg agaatagcac cagtctgtcc ttctggatt cctgtaacag 1440
cctcacgccc aagagcacac ctgttaagac cctgcccttc tcgccctccc agtttctgaa 1500
cttctggaac aaacaggaca cattggagct ggagagcccc tcgctgacat ccac cccagt 1560
gtgcagccag aaggtggtgg tcaccacacc actgcaccgg gacaagacac ccctgcacca 1620
gaaacatgct gcgtttgtaa ccccagatca gaagtactcc atggacaaca ctcccacac 1680
gccaaacccg ttcaagaacg ccctggagaa gtacggacce ctgaagcccc tgccacagac 1740
cccgcacctg gaggaggact tgaaggagg t gctgcgttct gaggtggca tcgaactcat 1800
catcaggagc gacatcaggc ccgagaagca gaagaggaag cctgggctgc ggccggagccc 1860
catcaagaaa gtccggaagt ctctggctct tgacattgtg gatgaggatg tgaagctgat 1920
gatgtccaca ctgcccaagt ctctatcctt gccgacaact gcccttcaa actcttcag 1980
cctcaccctg tcaggtatca aagaagaca cagcttgctc aaccagggct tcttgaggc 2040
caagcccag aaggcagcag tggcccagaa gccccaagc cacttcacga cacctgcccc 2100
tatgtccagt gcctggaaga cgggtggcctg cggggggacc agggaccagc ttttcatgca 2160
ggagaaagcc cggcagctcc tgggccgcct gaagcccagc ca cacatctc ggacctcat 2220
cttgctctga ggtgttgagg gtgtcacgag ccattctca tgtttacagg ggttgtggg 2280
gcagaggggg tctgtgaate tgaggtcat tcaggtgacc tctgcaggg agccttctgc 2340
caccagcccc tcccagact ctcaggtgga ggcaacagg ccatgtgctg ccctgttgcc 2400
gagcccagct gtggcg gct cctggtgcta acaacaagt tccacttcca ggtctgctg 2460
gttccctccc caaggccaca gggagctccg tcagcttctc ccaagcccac gtcaggcctg 2520
gcctcatctc agaccctgct taggatggg gatgtggcca ggggtgctcc tgtgctcacc 2580
ctctcttggg gcattttttt ggaagaataa aattgcctct ctctttg 2627
```

<210> 311

<211> 442

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(442)

<223> 3' terminal sequence. transforming growth
factor, beta receptor iii (betaglyc an, 300kd)

202/292

(TGFB3) gene.

<400> 311

```
cccagactca aggagttggt aaagggttaa tagccagata gtagaaccag tgaggagatg 60
cggccaaaga ttctttatat ctgaaccaag atgtaaaaca agaaatgctt tgaggctttc 120
taagcgatcc tcctgtctaa tttgcaacct tgtctggatg cacacttctg accttgctgc 180
cacaacctgt ggggttctga tgtgtccctt gatgggtgct gccctcaggg actgcacct 240
gacaagtgtt aaggcaacat tcctttcttg tgcccggggc caaaaccaat gctgatgacc 300
ttatcagctt cctgtttctt ccatacttg catacaccac tggcaaatg tottaatggc 360
aaattttgta tttcttacag ggnctacagg aaatttgaaa atgg accaaa ttcagggaac 420
cacaggtttt gtggcccatt tc                                         442
```

<210> 312

<211> 315

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(315)

<223> 5' terminal sequence. transforming growth
factor, beta receptor iii (betaglycan, 300kd)
(TGFB3) gene.

<400> 312

```
taacaaggag gtatcactga gcttatttta gctgcaaagt ggcatcatat tattccattt 60
aatgaaattc acctcaagcc ctttttgaca tattaatat atgggatata tttaa ggcaa 120
gagaagtaag gcaatccaaa tgagtgcctt tttccaatct cagcactgtc ttgngngaag 180
tggtgacact attcagataa ccaactggag accgacagat ttgccatgca tttgcatctt 240
gctagagttt ggtttttatg aaagggccta ttttttttta agttgacata ttttgagtgg 300
gaaacactca cccta                                         315
```

<210> 313

<211> 4208

<212> DNA/RNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(4208)

<223> transforming growth factor, beta receptor
iii (betaglycan, 300kd) (TGFB3) gene.

<400> 313

```
tctttaagat ttgtagctac taagaaagaa aggagctttt tttccttggg cttcaaact 60
gaaagaaccg catgagcctg acggcgcatg gtcttaacat caggctgtgc aggaagaagc 120
tatctgcaga tggatgccag cacacacaag gaagcagagc tctggcaaca ttgagtcaaa 180
gcaaggacac aacatcagag ggacggcaga gaatccttgt gtgtagtctt tgggtggcagt 240
ttgaaaattg caaggaggga cttaagact acttctgatt tgcaaagatg gtctgtgctc 300
cgagcaggct aaagtgactg gacgagacgc actgttggag aaataaaaaat gacttcccat 360
tatgtgattg ccatctttgc cctgatgagc ttctgtttag cca ctgcagg tccagagcct 420
ggtgcactgt gtgaactgtc acctgtcagt gcctcccatc ctgtccaggc cttgatggag 480
agcttcactg ttttgtcagg ctgtgccagg agaggcacia ctgggctgcc acaggagggtg 540
```

203/292

catgtcctga atctcgcact gcgccagggg cctggccagc tacagagaga ggtcacactt 600
 cacctgaatc ccattctcctc a gtccacatc caccacaagt ctgtttgtgtt cctgctcaac 660
 tccccacacc cctcgggtgtg gcattctgaag acagagagac ttgccactgg ggtctccaga 720
 ctgttttttg tgtctgaggg ttctgtggtc cagttttcat cagcaaacct ctcttgaca 780
 gcagaaacag aagaaaggaa cttcccccat ggaaatgaac atctgttaaa ttgggcccga 840
 aaagagtatg gagcagttac ttcatccacc gaactcaaga tagcaagaaa catttatatt 900
 aaagtggggg aagatcaagt gtccctcca aagtgaaca tagggaagaa tttctctca 960
 ctcaattacc ttgttgagta cttcaaccc aaagcagcag aagggtgtgt gatgtccagc 1020
 cagccccaga atgaggaagt acacatcatc gagctaatca cccccaactc taaccctac 1080
 agtgctttcc agtggtatat aacaattgat ataagacctt ctcaagagga tcttgaagt 1140
 gtcaaaaatc tcatcctgat cttgaagtgc aaaaagtctg tcaactgggt gatcaaatct 1200
 tttgatgtta agggaagcct gaaaattatt gctcctaaca gtattggctt tggaaaagag 1260
 agtgaagat ctatg acaat gaccaaatca ataagagatg acattccttc aaccaagg 1320
 aatctgttga atcgggcttt ggacaatggc tatagtccaa taacttcata cacaatggct 1380
 cctgtggcaa tagtatttca tcttcggctt gaaaataatg aggagatggg agatgaggaa 1440
 gtccacacta ttctcctga gctacggatc ctgctggacc ctggtgccct gcct gccctg 1500
 cagaaccgc ccatccgggg aggggaaggc caaaatggag gccttcggtt tcttttcca 1560
 gatatttcca ggagagtctg gaatgaagag ggagaagatg ggctccctcg gccaaaggac 1620
 cctgtcattc ccagcataca actgtttcct ggtctcagag agccagaaga ggtgcaagg 1680
 agcgtggata ttgcccctgc tgtcaaatg t gacaatgaga agatgatcgt ggctgtagaa 1740
 aaagattctt ttcaggccct tggctactcg gggatggacg tcacctgtt ggatcctacc 1800
 tgcaaggcca agatgaatgg cacacacttt gttttggagt ctctctgaa tggctgcgt 1860
 actcggcccc ggtggtcagc cttgatgggt gtggtctact ataactccat tgtgatacag 1920
 gttccagccc ttggggacag tagtggttgg ccagatggtt atgaagatct ggagtcaggt 1980
 gataatggat ttccgggaga tatggatgaa ggagatgctt cctgttcac ccgacctgaa 2040
 atcgtggtgt ttaattgcag ccttcagcag gtgaggaacc ccagcagctt ccaggaacag 2100
 cccaacggaa acatcacctt caacatggag ctatacaaca ct gacctctt tttggtgcc 2160
 tcccaggcgt tcttctctgt gccagagaat ggacacgttt atgttgaggt atctgttact 2220
 aaggctgaac aagaactggg atttgccatc caaacgtgct ttatctctcc atattcgaac 2280
 cctgatagga tgtctcatta caccattatt gagaatattt gtctaaaga tgaatctgtg 2340
 aaattctaca gtcccaa gag agtgcactc cctatccgc aagctgacat ggataagaag 2400
 cgattcagct ttgtcttcaa gcctgtcttc aacacctcac tgcctttct acagtgtgag 2460
 ctgacgtgt gtacgaagat ggagaagcac cccagaagt tgctaagt tgtgcctct 2520
 gacgaagcct gcacctcgt ggacgcctcg ataacttggg ccatgatgca gaataa gaag 2580
 acgttcacca agccccttgc tgtgatccac catgaagcag aatctaaaga aaaaggtcca 2640
 agcatgaagg aaccaaatcc aatttctcca ccaatttctc atggtctgga caccctaacc 2700
 gtgatgggca ttgcgtttgc agcctttgtg atcggagcac tctgacggg ggccttgtg 2760
 tacatctatt ctacacaggg ggagacagca ggaaggcagc aagtccccac ctcccgcga 2820
 gctcggaaa acagcagtg tgcccacagc atcggcagca cgcagagcac gccttgcctc 2880
 agcagcagca cggcctagcc caaccaggc ccaaccaggc ccaaccaggc ccagccagc 2940
 tcagctcagc tactccaagg gcaggaccaa tgcgtgagcc tctgttccag actcagagg 3000
 ctggattttg gttcccttgt aaagacagag tgaatttcag tataaagatc acccgttga 3060
 ttcacccac acccagggt agtataaaca tgacctggg cttctgtacc aactagaat 3120
 tcatgtgaga aagctaaaat ggtgtcttc tccaccagcc cctcacaggc ttgggggtt 3180
 tctatgtgaa acacatgcca gtttttaaaa tgcgtcttgg tcca ggtgag aacatccata 3240
 atttggggcc ctgagtttta ccagactca aggagttgg aaagggttaa tagccagata 3300
 gtagaaccag tgaggagatg cggccaaaga ttctttatat ctgaaccaag atgtaaaaca 3360
 agaaatgctt tgaggcttcc taagcgatcc tctgtctaa tttgcacctt tgtctggatg 3420
 cactctctg accttgcct c cacaacctgt ggggtctgat gtgtcccaag atgggtgctg 3480
 cctcaggga ctgcacctg acaagtgtta aggaacatt ccttgcctgt gccctgggccc 3540
 aaaaccaatg ctgatgacct tatcagcttc ctgtttcttc ccatactgca tacaccactg 3600
 caaaatgtct taatgcaaat tttgtatttc ttacaggcct acagaaattg aaaatgac ca 3660
 aaatcaggaa ccacagattt gtgcccattc ctaatatatt gttctgcaaa ttaatgtata 3720
 atttgaggtg aaattcagtt ataaagtcaa ggacgaatt gcacagtat atatttctat 3780
 gtgtatgcaa gtacaagtat ataatatgtc acctggcaca ttcattttct cagttgaaga 3840
 agagaaaatt tgaaaatgtc cttatgcttt ta gaggttgca acttaagtat atttggtagg 3900
 gtgagtggtt cactcaaaa tatgtcaact taataaaaaa taggcccctt cataaaaaacc 3960
 aaactgtagc aagatgcaaa tgcatggcaa atctgtcgg ctccagttgg ttatctgaat 4020
 agtgtacca attccaccaa gacagtgtg agattggaaa gggcactcat ttggattgcc 4080
 ttacttctc tgccttaaat atatcccata tatttaatat gtcaaaaagg gcttgaggtg 4140
 aatttcatta aatggaataa tatgatgcca ctttgcagct aaaataagct cagtataacc 4200

204/292

tccttggt

4208

<210> 314
<211> 468
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<220>
<221> misc_feature
<222> (1)..(468)
<223> 3' terminal sequence.. peroxiredoxin 2
(PRDX2) gene.

<400> 314
tnnttttttt tttncacctt tccctaatac ttnatnggtn acctctaggc ctgtgtgcgg 60
ctgggtgggc ttgggggagg gcgtcactat tcagcttcta ggtggaggca tgagaaggcc 120
ttggctaggc cctccagggt ccataactgt ggagtttggg ggggcaggtc tggcctttcc 180
tgggtcagca tagggcaccc aggtgggggn acaggtggac acccagcaca ggcacctagg 240
caggggcaca agtcantat ccnttagcca gcctaattgt ntttgg agaa atattccttg 300
ctgtcatcca cgttgggttt aatcgtgtca ctgccagggt tocagccagc gggacaaant 360
ttcccatgt tcgtttgtgt attgggaagg cctgggacca gccgcagagt tnatccacg 420
gagngtccca aaggnaaatc attaaacagt gattttggcn aaggaaaa 468

<210> 315
<211> 394
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<220>
<221> misc_feature
<222> (1)..(394)
<223> 5' terminal sequence. peroxiredoxin 2
(PRDX2) gene.

<400> 315
acttcaaggc cacagcgggt gttgatggcg ccttcaaaga ggtga agctg tcggactaca 60
aagggaagta cgtggctctc tttttctacc ctctggactt cacttttgtg tgccccaccg 120
agatcatcgc gttcagcaac cgtgcagagg acttccgcaa gctgggctgt gaagtgtctg 180
gcgtctcggg tggactctca gttaaccac ctggcttggg tcaacacccc ccggaagag 240
ggaggcttgg gccccctgaa catc ccctg cttgctgacg tgaccagacg cttgtctgag 300
gattacggcg tgctgaaaac agatgagggc attgctaaca ggggcctctt tatcatcgat 360
gggcaagggt gttcctttcg ccagatcaat gtta 394

<210> 316
<211> 937
<212> DNA/RNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<220>

205/292

<221> misc_feature
<222> (1)..(937)
<223> peroxiredoxin 2 (PRDX2) gene.

<400> 316
cgcgcccca gggctcactt ggcgctgaga acgcgggtgc agcgtgtgat cgtccgtgcg 60
tctagccttt gccacgcag ctttcagtca tggcctccgg taacgcg cgc atcggaagc 120
cagcccctga cttcaaggcc acagcgggtg ttgatggcg cttcaaagag gtgaagctgt 180
cggactacaa agggaagtac gtggtcctct ttttctaccc tctggacttc acttttgtgt 240
gccccaccga gatcatcgcg ttcaacaaccg tgaagaggac ttccgcaaag ctgggctgtg 300
aagtgtcggg cgtctcgggtg gactc tcagt tcaccacact ggcttggatc aacaccccc 360
ggaaagaggg aggcttgggc cccttgaaca tccccctgct tgctgacgtg accagacgct 420
tgtctgagga ttacggcgtg ctgaaaaacg atgagggcac tgcttacagg ggcctcttta 480
tcatcgatgg caagggtgtc cttcgccaga tcaactgttaa tgatttgct gtgggacgct 540
ccgtggatga ggtctgcgg ctggtccagg ccttccagta cacagacgag catggggaag 600
tttgtccggc tgcttgaag cctggacgtg acacgattaa gccgaacgtg gatgacagca 660
aggaatattt ctccaaacac aattaggctg gctaaccgat agtgagcttg tgcccctgcc 720
taggtgcctg tgctgggtgt ccacctgtgc cccacactgg gtgcc ctatg ctgaccagg 780
aaaggccaga cctgcccctc caaaatccac agtatgggac cctggagggc tagcaaggcc 840
ttctcatgcc tccacctaga agctgaatag tgacgccctc ccccaagccc acccagccgc 900
acacaggcct agaggtaacc aataaagtat tagggcc 937

<210> 317
<211> 451
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<220>
<221> misc_feature
<222> (1)..(451)
<223> 5' terminal sequence. v-fos fbj murine
osteosarcoma viral oncogene homolog (FOS) gene.

<400> 317
gctagcacca tgagctgaag accgagccct ttgatgactt cctgttccca gcatcatcca 60
ggcccagtgg ctctgagaca gcccgctcgg tgccagacat ggacctatct gggtccttct 120
atgcagcaga ctgggagcct ctgcacagtg gctccctggg gatggggccc atggcacagn 180
agctggagcc cctgtgact cccgtggtca cctgtactcc cagctgcaact gctta cacgt 240
cttccttcgt cttacactac cccgaggctg actncttccc cagctgtgca gctgcccacc 300
gcaaggcagc agcagcaatg agccttctc tgactcgttc agctnaccga cgggtcgtggc 360
cctgtgaggg ggcaggggaa ggggaggcag ncggcaacna caagttgccca ttgtccgagt 420
tngttgattt anagagagga gaaacaaatt t 451

<210> 318
<211> 2084
<212> DNA/RNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<220>
<221> misc_feature
<222> (1)..(2084)
<223> v-fos fbj murine osteosarcoma viral oncogene
homolog (FOS) gene.

<400> 318

```
aaccgcatct gcagcgagca actgagaagc caagactgag ccggcggccg cggcgcagcg 60
aacgagcagt gaccgtgctc ctacccagct ctgcttcaca gcgccaccc gtctccgccc 120
ctcggccccc cgcccggctt tgcctaaccg ccacgatgat gttctcgggc ttcaacgcag 180
actacgagcg gtcatactcc cgctgcagca gcgcgtcccc ggccggggat agcctctctt 240
actaccactc acccgagac tccttctcca gcatgggctc gcctgtcaac gcgcaggact 300
tctgcacgga cctggccgtc tccagtgcc aattcattcc caccgtcact gccatctcga 360
ccagtcggga cctgcagtgg ctggtgcagc ccgccctcgt ctctctgtg gccccatc gc 420
agaccagagc ccctcaccct ttccggagtc ccgccccctc cgctggggct tactccaggg 480
ctggcgttgt gaagaccatg acaggaggcc gagcgcagag cattggcagg aggggcaagg 540
tggaacagtt atctccagaa gaagaagaga aaaggagaat ccgaagggaa aggaataaga 600
tggctgcagc caaatgccgc aaccggagga gggagc tgac tgatacactc caagcggaga 660
cagaccaact agaagatgag aagtctgctt tgcagaccga gattgccaac ctgctgaagg 720
agaaggaaaa actagagttc atcctggcag ctaccgacc tgctgcaag atccctgatg 780
acctgggctt ccagaagag atgtctgtgg ctcccttga tctgactggg ggcctgccag 840
aggttgccac ccgcgagctt gaggaggcct tcaccctgcc tctcctcaat gaccctgagc 900
ccaagccctc agtggaaact gtcaagagca tcagcagcat ggagctgaag accgagccct 960
ttgatgactt cctgttccca gcatcatcca ggcccagtg ctctgagaca gcccgctccg 1020
tgccagacat ggacctatct ggttccttct atgcagcaga ctgggagcct ctgca cagtg 1080
gctccctggg gatggggccc atggccacag agctggagcc cctgtgcaact ccggtggtea 1140
cctgtactcc cagctgcact gcttacacgt ctctcttct ctccacctac ccgaggctg 1200
actcctccc cagctgtgca gctgcccacc gcaagggcag cagcagcaat gaggcttct 1260
ctgactcgtc cagctcacc acgtgctgg ccctgtgagg gggcagggaa ggggaggcag 1320
ccggcaccga caagtgccac tgcccagct ggtgcattac agagaggaga aacacatctt 1380
ccctagaggg ttcctgtaga cctagggagg accttatctg tgcgtgaaac acaccaggct 1440
gtgggcctca aggacttgaa agcatccatg tgtggactca agtccttacc tcttccggag 1500
atgtagcaaa acgcatggag tgtgtattgt tcccagtgac acttcagaga gctggtagtt 1560
agtagcatgt tgagccaggc ctgggtctgt gtctctttt tctttctct tagtcttctc 1620
atagcattaa ctaatctatt gggttcatta ttggaattaa cctgggtgctg gatattttca 1680
aattgtatct agtgcagctg attttaacaa taactactgt gtt cctggca atagtgtgtt 1740
ctgattagaa atgaccaata ttatactaag aaaagatacg actttatttt ctggtagata 1800
gaaataaata gctatatoca tgtactgtag ttttcttca acatcaatgt tcattgtaat 1860
gttactgac atgcattgtt gaggtggtct gaattgtctg acattaacag ttttccatga 1920
aaacgtttta ttgtgttt tt aatttattta ttaagatgga ttctcagata tttatatttt 1980
tattttattt ttttctacct tgaggctctt tgacatgtgg aaagtgaatt tgaatgaaaa 2040
atthaagcat tgtttgctta ttgttccaag acattgtcaa taaa 2084
```

<210> 319

<211> 240

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(240)

<223> 3' terminal sequence. retinoblastoma -binding
protein 7 (RBBP7) gene.

<400> 319

```
ctgcaaagcc aatcaagaag tggttgaagg aaaaagtgtg aaagttattc ttgcataatt 60
gggaacagca agcacttagt ttgagaaaat gaggacttaa aacagttgan tcaaaggcaa 120
taccctgcta cttgtattta aaatcaatgg tgatgttatt tcttangca cttcttctc 180
ttccctaata gctacaatnt gatacagtac gcaacagctc acttgaaagt gctagantca 240
```

<210> 320

207/292

<211> 457
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<220>
<221> misc_feature
<222> (1)..(457)
<223> 5' terminal sequence. retinoblastoma -binding
protein 7 (RBBP7) gene.

<400> 320
agatgtttga agatactgtg gaggagcgtg tcatcaatga agaatat aaa atctggaaga 60
agaatacacc gtttctatat gacctgggta tgacccatgc tcttcagtgg cccagtctta 120
ccgttcagtg gcttctctgaa gtgactaaac ctgaaggaaa agattatgcc cttcattggc 180
tagtgctggg gactcatacg tctgatgagc agaatcatct ggtgggtgct cgagtacata 240
ttcccaatga tgatgcacag tttgat gctt cccattgtga cagtgacaag ggtgaatttg 300
gtggcctttg ttctgtaaca ggnaaaattg aatgtgaaat taaaatcaat tcacgaagga 360
gaagttaaac cgtgctcgtt aacatggcgc cagantcctt cacatccatt gttacaaan 420
acaccctctt gcttgatggt gttggnnttt tgactat 457

<210> 321
<211> 1946
<212> DNA/RNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<220>
<221> misc_feature
<222> (1)..(1946)
<223> retinoblastoma -binding protein 7 (RBBP7)
gene.

<400> 321
gcctcgtcag ctgcctgggc gggc tgggag gcgcggggtg aaaagtctcg ttccaagttt 60
ggagagagag agaagagcgc ctcagacctc ggtacccgcg agcggggagg aggcaggaaa 120
gaaggacgcg gcgtctgggg agcaccagg cagcaagacg gggcccgggc tttcgacagt 180
ggggagtgtg acgcgcttgg gaaaggcagg agcgcagcgc gtcgggctgc tcttggttaa 240
cgagaggagt ccgaggcggc ggcgaggggc gaacgacccg acgcaagatg gcgagtaaag 300
agatgtttga agatactgtg gaggagcgtg tcatcaatga agaataaaa atctggaaga 360
agaatacacc gtttctatat gacctgggta tgacccatgc tcttcagtgg cccagtctta 420
ccgttcagtg gcttctctgaa gtgactaaac ctgaaggaaa agatt atgcc cttcattggc 480
tagtgctggg gactcatacg tctgatgagc agaatcatct ggtgggtgct cgagtacata 540
ttcccaatga tgatgcacag tttgatgctt cccattgtga cagtgacaag ggtgaatttg 600
gtggcctttg ttctgtaaca gaaaaattg aatgtgaaat taaaatcaat cacgaaggag 660
aagtaaaccg tgctcgttac atg ccgcaga atcctcacat cattgctaca aaaacaccat 720
cttctgatgt gttgggtttt gactatacaa aacaccctgc taaaccagac ccaagtggag 780
aatgtaatcc tgatctcaga ttaagaggtc accagaagga aggctatggt ctctcctgga 840
attcaaattt gagtggacat ctctaagtgc catctgatga ccatactgtt tgtctgtggg 900
atataaacgc aggacaaaa gaaggcaaaa ttgtggatgc taaagccatc tttactggcc 960
actcagctgt tgtagaggat gtggcctggc acctgctgca cgagtcattg tttggatctg 1020
ttgctgatga tcagaaactt atgatatggg acaccaggtc caataccacc tccaagccga 1080
gtcacttggg ggatgcgcac actgccgaag tcaactgcct c tcatccaat ccctacagcg 1140
aatttattct agccaccggc tctgcggata agaccgtagc tttatgggat ctgcgtaact 1200
taaaattaaa actccatacc ttogaatctc ataaagatga aattttccag gtccactggt 1260
ctccacataa tgaaactatt ctggcttcaa gtggtactga ccgccgcctg aatgtgtggg 1320

208/292

```

atttaagtaa aattggggaa gaacaatcag cagaagatgc agaagatggg cctccagaac 1380
tcctgtttat tcatggagga cacactgcta agatttcaga ttttagctgg aacccaatg 1440
agccttgggt catttgc tca gtgtctgagg ataacatcat gcagatatgg caaatggctg 1500
aaaatattta caatgatgaa gagtcagatg tcacgacatc cgaactggag ggaca aggat 1560
cttaaaccga aagtacgaga aatgtttctg ttgaatgtaa tgctacatga atgcttgatt 1620
tatcaagcgc caaaaaggca ttgtatagta ggaaatgtaa gtggggtggc ttatggcttc 1680
tttatcctct gattctagca ctttcaagt agctgttgcg tactgtatca tattgtagct 1740
attagggaag agaagaatgt tgcttaagaa agaacatcac cattgatttt aaatacaagt 1800
agcagggtat tgcctttgat tcaactgttt taagtctca ttttctcaaa ctaagtgcct 1860
gctgttccca aatatgcaag aataactttt acactttttc cttccaacac ttcttgattg 1920
gctttgcaga aataaagttt taaaat 1946

```

<210> 322

<211> 365

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(365)

<223> 3' terminal sequence. kiaa1075 protein
(KIAA1075) gene.

<400> 322

```

tatagaaatt ctttattatt agacaaaaat agactctctt tttccocta ttcatgtgat 60
cctactctga atctctgctc agaggaggca gtgactcgct cccacccct ctcccatccc 120
tgccgtgctg gcacctgcag ctgggtggaa ctggcagggg ctgatccct gggagggctg 180
acgttctcct gcagggtggg ctgctgctgc tccttcgggg ctcaactgct gatgcctcct 240
caccctcac acaccatct ctgccatctg ctacatggc aagggtcatc ttgtggggcc 300
tggtccactt taacttaggc agggctgggg ggcgggggaa gggagaggca gtgttcccag 360
gggcc 365

```

<210> 323

<211> 400

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(400)

<223> 5' terminal sequence. kiaa1075 protein
(KIAA1075) gene.

<400> 323

```

tcaagggtg cccagtgag cctactttg gcagcctgtc cgccttggtc tcccagcact 60
ccatctcccc catctccctg ccctgctgcc tgcgattcc cagcaaagat cctctggaag 120
agaccccaga ggtccagtg cccaccaaca tgagcacagc gncagacctc ctgctcagg 180
gtgctgcctg caggtnctc tacttgacct cagtggagac agagtactg acgggcccc 240
aagctgtggc ccgggccagc tctgcagctc tgagctgta g cccccgccg acaccagctg 300
ttgtccactt caaggtgtca gccaggga ttnacactga cgggacaacc aaaggaagct 360
ctttnttttc gccgccatta tccagtggaa cagcatcacc 400

```

209/292

<210> 324
<211> 489
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<220>
<221> misc_feature
<222> (1)..(489)
<223> 5' terminal sequence. atp-binding cassette,
sub-family c (cftr/mrp), member 5 (ABCC5) gene.

<400> 324
nttcggcaca gnaagataca actctgtgct gaacagctgc tgcctgaggc tgacctggcc 60
attcttccca gcacgcacct gacggagatt ggagagcgag tancaacctg agcgggtggc 120
agcgcagagg atcagccttg cccgggcctt gtatagtac aggagcatct acatcctgga 180
cgacccctc agtgcccttag atgcccattg ggaanccaca tncctcaata gtgctatccg 240
gaaacatctc aagtccaaga cagttctgtt tgttaccac cagt tacagt acctgggttg 300
actgtgatga agtgatcttc atgaaagagg gctgtattta cgggaaagag ggcaccntg 360
gaggaantg atggatttta aatgggtgatt atggttacct ttttaattaa cntgttggtg 420
ggggagagac accgccattg agntcatttc aaaaagggga accgtnggtt cacagaggag 480
ttcacagtt 489

<210> 325
<211> 5838
<212> DNA/RNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<220>
<221> misc_feature
<222> (1)..(5838)
<223> atp-binding cassette, sub-family c
(cftr/mrp), member 5 (ABCC5) gene.

<400> 325
ccgggcaggt ggctcatgct cgggagcgtg gttgagcggc tggcgcggtt gtcctggagc 60
aggggcgcag gaattctgat gtgaaactaa cagtctgtga gccctggaac ctccgctcag 120
agaagatgaa ggatatcgac ataggaaaag agtatatcat cccagtcct gggtagaaga 180
gtgtgaggga gagaaccagc acttctggga cgcacagaga ccgtgaagat tccaagttca 240
ggagaactcg accgttgga tgccaagatg ccttggaac agcagcccga gccgagggcc 300
tctctcttga tgcctccatg cattctcagc tcagaatcct ggatgaggag catccaagg 360
gaaagtacca tcatggcttg agtgcctga agcccatccg ga ctacttcc aaacaccagc 420
accagtgga caatgctggg ctttttctct gtatgacttt ttcgtggctt tcttctcttg 480
ccgtgtggc ccacaagaag gggagctct caatggaaga cgtgtggtct ctgtccaagc 540
acgagtcttc tgacgtgaac tgcagaagac tagagagact gtggcaagaa gagctgaatg 600
aagtggggc agacgctgct tccctgcgaa gggttgtgtg gatcttctgc cgcaccaggc 660
tcatcctgtc catcgtgtgc ctgatgatca cgcagctggc tggcttcagt ggaccagcct 720
tcatggtgaa acacctcttg gagtataccc aggcaacaga gtctaacctg cagtacagct 780
tgttgtagt gctgggctc ctctgacgg aaatcgtgcg gtcttggtcg cttgactga 84 0%
cttggaatt gaattaccga accggtgtcc gcttgcgggg ggccatccta accatggcat 900
ttaagaagat ccttaagtta aagaacatta aagagaaatc cctgggtgag ctcatcaaca 960
tttgcctcaa cgatgggcag agaattgttg aggcagcagc cgttggcagc ctgctggctg 1020
gaggaccggt tgttgccatc ttaggcatga tttataatgt aattattctg ggaccaacag 1080
gcttctctgg atcagctgtt tttatcctct tttaccagc aatgatgtt gcatacggc 1140
tcacagcata tttcaggaga aaatgcgtgg ccgccacgga tgaacgtgtc cagaagatga 1200

210/292

atgaagttct tacttacatt aaatttatca aaatgtatgc ctgggtcaaa gcattttctc 1260
 agagtgttca aaaaatccgc gaggaggagc gtcggatatt ggaaaaagcc ggggtacttcc 1320
 aggggtatcac tgtgggtgtg gctcccattg tgggtgtgat tgccagcgtg gtgaccttct 1380
 ctgttcatat gaccttgggc ttcgatctga cagcagcaca ggctttcaca gtgggtgacag 1440
 tcttcaattc catgactttt gctttgaaag taacaccgtt ttcagtaaag tcc ctctcag 1500
 aagcctcagt ggctgttgac agatttaaga gtttgtttct aatggaagag gttcacatga 1560
 taaagaacaa accagccagt cctcacatca agatagagat gaaaaatgcc accttggcat 1620
 gggactcctc ccactccagt atccagaact cgcccaagct gaccccaaaa atgaaaaaag 1680
 acaagagggc ttccaggggc aagaaaga ga aggtgaggca gctgcagcgc actgagcatc 1740
 aggcgtgtct ggcagagcag aaaggccacc tcctcctgga cagtgcagag cggcccagtc 1800
 ccgaagagga agaaggcaag cacatccacc tgggccacct gcgcttacag aggacactgc 1860
 acagcatcga tctggagatc caagagggta aactgtgttg aatctgcggc agtgtgggaa 1920
 gtggaaaaac ctctctcatt tcagccattt taggccagat gacgcttcta gagggcagca 1980
 ttgcaattac tggaaacctc gcttatgttg ccagcaggc ctggatcctc aatgctactc 2040
 tgagagacaa catcctgttt gggaaggaa atgatgaaga aagatacaac tctgtgtgta 2100
 acagctgtct cctgaggcct gacctggcca ttcttcccag c agcgacctg acggagattg 2160
 gagagcgagg agccaacctg agcgtgtggc agcgcagag gatcagcctt gcccgggcct 2220
 tgtatagtga caggagcatc tacatcctgg acgacccctc cagtgcctta gatgcccatg 2280
 tgggcaacca catcttcaat agtgcctatc ggaaacatct caagtccaag acagttctgt 2340
 ttgttaccga ccagttacag tacctgtgtg actgtgatga agtgatctt atgaaagagg 2400
 gctgtattac ggaaagagc acccatgagg acctgatgaa tttaaatggt gactatgcta 2460
 ccatttttaa taacctgttg ctgggagaga caccgccagt tgagatcaat tcaaaaaagg 2520
 aaaccagtgg ttacagaag aagtcacaag acaagggtcc taaaacagga tcagt aaaga 2580
 aggaaaaagc agtaagcca gaggaagggc agcttgtgca gctggaagag aaagggcagg 2640
 gttcagtgcc ctggtcagta tatgtgtgtc acatccaggc tgctgggggc cccttggcat 2700
 tctgtgttat tatggccctt ttcagtctga atgtaggcag caccgccttc agcacctggt 2760
 ggttgagtta ctggtacag caaggaagcg ggaacaccac tgtgactcga ggaacgaga 2820
 cctcggtgag tgacagcatg aaggacaatc ctcatatgca gtactatgcc agcatctacg 2880
 cctctccat ggcagtcctg ctgatcctga aagccattcg aggagttgtc tttgtcaagg 2940
 gcacgctgag agcttctctc cggtgcatg acgagctttt ccgaaggatc cttcgaagcc 3000
 ctatgaaagt ttttgacacg acccccacag ggaggattct caacagggtt tccaaagaca 3060
 tggatgaagt tgacgtgagg ctgccgttcc aggcagagat gttcatccag aacgttatcc 3120
 tgggtgttct ctgtgtggga atgatgcag gactcttccc gtgggttctt gtggcagtgg 3180
 ggcccttgt catctctttt tcagtctctc acattgtctc cag ggtcctg attcgggagc 3240
 tgaagcgtct ggacaatatc acgcagtcac ctctctctc ccacatcag tccagcatac 3300
 agggccttgc caccatccac gcctacaata aagggcagga gtttctgcac agataccagg 3360
 agctgtcgtga tgacaacca gctccttttt tttgttttac gtgtgcgatg cgggtgctgg 3420
 ctgtgcggct ggacctca tc agcatcgccc tcatcaccac caccgggctg atgatcgttc 3480
 ttatgcacgg gcagattccc ccagcctatg cgggtctctc catctcttat gctgtccagt 3540
 taacggggct gttccagttt acggtcagac ttgcatctga gacagaagct cgattcacct 3600
 cgttgagagag gatcaatcac tacattaaga ctctgtcctt ggaagcacct gccagaa tta 3660
 agaacaaggc tccctccctt gactggcccc agggaggaga ggtgacctt gagaacgcag 3720
 agatgaggtg ccgagaaaa ctcctctctg tcctaaagaa agtatccttc acgatcaaac 3780
 ctaaagagaa gattggcatt gtggggcgga caggatcagg gaagtcctcg ctggggatgg 3840
 ccctcttccg tctggtggag ttatctggag g ctgcatcaa gattgatgga gtgagaatca 3900
 gtgatatggc ccttgccgac ctccgaagca aactctctat cattctcaa gagccggtgc 3960
 tgttcagtgg cactgtcaga tcaaatttgg accccttcaa ccagtacact gaagaccaga 4020
 tttgggatgc cctggagagg acacacatga aagaatgtat tgctcagcta cctctgaaac 4080
 ttgaatctga agtgatggag aatggggata acttctcagt gggggaacgg cagctcttgt 4140
 gcatagctag agccctgctc cgccactgta agattctgat tttagatgaa gccacagctg 4200
 ccatggacac agagacagac ttattgattc aagagaccat ccgagaagca tttgcagact 4260
 gtaccatgct gaccattgcc catcgccctg acacggttct aggt ccgat aggattatgg 4320
 tgctggccca gggacagggt gtggagtttg acacccctc ggtcctctg tccaacgaca 4380
 gttcccgatt ctatgctatg ttgctgctg ccagaaacaa ggtcgtctg aagggtgac 4440
 tcctccctgt tgacgaagtc tcttttcttt agagcattgc cattccctgc ctggggcggg 4500
 ccctcatcg cgtcctcta ccgaaacctt gcctttctcg attttatctt tcgcacagca 4560
 gttccggatt ggctgtgtg tttcactttt agggagagtc atattttgat tattgtattt 4620
 attccatatt catgtaaaaa aaatttagtt tttgttctta attgcactct aaaaggttca 4680
 gggaaccgtt attataattg tatcagaggc ctataatgaa gctttatacg tgtagctat a 4740
 tctatatata attctgtaca tagcctatat ttacagtga aatgtaagct gtttatttta 4800
 tattaataata agcactgtgc taataacagt gcatattcct ttctatcatt tttgtacagt 4860

211/292

```

ttgctgtact agagatctgg ttttcttatt agactgtagg aagagtagca tttcattctt 4920
ctctagctgg tggtttcacg gtgccagggtt ttc tgggtgt ccaaaggaag acgtgtggca 4980
atagtgggcc ctccgacagc cccctctgcc gcctccccac agccgctcca ggggtggctg 5040
gagacgggtg ggcggctgga gaccatgcag agcgcctga gttctcaggg ctctgcctt 5100
ctgtcctggg gtcacttact gtttctgtca ggagagcagc ggggcgaagc ccaggccctt 5160
tttcaactcc tccatcaaga atggggatca cagagacatt cctccgagcc ggggagtttc 5220
tttctgcct tcttcttttt gctgttgtt ctaaacaaga atcagtctat ccacagagag 5280
tcccactgcc tcaggttcct atggctggcc actgcacaga gctctccagc tccaagacct 5340
gttggttcca agccctggag ccaactgctg ctttttgagg tggcact ttt tcatttgcct 5400
attcccacac ctccacagtt cagtggcagg gctcaggatt tcgtgggtct gttttccttt 5460
ctcaccgcag tcgtcgaca gtctctctct ctctctcccc tcaaagtctg caactttaag 5520
cagctcttgc taatcagtg ctcacactgg cgtagaagtt tttgtactgt aaagagacct 5580
acctcagggt gctgggtgct g tgtggttg gtgtgttccc gcaaaccccc tttgtgctgt 5640
ggggtggtga gctcagggtg gcgtggtcac tgctgtcatc agttgaatgg tcagcgttgc 5700
atgtcgtgac caactagaca ttctgtgcgc ttagcatgtt tgctgaacac cttgtggaag 5760
caaaaatctg aaaatgtgaa taaaattatt ttggattttg taacaaaaaa aaaaaaaa 5820
aaaaaaaaa aaaaaaaa
5838

```

<210> 326

<211> 385

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(385)

<223> 3' terminal sequence. cadherin 1, type 1,
e-cadherin (epithelial) (CDH1) gene.

<400> 326

```

aanganatat taacaaaatt gtttaataaa atttataaaa atgcatcttt gagaatactt 60
tnctcagctt gaattgtttt ccttttccac ccccaaagaa aatacacaat tatcagcacc 120
cacacatgta tacactcaaa actacagtga catt ctctac acagnnctat attcgatata 180
gcttgaactg ccgaaaaatc angacaattc caaaagggtga ttgcagggtt gatttttttc 240
tccaaaacac ttgaganaca gtaaagctat ttcaacaaag gtotttncct tgattgtcaa 300
aggttgaaat tcacatttna ntannagggg ntcnaatca ngntcctcac taccctctac 360
ccctcancta accccctttg gggcc
385

```

<210> 327

<211> 423

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(423)

<223> 5' terminal sequence. cadherin 1, type 1,
e-cadherin (epithelial) (CDH1) gene.

<400> 327

```

ggcagagca aganaggagt tctctgatgc agaaattatt gggctctttt agggtaagaa 60
gtttgtgtct ttgtctggcc acatcttgac taggtattgt ctactctgaa gacctttaat 120
ggcttccctc tttcatctcc tgagtatgta acttgcaatg ggcagctatc c agtgacttg 180

```

212/292

```

ttctgagtaa gtgtgttcat taatgtttat ttagctctga agcaagagt atatactcca 240
gggacttaga atagtgccta aagtgtgca gccaaagaca gagcggaact atgaaaagt 300
ggcttgagaga tggcaggaga gcttgtcatt gagcctgggc aatttnagca aactgatgtc 360
tgaggatgat tcgagggtggg tcttacctca tctactgnaa aattctggta aggaatggga 420
ggg 423

```

<210> 328

<211> 4828

<212> DNA/RNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(4828)

<223> cadherin 1, type 1, e-cadherin (epithelial)
(CDH1) gene.

<400> 328

```

agtggcgctg gaactgcaaa gcacctgtga gcttgccgaa gtcagttcag actccagccc 60
gctccagccc ggcccgaacc gaccgcaccc ggcgccctgcc ctgcctcggc gtcccgcggc 120
agccatgggc ccttgagacc gcagcctctc ggcgctgctg ctgctgctgc aggtctcctc 180
ttggctctgc caggagccgg agccctgcca ccctggcctt gacgccgaga gctacacgtt 240
cacggtgccc cggcgccacc tggagagagg ccgcgtcctg ggcagagtga attttgaaga 300
ttgcaccggg cgacaaagga cagcctatct tccctcgac acccgattca aagtgggcac 3 60
agatgggtgtg attacagtca aaaggcctct acggtttcat aaccacaga tccatttctt 420
ggtctacgcc tgggactoca cctacagaaa gttttccacc aaagtacgc tgaatacagt 480
ggggcaccac caccgcccc cgcccatca ggctccgtt tctggaatcc aagcagaatt 540
gtccacattt cccaactcct ctctggcct cagaagacag aagagagact gggttattcc 600
tcccacagc tgcccagaaa atgaaaaagg ccatttctt aaaaacctgg ttcagatcaa 660
atcccaaaaa gacaaagaag gcaaggcttt ctacagcatc actggccaag gagctgacac 720
acccctgtgt ggtgtcttta ttattgaaag agaaacagga tggctgaagg tgacagagcc 780
tctggataga gaacgcag tg ccacatacac tctcttctc cagctgtgt catccaacgg 840
gaatgcagtt gaggatccaa tggagatttt gatcacggta accgatcaga atgacaacaa 900
gcccgaattc acccaggagg tctttaaggg gtctgtcatg gaagggtgct tccaggaaac 960
ctctgtgatg gaggtcacag ccacagacgc ggacgatgat gtgaacacct acaatgccgc 1020
catcgcttac accatcctca gccaaagatcc tgagctccct gacaaaaata tgttcacat 1080
taacaggaac acaggagtca tcagtgtggt caccactggg ctggaccgag agagtttccc 1140
tacgtatacc ctggtgtgtc aagtgtctga ccttcaaggt gaggggttaa gcacaacagc 1200
aacagctgtg atcacagtc ctgacaccaa cgat aatcct ccgatcttca atcccaccac 1260
gtacaagggt caggtgcctg agaacgaggg taacgtcgta atcaccacac tgaaagtgaac 1320
tgatgtgatg gcccacaata cccagcgtg ggaggtgtg tacaccatat tgaatgatga 1380
tgggtggaca tttgtcgtca ccacaaatcc agtgaacaac gatggcattt tgaaaacagc 1440
aaagggttg gattttgagg ccaagcagca gtacattcta cagtagcag tgacgaatgt 1500
ggtacctttt gaggtctctc tcaccacctc cacagccacc gtcaccgtgg atgtgctgga 1560
tgtgaatgaa gcccctatct ttgtgcctcc tgaaaagaga gtggaagtgt ccgaggactt 1620
tggcgtgggc caggaaatca catcctacac tgcccaggag ccagacac at ttatggaaca 1680
gaaaataaca tatcgattt ggagagacac tgccaactgg ctggagatta atccggacac 1740
tgggtgccatt tccactcggg ctgagctgga caggaggagt tttgagcac tgaagaacag 1800
cacgtacaca gccctaatac tagctacaga caatggttct ccagttgcta ctggaacagg 1860
gacactctcg ctgatctgt ct gatgtgaa tgacaacgcc ccataaccag aacctogaac 1920
tatattcttc tgtgagagga atccaaagcc tcaggtcata aacatcattg atgcagacct 1980
tctcccaat acatctccct tcacagcaga actaacacac gggcgagtg ccaactggac 2040
cattcagtag aacgacccaa ccaagaatc tatcattttg aagccaaaga tggccttaga 2 100
ggtgggtgac taaaaaatca atctcaagct catggataac cagaataaag accaagtgaac 2160
caccttagag gtcagcgtgt gtgactgtga aggggccgcc ggcgctctgta ggaaggcaca 2220
gcctgtcgaa gcaggattgc aaattcctgc cattctgggg attcttgag gaattcttgc 2280
tttgctaatt ctgattctgc tgcctctgct gtttct tcgg aggagagcgg tggtaaaga 2340

```

213/292

```

gcccttactg cccccagagg atgacacccg ggacaacggt tattactatg atgaagaagg 2400
aggcggagaa gaggaccagg actttgactt gagccagctg cacagggggc tggacgctcg 2460
gcctgaagtg actcgtaacg acgttgaccc aaccctcatg agtgtccccc ggtatcttcc 2520
ccgccttgcc aatcccgatg aaattggaaa ttttattgat gaaaatctga aagcggctga 2580
tactgacccc acagcccgcg cttatgattc tctgctcgtg tttgactatg aaggaagcgg 2640
ttccgaagct gctagtctga gctccctgaa ctccctcagag tcagacaaag accaggacta 2700
tgactacttg aacgaatggg gcaatcgctt caagaagctg gctgacatgt acggaggcgg 2760
cgaggacgac taggggactc gagagaggcg ggccccagac ccatgtgctg ggaaatgcag 2820
aaatcacggt gctggtggtt tttcagctcc ctcccttga gatgagtttc tggggaaaaa 2880
aaagagactg gttagtgatg cagttagtat agctttatac tctctccact ttatagctct 2940
aataagtttg tgttagaaaa gttt cgactt atttcttaaa gctttttttt ttttcccatc 3000
actctttaca tgggtggtgat gtccaaaaga tacccaaatt ttaatatcc agaagaacaa 3060
ctttagcatc agaaggttca cccagcacct tgcagatttt ctttaaggaa tttgtctcac 3120
ttttaaaaaa aaggggagaa gtcagctact ctagtctgtg tgttttgtgt atataatttt 318 0
ttaaaaaaaa tttgtgtgct tctgctcatt actacactgg tgtgtccctc tgcctttttt 3240
ttttttttta agacagggtc tcattctatc ggccaggctg gagtgcagtg gtgcaatcac 3300
agctcactgc agccttgtcc tcccaggctc aagctatcct tgcacctcag cctcccaagt 3360
agctgggacc acaggcatgc accactacgc atgactaa tt ttttaaatat ttgagacggg 3420
gtctccctgt gttaccaggg ctggtctcaa actcctgggc tcaagtgatc ctcccatctt 3480
ggcctcccag agtattggga ttacagacat gagccactgc acctgcccag ctccccaact 3540
ccttgccatt ttttaagaga cagtttcgct ccatcgccca ggctgggat gcagtgatgt 3600
gatcatagct cactgtaacc tcaaactctg gggctcaagc agttctccca ccagcctcct 3660
ttttattttt ttgtacagat ggggtcttgc tatgttgccc aagctggtct taaactcctg 3720
gcctcaagca atccttctgc cttggccccc caaagtgctg ggattgtggg catgagctgc 3780
tgtgcccagc ctccatgttt taatatcaac tctcactcct gaattcagtt g ctttgccca 3840
agataggagt tctctgatgc agaaattatt gggctctttt agggtaagaa gtttgtgtct 3900
ttgtctggcc acatcttgac taggtattgt ctactctgaa gacctttaat ggcttccctc 3960
tttcatctcc tgagtatgta acttgcaatg ggcagctatc cagtgacttg ttctgagtaa 4020
gtgtgttcat taatgtttat ttagct ctga agcaagagt atatactcca ggacttagaa 4080
tagtgccata agtgctgcag ccaaagacag agcggaaacta tgaaaagtgg gcttgagat 4140
ggcaggagag cttgtcattg agcctggcaa tttagcaaac tgatgctgag gatgattgag 4200
gtgggtctac ctcatctctg aaaattcttg aaggaatgga ggagtctcaa catgtgtttc 4260
tgacacaaga tccgtggttt gtactcaaag cccagaatcc ccaagtgcct gcttttgatg 4320
atgtctacag aaaatgctgg ctgagctgaa cacatttgcc caattccagg tgtgcacaga 4380
aaaccgagaa tattcaaaat tccaaatttt ttcttaggag caagaagaaa atgtggccct 4440
aaagggggtt agttgagggg tagggggtag tgaggatctt gatttggatc tctttttatt 4500
taaattgtgaa tttcaacttt tgacaatcaa agaaaagact tttgttgaaa tagctttact 4560
gtttctcaag tgttttgag aaaaaaatca accctgcaat cacttttttg aattgtcttg 4620
atttttcggc agttcaagct atatcgata tagttctgtg tagagaatgt cactgtagtt 4680
ttgagtgtat acatgtgtgg gtgctgataa ttgtgtattt tctttggggg tggaaaagga 4740
aaacaattca agctgagaaa agtattctca aagatgcatt tttataaatt ttattaaaca 4800
attttgttaa accataaaaa aaaaaaaa
4828

```

<210> 329

<211> 471

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(471)

<223> 5' terminal sequence. zinc finger protein
144 (mel-18) (ZNF144) gene.

<400> 329

```

attcggcaca tgattccact tccgtttccc agggcaacgc tccccagtcc cccacccc cc 60
gaccccgga tcatgcatcg gactacacgg atcaaaatca cagagctgaa cccccacctc 120

```

214/292

```
atgtgtgccc tctgcggggg gtacttcacg gacgccacca ctatcgtgga gtgcctgcat 180
tccttctgca aaacctgcat cgtgcgctac ctggagacca acaaatactg ccccatgtgt 240
gacgtgcagg tccataaaac ccggcgcgtg ctgagca ttc aggtctgaca aaacatttca 300
agacattgtc ttacaaattg gtccctgggg ctttttaaag atggagattg aaacggggcg 360
cgggatttct tatggcaggc gttaccctt ggacgggagg ttcccccaac ggnttccaat 420
tgagggaccg ngggcgaggg ttttnggga ggcagggaga aggggggttt t 471
```

<210> 330

<211> 2227

<212> DNA/RNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(2227)

<223> zinc finger protein 144 (mel -18) (ZNF144)
gene.

<400> 330

```
gagagccga acaggaagag ggtacagctt tgtg caggtc acatgccac tgcagccctc 60
cagcctctgg tccccagagc ggactttgga agctgaactg cttttgttgc tggaaagactt 120
atgttataat ttaccctggg tggaccaggg tcgtacaaaa gggcaacgct cccagctccc 180
ccactcccg accccggaat catgcacgga actacacgga tcaaaatcac agagctgaac 240
ccccacctca tgtgtgcct ctgcgggggg tacttcacg acgccaccac tatcgtggag 300
tgctgcatt cttctgcaa aacctgcac gtgcgtacc tggagaccaa caaatactgc 360
ccatgtgtg acgtgcagg ccataaaacc cggcgcgtgc tgagcatcag gtctgacaaa 420
acactcaag acattgtcta caaattggtc cctgggcttt ttaaagatga gatga aacgg 480
cggcgggatt tctatgcagc gtacccctg acggaggctc ccaacggctc caatgaggac 540
cgcggcgagg tcttgagca ggagaagggg gctctgagtg atgatgagat tgtcagcctc 600
tccatcgaat tctacgaagg tgccaggggac cgggatgaga agaaggggccc cctggagaat 660
ggggatgggg acaaagagaa aacaggggtg cgc ttctctgc gatgccagc agccatgacc 720
gtcatgcac ttgccaagtt tctccgcaac aagatggatg tgcccagcaa gtacaagggtg 780
gaggttctgt acgaggacga gccactgaag gaatactaca cctcatgga catcgctac 840
atctaccctt ggcggcgga cgggcctctc cccctcaagt accgtgtcca gccagcctgc 900
aagcggctca ccctagccac ggtgccacc ccctcggagg gcaccaacac cagcggggcg 960
tccgagtgtg agtcagtcag cgacaaggct cccagccctg ccaccctgcc agccacctcc 1020
tcctccctgc ccagccagc caccocatcc catggctctc ccagttcca tgggcctcca 1080
gccaccacc ctacctccc cactccccct tcgacagcca gtggggccac c acagctgcc 1140
aacgggggta gcttgaactg cctgcagaca ccactctcca ccagcagggg gcgcaagatg 1200
actgtcaacg gcgtcccggt gcccccctta acttgaggcc agggaccctc tcccttcttc 1260
cagccaagcc tctccactcc ttccactttt tctgggcctt tttttccact tcttctactt 1320
tccccagctc tccccacctt ggggggt gggg ggcgggtttt ataaataaat atatatatat 1380
atgtacatag gaaaaacaa atatacatat ttattttcta tggaccaacc agattaattt 1440
aaatgccaca ggaacaaaac tttatgtgtg tgtgtatgtg tggaaaatgg tgttcatttt 1500
ttttgggggg ggtcttgtgt aatttgctgt ttttgggggt gcctggagat gaactggatg 1560
ggccaactga gtctcaataa agctctgcac catcctcgt gtttcccaag gcagtggtg 1620
tggtgggggc cccttcagac ccaaagcttt aggcgatgatt ccaactggct gcataatagga 1680
gtcagttaga attgtttctt tctctccccg tttctctccc catcttggct gctgtcctgc 1740
ctctgaccag tggccgcccc ccgcgttgtt gaatgtccag aaattgctaa gaacagtgcc 1800
ttttacaaat gcagtttatc cctggttctg aggagcaagt gcagggtgga ggtggcacct 1860
gcatacctc ctctcttgc agtggaact ttgtgcaaag aatagatagt tctgcctctt 1920
ttttttttt ttctgtgtg tgtggccttt gcatacttta tcttgtggaa aagaagattc 1980
aggccctgag aggtctcagc tcttgaggga gggctaaggc ttttagcattg tgaagcgctg 2040
caccctcacc aaccttacc tcaccgggga accctacta gcaggactgg tggaggagtc 2100
tcacctgggg cctagagtgg aagtgggggt gggttaacct cacacaagca cagatcccag 2160
actttgccag aggcaaacag ggaattccgc cgatactgac gggctccagg agt cgtcgcc 2220
acactcg 2227
```

<210> 331
<211> 254
<212> DNA
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(254)

<223> 3' terminal sequence. macrophage stimulating
1 (hepatocyte growth factor -like) (MST1) gene.

<400> 331

```
gcataaagag gaaacatggc tttatgtctg acaagaagtt ttgtcctccc caaggcatat 60
ggcatcaagg ctgggctaac ccagtctcat gaccttgtga atccagtcca caaacacaga 120
gacacgcgtg aagacagctg gccagcggga ccttgcgcat actcggttgg ggattataat 180
tccttcagg gaccagcag ttgtgggtaa agcaggcaag tgggcccccg tagtcaccct 240
cacaggcccc caca                                     254
```

<210> 332
<211> 362
<212> DNA
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(362)

<223> 5' terminal sequence. macrophage stimulating
1 (hepatocyte growth factor -like) (MST1) gene.

<400> 332

```
gccatggnc tggtgctaca cgatggaccc aaggacccca t tcgactact gtgccctgog 60
acgtctgcgt gatgaccagc cgccatcaat cctggacccc ccagaccagg tgcagtttga 120
gaagtgtggc aagaggttgg atcggctgga tcagcggcgt tccaagctgc gctggttggg 180
ggccatccgg gcaactcacc ctggacagtc agcttgcgga atcggcaggg ccagcatttc 240
tgcggngngt ctctagttaa ggagcagtn gatactgactn cccggaagtg cttctcctcc 300
tnccatatnc ctctcacggg ctatgaggta tggttngggc ancctttttc cagaaccac 360
ag                                     362
```

<210> 333
<211> 2219
<212> DNA/RNA
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(2219)

<223> macrophage stimulating 1 (hepatocyte growth
factor-like) (MST1) gene.

216/292

<400> 333

agccagaagg atgggggtggc tccactoct gctgcttctg actcaatgct taggggtccc 6 0
tgggcagcgc tcgccattga atgacttoca agtgctccgg ggcacagagc tacagcacct 120
gctacatgcg gtgggtgccg ggccttggca ggaggatgtg gcagatgctg aagagtgtgc 180
tggtcgctgt gggcccttaa tggactgccg ggccttccac tacaacgtga gcagccatgg 240
ttgccaaactg ctgccatgga ctcaacactc gcccacacg aggtgcggc gttctggggc 300
ctgtgacctc ttccagaaga aagactacgt acggacctgc atcatgaaca atgggggttg 360
gtaccggggc accatggcca cgacctggg tggcctgcc tgccaggctt ggagccacaa 420
gttcccgaat gatcacaagt acacgccac tctccgaat ggctggaag agaacttctg 480
ccgtaaccct gatggcgac c cggaggtcc ttgggtgtac acaacagacc ctgtgtgctg 540
cttccagagc tgcggcatca aatcctgccg ggaggccgcg tgtgtctggt gcaatggcga 600
ggaataccgc ggcgcgtag accgcacgga gtcagggcgc gagtgccagc gctgggatct 660
tcagcaccgc caccagcacc ccttcgagcc gggcaagttc ctcgaccaag gtctggacga 720
caactattgc cggatcctg acggctccga cgggccatgg tgctacacta cggatccgca 780
gatcgagcga gaggttctgt acctccccg ctgcgggtcc gaggcacagc cccgccaa 840
ggccacaact gtcagctgct tccgcgggaa ggtgagggc taccggggca cagccaatac 900
caccactgcg ggcgtacct gccagcgttg ggacgcga a atccgcctc agcaccgatt 960
taogccagaa aaatacgcgt gcaaagacct tcgggagaac ttctgccgga accccgacg 1020
ctcagaggcg ccttggtgct tcacactgcg gcccgcatg cgcgcggcct ttgtctacca 1080
gatccggcgt tgtacagagc acgtgcggcc ccaggactgc taccacggcg caggggagca 1140
gtaccgcggc acgg tcagca agaccgcaa ggtgtccag tgccagcgt ggtccgctga 1200
gacgccgcac aagccgcagt tcacgtttac ctccgaaccg catgcacaac tggaggagaa 1260
cttctgccgg aaccagatg gggatagcca tggccctgg tgctacacga tggaccaag 1320
gaccccatc gactactgtg cctgcgcagc ctgcgtgat gaccagccgc cat caatcct 1380
ggacccccca gaccaggtgc agtttgagaa gtgtggcaag aggttgatc ggctggatca 1440
cggcgcttcc aagctgcgcg tggttgggg ccacccggc aactcaccct ggacagtcag 1500
cttgcggaat cggcagggcc agcatttctg cggggggtct ctagtgaagg agcagtggt 1560
actgactgcc cggcagtgct tctcctcc tg ccatatgcct ctacgggct atgaggtatg 1620
gttgggcacc ctgttccaga accacagca tggagagcca agcctacagc gggctccagt 1680
agccaagatg gtgtgtggc cctcaggctc ccagcttgc ctgctcaagc tggagagatc 1740
tgtgacctg aaccagcgtg tggccctgat ctgcctgcc cctgaatggt atgtggtgcc 1800
tccagggacc aagtgtgaga ttgcaggctg ggtgagacc aaaggtacgg gtaatgacac 1860
agtcctaaat gtggccttcc tgaatgttat ctccaaccag gagtgttaaca tcaagcaccg 1920
aggacgtgtg cgggagagtg agatgtgcac tgagggactg ttggccctg tgggggcctg 1980
tgagggtgac tacgggggccc cacttgctg ctttaccac a actgctggg tcttggagg 2040
aattataatc cccaaccgag tatgcgcaag gtcccgctg ccagctgtct tcacgcgtgt 2100
ctctgtgttt gtggactgga ttcacaaggt catgagactg ggttaggcc agccttgatg 2160
ccatatgcct tggggaggac aaaacttctt gtcagacata aagccatgtt tcctcttta 2219

<210> 334

<211> 431

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(431)

<223> 3' terminal sequence. glutathione
s-transferase pi (GSTP1) gene.

<400> 334

gaaaggaagg caaactctgc ccccc gctca gagtcccccc aaccctcact gtttcccggt 60
gccattgatg gggagggtca cgtactcagg ggaggccagg naggcntgna gcttggggccg 120
ggcactgagg cgcacacat atgtgagag cagggggaac gcatccaggc agccagggt 180
agggaccnca tggatcagca gcaagtccag caggttntag tcagcgaagg agntctggtc 240
tcccacaatg aaggtcttgc ctccctggtt ctgggacagc aggtctcaa aaggcttcag 300

217/292

ttgcccgggc agtgccttca catagtcac cttgcccgcc tcatagttgg tntagatgag 360
ggagatgtat ttgcagcgga ggtcctccac gccgttcatt tcacctgtcc accagggtg 420
nctccntttt t 431

<210> 335
<211> 305
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<220>
<221> misc_feature
<222> (1)..(305)
<223> 5' terminal sequence. glutathione
s-transferase pi (GSTP1) gene.

<400> 335
nattcggcac aggtcgccac catgccgccc tacaccgtgg tctatttccc agttcgaggc 60
cgctgcctgt cggcaatgct gctggcagat cagggccaga gctggaagga ggaggtngtg 120
accgtggaga cgtggcagga gggctcactc aaagcctcct gcctatacgg gcagctcccc 180
aagttccagg acggagacct naccctgtac cagt ccaata ccacctgctg tcacctgggc 240
cgcacccttg ggctnctatg ggaaggacca gcaggangca gccctggtgg acatngtgaa 300
tgacg 305

<210> 336
<211> 737
<212> DNA/RNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<220>
<221> misc_feature
<222> (1)..(737)
<223> glutathione s-transferase pi (GSTP1) gene.

<400> 336
ggagtttcgc cgccgcagtc ttgccacca tgccgcccta caccgtggtc tatttcccag 60
ttcgaggccg ctgcgcggcc ctgcgcatgc tgctggcaga tcagg gccag agctggaagg 120
aggaggtggt gaccgtggag acgtggcagg agggctcact caaagcctcc tgcctatac 180
ggcagctccc caagttccag gacggagacc tcaccctgta ccagtccaat accatcctgc 240
gtcacctggg cgcaccctt gggtctatg ggaaggacca gcaggaggca gccctggtgg 300
acatggtgaa tgacggcgtg gag gacctcc gctgcaaata catctccctc atctacacca 360
actatgaggc gggcaaggat gactatgtga aggcactgcc cgggcaactg aagccttttg 420
agaccctgct gtcccagaac cagggaggca agaccttcat tgtgggagac cagatctcct 480
tcgctgacta caacctgctg gacttgctgc tgatccatga ggtcctagcc cctggctgcc 540
tggatgcgtt cccctgctc tcagcatatg tggggcgcc cagcgcccg cccaagctca 600
aggccttctt ggcctccct gagtacgtga acctcccat caatggcaac gggaaacagt 660
gagggttggg gggactctga gcgggaggca gagtttgctt tcttttctcc aggaccaata 720
aaatttctaa gagagct 737

<210> 337
<211> 372
<212> DNA
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(372)

<223> 3' terminal sequence. b-cell cll/lymphoma 2
(BCL2) gene.

<400> 337

```
gtgggnctgt gttgaaacag gccacgtaaa gcaactctct aaagggtcaaa ccaccataga 60
tttgaatctg ctgggtcattc gccatctgga tttttaactg aatgaatctc atgggtttta 120
ccaaacatgc atgtaatcct gaataccatg anttaaatgc gganttgccc agggacgagg 180
aaaccttcaa gaaacaaggt caaagggaca ncagatata a ctgtcacant aaacanttct 240
gttgacgtgg gaaatgcaca tgacttggtt gaaacaaagc tcctcagtgg gccagtgaca 300
tcnngggttt ttcttagggt aggctgagga ctgagggtct tatctcacct tctcaggaat 360
gctttttgaa gg                                     372
```

<210> 338

<211> 508

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(508)

<223> 5' terminal sequence. b-cell cll/lymphoma 2
(BCL2) gene.

<400> 338

```
nttcggcaca gacttttttt aagctaccaa ttg tgccgag aaaagcattt tagcaattta 60
tacaatatca tccagtaacct taaaccctga ttgtgtatat tcatatattt tggatacgca 120
ccccccaact cccaatactg gctctgtctg agtaagaaac agaatoctct ggaacttgag 180
gaagtgaaca tttcgggtgac ttccgcatca ggaaggctag agttaccagc agcatcaggc 240
cgccacaagt gcctgctttt aggagaccga agtccgcaga acctgcctgt gtcccagctt 300
ggaggcctgg gtocctggga ctgagccggg gccctcactg gccttcttc caggggatgg 360
atcaacaggg gcagtgtggt cttccgaatg tctgggaagc tgatgggagc tcagantttc 420
cactgtcaag aaagaggcag ttaggagggg tttgggtggg gcttggtcac ctgg ggggcc 480
ttccaggtag ggcccttttt aagtggga                                     508
```

<210> 339

<211> 445

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(445)

<223> 3' terminal sequence. proliferating cell
nuclear antigen (PCNA) gene.

<400> 339

219/292

tttttttant caaaagtttg aaattcaagt aactttatatt aaattcaaaa acaattctta 60
aaactgcatt tagagtcaag acccttttgt attataaaaa tcacaagtat ttctaagaga 120
caaaaataact tctagggttaa ctagaccaga tctgactt tg gactttattc tttaaacaan 180
ttgcagagan tagagaaaaa antagggttat ttacagaaaa caatatctac atatgtactt 240
ngnggtacaa ntttgggtga cagaaaagac ttcaggtata tgctgggcac cttaggaagn 300
cagttctcaa agggnccttag gttttatttn cttggatttt taaggattgc cctaagganc 360
ccttcttcat cctcgn tctt gggggnggcc aggtaggtn tttagggtgc cccntatccc 420
ganttttata ctctncaccg ggggg 445

<210> 340

<211> 437

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(437)

<223> 5' terminal sequence. proliferating cell
nuclear antigen (PCNA) gene.

<400> 340

gctccagcgt tgtaaacctg cagagatgga ctggtccac gtctctttgg tgcagctcac 60
cctgcggtct gagggcttcg acacctaccg ctgcgaccgc aacctggcca tggggtgaaac 120
ctcaccagta tgtccaaaat actaaaatgc gccggcaatg aagatatcat tacactaagg 180
gccgaagata acgcggatag cttggcgcta gtatttgaag caccaaacca ggagaaagtt 240
tcagactatg aaatgaagtt gatggattta gatgttgaac aacttngaag tccagaacag 300
gagtacagct gtgtagtaaa gatgcntct ggtgaatttg c acgtatatg ccgagatctc 360
agccatattg ggagatgctg ttgtaatttc ctgtgncaaa agacgggagt gaaaattttt 420
ctgcaagtgg gagnact 437

<210> 341

<211> 1231

<212> DNA/RNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(1231)

<223> proliferating cell nuclear antigen (PCNA)
gene.

<400> 341

aggtctcagc cggctcgtgc gacgttcgcc cgctcgtct gaggtcctg aagccgaaac 60
tagctagact ttctctcttc ccgctgcct gtacggcgt tgttgccact ccgccaccat 120
gttcgaggcg cgctgggtcc agggctccat cctcaagaag gtgttgagg cactcaagga 180
cctcatcaac gaggcctgct gggatattag ctccagcggg gtaaacctgc agagcatgga 240
ctggtccac gtctctttgg tgcagctcac cctgcggtct gagggcttcg acacctaccg 300
ctgcgaccgc aacctggc ca tgggcgtgaa cctcaccagt atgtccaaaa tactaaaatg 360
cgccggcaat gaagatatca ttactaag gccggaagat aacgcggata ccttggcgct 420
agtatttgaa gcaccaaacc aggagaaagt ttcagactat gaaatgaagt tgatggattt 480
agatgttgaa caacttgga ttccagaaca ggagtacagc tgtgtagtaa agatgccttc 540
tgggtgaattt gcacgtatat gccgagatct cagccatatt ggagatgctg ttgtaatttc 600
ctgtgcaaaa gacggagtga aattttctgc aagtggagaa cttggaaatg gaaacattaa 660

220/292

```

attgtcacag acaagtaatg tcgataaaga ggaggaagct gttaccatag agatgaatga 720
accagttcaa ctaacttttg cactgaggta cctgaact tc ttacaaaag ccactccact 780
ctcttcaacg gtgacactca gtatgtctgc agatgtaccc cttgttgtag agtataaaat 840
tgcggatatg ggacacttaa aatactactt ggctcccaag atcgaggatg aagaaggatc 900
ttaggcattc ttaaaattca agaaaataaa actaagctct ttgagaactg cttctaagat 960
gccagcatat actgaa gtct tttctgtcac caaatttgta cctctaagta catatgtaga 1020
tattgttttc tgtaaataac ctattttttt tctctattct ctccaatttg tttaaagaat 1080
aaagtccaaa gtctgatctg gtctagttaa cctagaagta tttttgtctc ttagaaatac 1140
ttgtgatttt tataatacaa aagggtcttg actctaaatg cagttttaag aagtg ttttt 1200
gaatttaaat aaagttactt gaatttcaaa c

```

1231

<210> 342

<211> 383

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(383)

<223> 3' terminal sequence. adenovirus 5' el
binding protein (BS69) gene.

<400> 342

```

tttttttttt aaacacacan gttttcacgc tgtagtaact tggaaatgtg caaccctgtg 60
caacagagac agaaaagcca aagtaacacg aatctcactt tcatgcagct atcagttaaa 120
tattacatac tctggaatga ttttacacca aaaatattt c cacaattact tgcttcata 180
ggggtggatc gaagtcttaa aacttgaaaa acaatcaaag aaggttaagt gttctcggtt 240
ctgacatctc catcagcgcc acacactgtg gngaacactg gactaattac acagcaacaa 300
ggaggggaac gatgatgcca agttactgca taatttaggg tacattgtat ggaatggggg 360
gctactgggg gtactttttt tac

```

383

<210> 343

<211> 483

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(483)

<223> 5' terminal sequence. adenovirus 5' el
binding protein (BS69) gene.

<400> 343

```

gttnaaattg cagggactgg ggtaatcttt tactgagctg gatcttagag aaaatgaata 60
tttaaatttt aaagtttgca catttcactt ttgtcctaac atgagtgtt gtaacaaaat 120
aaacaacaaa aacaaagcca aaaactacct ttatccatat gtgaaattat agatgaggca 180
tacgaatttg ttaaatgctt cccttcctt ccacatatc atctcactgc ctattatctg 240
gtgtcacctc atgtatcgta agttaatact aaaagaagag aaagcactta agtttcacag 300
aagccgttat gttttaggtt aatgggtgca ttgcctaag gaactccatc actgtacaca 360
gaatgaagga nttaatgcca tgtaatttt cttgttattt aagg atgccg tggatttggt 420
aaaaggtctg gtattttgcg gggatgtctg gggttaggga ggccttacc ataggggntg 480
ggg

```

483

<210> 344
<211> 2722
<212> DNA/RNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<220>
<221> misc_feature
<222> (1)..(2722)
<223> adenovirus 5 ela binding protein (BS69)
gene.

<400> 344
ggagcataat gctaaagaag taaacaggtc atggcacgtt taacaaaaag acgacaggcg 60
atacaaaagc tatccagcat ctttgggcag ccattgagat tata cggaac cagaagcaga 120
ttgccaaacat tgaccgtatt acaaaatgtg aaacaactac attattcttg aacctatggt 180
gattttttaca tcattacaca gatattgcat ttctattagt tgcattcattg ttataaactg 240
gtatatgtct cgagtcacag gtatgcaccc taaagagacc acccgtcagc tgagcttagc 300
tgtgaaagat ggtcttattg tc gaaactct aacagtgggc tgcaaaaggtt caaaagctgg 360
tattgaacaa gaaggatatt ggttgccagg agatgagatt gactgggaaa cagaaaatca 420
tgactgggtat tgttttgaat gccatttgc tggagagggtg ttgatattgtg acctgtgttt 480
tcgtgtgtat cattccaagt gtttgtctga tgagttcagg cttagagaca gcagtagtcc 540
ctggcagtgcc ccagtttgca ggagcattaa gaagaagaat acaaaacaaac aggagatggg 600
cacatacctc agattcattg tctcccgcat gaaggagagg gctatagatc ttaataaaaa 660
ggggaaggac aataaacacc cgatgtacag gaggctgggtg cactcagctg tggacgttcc 720
caccattcaa gagaaagtga atgaaggga ataccgaagt ta tgaagagt tcaaaagctga 780
tgcccaattg cttctccaca ataccgtgat ttctatgga gcagacagtg agcaagctga 840
cattgcgagg atgctatata aagacacatg tcatgagctg gatgaactgc agctttgcaa 900
gaattgcttt tacttgtcaa atgctcgtcc tgacaactgg ttctgttacc cttgtatacc 960
taatcatgag ctggtttggg ctaaaatgaa aggttttggg ttttggccag ccaaagtcac 1020
gcagaaagaa gacaatcaag tgcacgttcg cttctttggc caccaccacc agagggcctg 1080
gattccttct gaaaacattc aagatatcac agtcaacatt catcggtgc acgtgaagcg 1140
cagtatgggt tggaaaaagg cctgtgatga gctggagctg catcagcgtt tcctacgaga 1200
agggagattt tggaaatcta agaagagga ccgaggtgag gaagaggcag aatccagtat 1260
ctcctccacc agtaatgagc agctaaaggt cactcaagaa ccaagagcaa agaaaggacg 1320
acgtaatcaa agtgtggagc caaaaagga agaaccagag cctgaaacag aagcagtaag 1380
ttctagccag gaaataccca cgatgcctca gcc atcgaa aaagtctccg tgtaactca 1440
gacaaagaag ttaagtgcct cttcaccga aatgctgcac cggagcacc agaccacaaa 1500
cgacggcgtg tgcagagca tgtgccatga caaatacacc aagatcttca atgacttcaa 1560
agaccggtg aagtcggacc acaagcggga gacagagcgt gttgtccgag aagctctgga 1620
gaagctcgt tctgaaatgg aagaagaaa gagacaagct gtaaataaag ctgtagccaa 1680
catgcagggt gagatggaca gaaaatgtaa gcaagtaaag gaaaagtgtg aggaggaatt 1740
tgtagaagaa atcaagaagc tggcaacaca gcacaagcaa ctgatttctc agaccaagaa 1800
gaagcagtg tgcatacaact gtgaggagga ggcacgtac cactgctg ct ggaacacatc 1860
ctactgctcc atcaagtgc agcaggagca ctggcacgcg gagcacaagc gcacctgccg 1920
ccggaagaa tgaagctggc ccttcccgga gtcaccccgga tgattactct tttcagacac 1980
agcgtttttt gtttccaaga agccaaaatt gtttagaatt tgcttcccat tttgcaccag 2040
cctttaaaca cttttcgtga ag aaattttg cacagtagtt taaatctttt gttaatgctc 2100
ctccgaagtt tttcagggg taaaagttaac atcagtgag ggtattattt taaataaatt 2160
ttaattgaga atttgttgca ttttcagcaa attttaaaac atttttaggt tttacagaga 2220
ttttaacctt taaacaacag atctttaaaa aacagtgtaa tacaagtga ttaacaaag 2 280
aaacatttag aatagatctg aatgtaagaa ctacagaact gtttcagaaa taaaacatac 2340
taccttgatg tgacattttt ttcttaacct tgttgagctg gttttgttca gcttaattta 2400
ctgttcaaag gcattatctg ttggtcacac cagtggtgat atgattgaat ttagggaaca 2460
gggttgacac agcagggtc gtcctgcata tttttt ctta aatatttccc aattgtgttt 2520
ttcattattt cttttcaata tataactttt ataacaaatt attagctttg atcttgtagt 2580
ttaaaattgc agggaaactg ggtaatcttt tactgagctg gatcttagag aaaatgaata 2640
tttaaatattt aaagtgtgcc acatttcac tttgtcctaa catgagtgct tgtaacaaaa 2700

222/292

taaaacaaca aaaacaaagc ct

2722

<210> 345

<211> 363

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(363)

<223> 3' terminal sequence. matrix
metalloproteinase 11 (stromelysin 3) (MMP11) gene.

<400> 345

```
gcacgcagca tctcgagtgg tagcgctgat ctacagagggc acccctctcc agtcagtggc 60
cctgcgggna cggngactgt ctacacgccc ggtgctgggg tggaaacgcc agtagtcctc 120
gcctcggaag aagtagatct tggtcttctc gggaccccag accaaggc ag catggaccgg 180
gaacctcacc agggcccagc tcggtgaggg gtgcggggcc cagggaactgg cttttcaccg 240
tcgtacaccc agtacttgag caccttgga agaaccaaat gtgggcccgg cttaccagc 300
attggccttt tcgccacagg gctggggcag tccctgccag tngcgagaag ccaattttgg 360
gca
```

363

<210> 346

<211> 2260

<212> DNA/RNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(2260)

<223> matrix metalloproteinase 11 (stromelysin 3)
(MMP11) gene.

<400> 346

```
aagcccagca gcccggggc ggatggctcc ggccgcctgg ctccgcagcg cggccgcgcg 60
cgccctcctg ccccgatgc tgctgctgct gctccagccg ccgcccgtgc tggcccgggc 120
tctgccgccc gacgtccacc acctccatgc cgagaggagg gggccacagc cctggcatgc 180
agccctgccc agtagcccg caccctgccc tgccacgcag gaagccccc ggccctgccag 240
cagcctcagg cctcccgcgt gtggcggtgc cgacctatct gatgggctga gtgcccgcaa 300
ccgacagaag aggttcgtgc tttctggcgg gcgctgggag aagacggacc tcacctacag 360
gatccttcgg ttcccatggc agttggtgca ggagcaggtg cggcagacga tggcaga ggc 420
cctaaaggta tggagcgatg tgacgccact cacctttact gaggtgcacg agggccgtgc 480
tgacatcatg atcgacttcg ccagggtactg gcattggggac gacctgccgt ttgatgggcc 540
tgggggcatc ctggcccatg ccttcttccc caagactcac cgagaagggg atgtccactt 600
cgactatgat gagacctgga ctatcgggga tgacc agggc acagacctgc tgcaggtggc 660
agcccatgaa tttggccacg tgctggggct gcagcacaca acagcagcca aggccctgat 720
gtccgccttc tacacctttc gctaccact gagtctcagc ccagatgact gcagggcgct 780
tcaacaccta tatggccagc cctggcccac tgccacctcc aggaccccag ccctggggcc 840
ccaggctggg atagacacca atgagattgc accgctggag ccagacgccc cgccagatgc 900
ctgtgaggcc tcctttgacg cgggttccac catccgaggc gagctctttt tcttcaaagc 960
gggctttgtg tggcgccctc gtgggggcca gctgcagccc ggctaccagc cattggcctc 1020
tcgccactgg cagggaactgc ccagccctgt ggacgctgcc ttcgaggatg ccca gggcca 1080
catttggttc ttccaagggt ctcagtactg ggtgtacgac ggtgaaaagc cagtcctggg 1140
```

223/292

```

ccccgcaccc ctcaccgagc tgggcctggt gaggttcccg gtccatgctg ccttggtctg 1200
gggtcccgag aagaacaaga tctacttctt ccgaggcagg gactactggc gtttccaccc 1260
cagcaccogg cgtgtagaca gtcccgctgc c ccgcagggcc actgactgga gaggggtgcc 1320
ctctgagatc gacgctgcct tccaggatgc tgatggctat gcctacttcc tgcgcggccg 1380
cctctactgg aagtttgacc ctgtgaaggt gaaggctctg gaaggcttcc ccggtctcgt 1440
gggtcctgac ttctttggct gtgccgagcc tgccaacact ttctctgac catggcttgg 1500
atgccctcag ggggtgctgac cctgcccagg ccacgaatat caggctagag acccatggcc 1560
atctttgtgg ctgtgggcac caggcatggg actgagccca tgtctcctgc agggggatgg 1620
ggtggggtag aaccaccatg acaactgccg ggagggccac gcaggctcgtg gtcacctgcc 1680
agcgactgtc tcagactggg caggagggtt ttggcatgac tt aagaggaa gggcagtctt 1740
gggaccgct atgcaggctc tggcaaacct ggctgccctg tctcatccct gtccctcagg 1800
gtagcaccat ggcaggactg ggggaactgg agtgtccttg ctgtatccct gttgtgaggt 1860
tccttccagg ggtggcact gaagcaagg tgctggggcc ccatggcctt cagccctggc 1920
tgagcaactg ggtgta ggg cagggccact tcctgaggtc aggtcttggg aggtgcctgc 1980
atctgtctgc cttctggctg acaatcctgg aaatctgttc tccagaatcc aggccaaaaa 2040
gttcacagtc aaatggggag ggttattctt catgcaggag accccaggcc ctggaggctg 2100
caacatacct caatcctgtc ccaggccgga tcctcctgaa gcccttttcg cagcac tgct 2160
atcctccaaa gccattgtaa atgtgtgtac agtgtgtata aacottcttc ttcttttttt 2220
tttttaaact gaggattgtc attaaacaca gttgttttct 2260

```

<210> 347

<211> 273

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(273)

<223> 3' terminal sequence. hypothetical protein
mgl13071 (MGC13071) gene.

<400> 347

```

atgtttattg aacgtaacag tatatttcat gtagtttccc ataatttttt catgtactaa 60
ctcatgtaat tctttgtttt ttagagatct gaagtgat tt tacctttact tccttcaatt 120
taagccaatc atgaaatttc agtgatttct ggggtgaggg cgaaaggtagg tgttacgaat 180
catcggggct gtggccagnt tgctcaccg aggtgcagg aggtcggggc ctactaggg 240
canctggagg agcacggact gccctgccg cag 273

```

<210> 348

<211> 330

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(330)

<223> 5' terminal sequence. hypothetical protein
mgl13071 (MGC13071) gene.

<400> 348

```

ggagtacaga acattgtggt aggggaagg actcacttcc tcatcccatg tgtacaaaaa 60
ccaattatct ttgactgctg ttctcaacca cgtagtcgnc cagtcacac tggtagcaaa 120
gatttacaga atgtcaacat cacactgtgc atcctcttcc ggcccatcac tagccagctt 180

```


224/292

```
cctcgcatct tcaccagcat tggagaggac tacgatgagt gtgtgctgcc gttcattacc 240
acggagatcc tcaagtcact ggtggctcgc tttgatgctg gagaactaat caccagagg 300
gagcttggtt tccagccngg tgaagnacca                               330
```

<210> 349

<211> 1168

<212> DNA/RNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:prime r

<220>

<221> misc_feature

<222> (1)..(1168)

<223> hypothetical protein mgc13071 (MGC13071)
gene.

<400> 349

```
aaatgatgat agtagtacct acagtatagt gctgttagaa ttacatgagt tagatgtgga 60
ggtcagagtg gaagcaggtg tgagagggtc ccgcagaaga aaacatggct gccaaagtgt 120
ttgagtccat cggcaagttt ggccctggcct tagctgttgc aggaggcatg gtgacctctg 180
ccttatgtaa tgtggatgct gggcacagag ctgccatctt tgaccaattc cgtggagtac 240
agaacattgt ggtaggggaa gggactcact ttctcatccc atgtgtacaa aaaccaatta 300
tctttgactg ctgttctcaa ccacgtagtg cgccagtcac c actggtagc aaagatttac 360
agaatgtcaa catcacactg tgcacacctt tccggcccat cactagccag ctctctcgca 420
tcttcaccag cattggagag gactacgatg agtgtgtgct gccgttcatt accacggaga 480
tcttcaagtc actggtggct cgctttgatg ctggagaact aatcaccag agggagctgg 540
tctccagcca ggtgagcaac aaccttatgg agtgagcagc cacctttggg ctcattctgg 600
acgacgtgtc tttagacacat ctgaccttct tgaaggagtt aacagacagg tggcccccca 660
ggaagcagag agcgccagat ttgtggtgga aaaggcggcc atcatctctg ctgaggggtga 720
ctccaaggca gctgagctga tcgccaaetc actggccact gcaggggacg gccagagcga 7 80
gctgtgcaag ctggaagctg cagaagacat tgcataccag ctctcatgct ctcggaacat 840
cacctgcctg ccggcagggc agtcctgtct cctccagctg ccctagttag gccccagcct 900
acctgcacct ccgtgaggca actggggcac agccccgatg attcgttaaca ccacctttcg 960
ccctcacccc agaaatcact gaaatttcat gattggctta aagtgaagga agtaaaggta 1020
aaatcacttc agatctctaa aaaacaaaga attacatgag ttagtacatg aaaaaattat 1080
gggaaactac atgaaatata ctgttacgtt caataaacat tagcttctgt atataaaaaa 1140
aaaaaaaaaa aaaaaaaaaa aaaaaaaa                               1168
```

<210> 350

<211> 315

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(315)

<223> 5' terminal sequence. interleukin enhancer
binding factor 2, 45kd (ILF2) gene.

<400> 350

```
ctggctttga aatcagttct ncgtgatgct acagtgaaga ttctcattac aacagtgcc 60
cccaatcttc gaaaactgga tccagaactc catttgata tcaaagtatt gcagagtgcc 120
ttagcagcca tccgacatgc ccgctggttc gaggaaatg cttctcagtc cacagttaaa 180
gttcnccanc agantactga aggacttgag gattcgtttt ccnggctttg agc cctcaca 240
```

225/292

cccnggatnc ttgaactact aggn cattat gctgtgatga acaacccac caganagcct 300
ttggcnctaa acgtt 315

<210> 351
<211> 1552
<212> DNA/RNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<220>
<221> misc_feature
<222> (1)..(1552)
<223> interleukin enhancer binding factor 2, 45kd
(ILF2) gene.

<400> 351
cgggttggtgc ggcctccatt gttcgtgttt taaggcgcca tgaggggtga cagaggccgt 60
ggtcgtggtg ggcgcttttg ttccagagga ggcccaggag gag ggttcag gccctttgta 120
ccacatatcc catttgactt ctatttgtgt gaaatggcct ttccccgggt caagccagca 180
cctgatgaaa cttccttcag tgaggccttg ctgaagagga atcaggacct ggctcccaat 240
tctgctgaac aggcatctat cctttctctg gtgacaaaaa taaacaatgt gattgataat 300
ctgattgtgg ctccaggggac a tttgaagtg caaattgaag aagttcgaca ggtgggatcc 360
tataaaaagg ggacaatgac tacaggacac aatgtggctg acctggtggt gatactcaag 420
attctgccaa cgttggaagc tgttgctgcc ctggggaaca aagtcgtgga aagcctaaga 480
gcacaggatc cttctgaagt ttttaaccatg ctgaccaacg aaactggctt tgaaatcagt 540
tcttctgatg ctacagtga gattctcatt acaacagtgc cacccaatct tcgaaaactg 600
gatccagaac tccatttgga tatcaaagta ttgcagagtg ccttagcagc catccgacat 660
gcccgctggt tcgaggaaaa tgcttctcag tccacagtta aagttctcat cagactactg 720
aaggacttga ggattcggtt tcttggtctt gagccctca c acctggat ccttgaccta 780
ctaggccatt atgctgtgat gaacaacccc accagacagc ctttgccct aaacgttgca 840
tacaggcgct gcttgagat tctggctgca ggactgttc tgccagggtc agtgggtatc 900
actgaccct gtgagagtgg caactttaga gtacacacag tcatgacct agaacagcag 960
gacatggtct gctatacagc tcagactctc gtccgaatcc tctcacatgg tggctttagg 1020
aagatccttg gccaggagg tgatgccagc tatcttgctt ctgaaatata tacctgggat 1080
ggagtgatag taacaccttc agaaaaggct tatgagaagc caccagagaa gaaggaagga 1140
gaggaagaag aggagaatac agaaagaacc acctcaagga gaggaagaag aaagcatgg a 1200
aactcaggag tgacattccc ttcactcctt ttcctaccca agggaaagac tggagcctaa 1260
gctgcctgct actggcttta catggtgaca gacattccgt ggataggaag atagcaggag 1320
aaagtaactc catagagtgt cattccactg gttgatattg gcttagctgc cagtctccca 1380
tttgtgacct atgccatcca tctataatgg agg ataccaa catttcttcc taatattcta 1440
taatctcaa ctctgaaaa cccctctctc aactaatact ttgctgttga aatgttgtga 1500
aatgttaagt gtctggaaat tttttttct aagaaaaact attaaagtac tt 1552

<210> 352
<211> 396
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<220>
<221> misc_feature
<222> (1)..(396)
<223> 3' terminal sequence. hypothetical protein
flj11307 (FLJ11307) gene.

226/292

<400> 352

ctccattaca ggggtttttgc cacttgctgt gaggataggg ccctgagttc ttacctctaa 60
ggtagctggag gtttcagttg tagaatttcc agtattattg cttgagtttg aagacactgt 120
ttcattttta ctttcattat ctgatttttc atcggaactc atacattcaa tatctgcac 180
aaagcctgtt ggatatccca ttgcctgcaa taccttcacc gctacgtgaa agttttgctg 240
ttttcttgga tggctctgag gcttcatatg ttgtgccatc cacatctaca gacattg tga 300
agactggggg catgaacggg ggccagactg aagataagaa gctatactga agcacaggcc 360
tgatctgaat taagcntcat tagtggcatt ccataa 396

<210> 353

<211> 1858

<212> DNA/RNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: primer

<220>

<221> misc_feature

<222> (1)..(1858)

<223> hypothetical protein flj11307 (FLJ11307)
gene.

<400> 353

tcgatgaaag atcctccgga cttattggac aggcagaaat gcccgaacgc cttggcgtct 60
cttcgacatg ccaaatgggt tcaggcaagg gcaaatggat taaaatcatg tgtaat tgtc 120
ctccgcattc tgcgtgattt gtgcaacaga gtccccacat gggcaccatt gaaaggatgg 180
ccactagaac ttatatgtga aaagtctata ggtacttgta atagaccttt gggcgctggg 240
gaggccctga gacgagtaat ggagtggttg gcatctggaa tactacttcc tgggggtcct 300
ggtcttcatg atccttgtga gcgagaccca acag atgctc tgagctatat gaccatccag 360
caaaaagaag atattacca cagtgcacag catgcaacta gactatcagc ctttggccag 420
atttacaaag tgctggagat ggacccctt ccatctagta agccttttca gaagtattcc 480
tggtcagtta ctgataaaga aggtgctggg tcttcagctc taaagaggcc atttgaagat 540
ggattagggg atgataaaga cccaacaag aagatgaaac gaaacttaag gaaaattctg 600
gatagtaaag caatagacct tatgaatgca ctaatgaggc taaatcagat caggcctggg 660
cttcagtata agctcctatc tcagtctggc ccggttcagc cccagctctt cacaatgtct 720
gtagatgtgg atggcacaac atatgaagcc tcaggaccat ccaagaaaac agca aaactt 780
cacgtagcgg tgaaggatatt gcaggcaatg ggatatccaa caggctttga tgcagatatt 840
gaatgtatga gttccgatga aaaaacagat aatgaaagta aaaatgaaac agtgtcttca 900
aactcaagca ataatactgg aaattctaca actgaaacct ccagtacctt agaggtaaga 960
actcagggcc ctatcctcac agcaagtggc aa aaaccctg taatggagct caatgaaaaa 1020
agaagagggtc tcaagtatga actcatctca gagactgggt gaagccatga caagcgcttt 1080
gtaatggagg tagaagtaga tggacagaaa ttcagaggcg cagggtccaa taagaaagt 1140
gcaaaggcga gtgcagcttt agctgccttg gagaaactgt tttctggacc caatgcggca 1200
aataataaga aaaagaagat tatccctcag gcaaagggcg ttgtgaatac agctgtgtct 1260
gcagcagtc aagctgttcg gggcagagga agaggaaactc taacaagggg agcttttgtt 1320
ggggcgacag ctgctcctgg ctacatagct ccaggctatg gaacaccata tggttacagc 1380
acagctgccc ctgcctatgg tttacccaag agaattgggt tgttac ccgt tatgaaattt 1440
ccaacatata ctgttcccc ctactcattc ttttagcaaa tgacagaagc taattcctat 1500
tgaacaacaa tacagtacaa cacagaatgt tagagaaaaa gcctttttat cctgctttct 1560
ttgaacacat acttgatcaa aattatttgt aaagaacatc tttcctactt tttgatttta 1620
acaaatgcaa atttagttct ctaaaacttg aaaaaaaaaa aagaaaccag ttctgtgaaa 1680
acggtacctc atttctggaa aataacttat accagccctt ctgttctagg gaaataaaag 1740
tctagcagtt caaagtttaa gttttaagag acgtatcaga ttatgtaaaa ttaaatttgt 1800
gaaggatgta tagagtctca aacactgac acaataaac tgctttgtt taacacag 1858

<210> 354

<211> 242

<212> DNA

227/292

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(242)

<223> 5' terminal sequence. v-myb avian
myeloblastosis viral oncogene homolog (MYB) gen e.

<400> 354

```
agaacccag ctatcaaaag gtcaatctta gaaagctctc caagaactcc tacaccattc 60
aaacatgcac ttgcagctca agaaattaaa tacggtcccc tgaagatgct acctcagaca 120
ccctctcatc tagtagaaga tctgcaggat gtgatcaaac aggaatctga tgaatctgga 180
attgttgctg agtttcaacg aaaatggacc acccttactg aacgaaaatc ntacaacgag 240
gt                                         242
```

<210> 355

<211> 3225

<212> DNA/RNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(3225)

<223> v-myb avian myeloblastosis viral oncogene
homolog (MYB) gene.

<400> 355

```
ggcggcagcg ccctgccgac gccggggagg gacgcaggca ggcggcgggc agcgggaggc 60
ggcaccgccg tgctccccgc ggctctcggc ggagccccgc cgcccgccgc gccatggccc 120
gaagaccceg gcacagcata tatagcagtg acgaggatga tgaggacttt gagatgtgtg 180
accatgacta tgatgggctg cttccaagt ctggaaagcg tcaacttggg aaaacaagggt 240
ggacccgga agaggatgaa aaactgaaga agctggtgga acagaatgga acagatgact 300
ggaaagttaa tgccaattat ctccgaatc gaacagatgt gcagtgccag caccgat ggc 360
agaaagtact aaaccctgag ctcatcaagg gtccttggac caaagaagaa gatcagagag 420
tgatagagct tgtacagaaa tacggtccga aacgttgggc tgttattgcc aagcacttaa 480
aggggagaat tggaaaacaa tgtagggaga ggtggcataa ccacttgaat ccagaagtta 540
agaaaacctc ctggacagaa gaggaagaca gaatt attta ccaggcacac aagagactgg 600
ggaacagatg ggcagaaatc gcaaagctac tgcctggacg aactgataat gctatcaaga 660
accactggaa ttctacaatg cgtcggaagg tcgaacagga aggttatctg caggagtctt 720
caaaagccag ccagccagca gtggccacaa gcttcagaa gaacagtcac ttgatggggt 780
ttgctcaggc tccgcctaca gctcaactcc ctgccactgg ccagccact gttacaacag 840
actattccta ttaccacatt tctgaagcac aaaatgtctc cagtcatgtt ccataccctg 900
tagcggtaca tgtaaatata gtcaatgtcc ctgagccagc tgccgcagcc attcagagac 960
actataatga tgaagaccct gagaaggaaa agcgaataaa ggaattagaa ttgct cctaa 1020
tgtcaaccga gaatgagcta aaaggacagc aggtgctacc aacacagaac cacacatgca 1080
gctaccgccg gtggcacagc accaccattg ccgaccacac cagacctcat ggagacagtg 1140
cacctgtttc ctgtttggga gaacaccact ccaactccatc tctgccagcg gatcctggct 1200
ccctacctga agaaagcgcc tcgccagcaa ggtgcatgat cgtccaccag ggcaccattc 1260
tggaataatg taagaacctc ttagaatttg cagaaacact ccaatttata gattctttct 1320
taaacacttc cagtaaccat gaaaactcag acttggaat gccttcttta acttccaccc 1380
ccctcattgg tcacaaattg actgttacaa caccatttca tagagaccag actgtgaaaa 1440
ctcaaaagga aaatactgtt tttagaacc cagctatcaa aaggtcaatc ttagaaagct 1500
ctccaagaac tcctacacca ttcaaacatg cacttgacgc tcaagaaatt aaatacggtc 1560
ccctgaagat gctacctcag acaccctctc atctagtaga agatctgcag gatgtgatca 1620
```

228/292

```

aacaggaatc tgatgaatct ggatttggtg ctgagtttca aga aaatgga ccacccttac 1680
tgaagaaaat caaacaagag gtggaatctc caactgataa atcaggaaac ttcttctgct 1740
cacaccactg ggaaggggac agtctgaata cccaactgtt cacgcagacc tcgcctgtgc 1800
gagatgcacc gaatattctt acaagctccg ttttaatggc accagcatca gaagatgaag 1860
acaatgttct caaagcat tt acagtaccta aaaaacaggtc cctggcgagc cccttgacgc 1920
cttgtagcag tacctgggaa cctgcatcct gtggaagat ggaggagcag atgacatctt 1980
ccagtcaagc tcgtaaatac gtgaatgcat tctcagcccg gacgctggtc atgtgagaca 2040
tttccagaaa agcattatgg ttttcagaac agttcaagtt gacttgggat atatcat tcc 2100
tcaacatgaa acttttcatg aatgggagaa gaacctatct ttgttgtggt acaacagttg 2160
agagcacgac caagtgcatt tagttgaatg aagtcttctt ggatttcacc caactaaaag 2220
gatttttaaa aataaataac agtcttacct aaattattag gtaatgaatt gtagccagtt 2280
gttaatatct taatgcagat ttttttaaaa aaaaacataa aatgatttat ctggtatttt 2340
aaaggatcca acagatcagt attttttcct gtgatgggtt ttttgaaatt tgacacatta 2400
aaagtgactc cagtatttca cttttctcga tcaactaaaca tatgcatata tttttaaaaa 2460
tcagtataag cattactcta agtgtagact taataccatg tgacatttaa tccagattgt 2520
aaatgctcat ttatggttaa tgacattgaa ggtacattta ttgtaccaa ccattttatg 2580
agttttctgt tagcttgctt taaaaattat tactgtaaga aatagtttta taaaaaatta 2640
tatttttatt cagtaattta attttgtaaa tgccaaatga aaaacgtttt ttgctgctat 2700
ggtcttagcc ttagacatg ctgctagtat cagaggggca gtaga gcttg gacagaaaga 2760
aaagaaactt ggtgttaggt aattgactat gcaactagat ttcagacttt ttaattttat 2820
atatatatac atttttttcc cttctgcaat acatttgaaa acttggttgg gagactctgc 2880
attttttatt gtggtttttt tgttattgtt ggtttataca agcatgcgtt gcacttcttt 2940
tttgggagat gtgtgttgtt catgttttat gttttgtttt gtgtgtagcc tgactgtttt 3000
ataatttggg agttctcgat ttgatccgca tcccctgtgg tttctaagtg tatggtctca 3060
gaactgttgc atggatcctg tgtttgcaac tggggagaca gaaactgtgg ttgatagcca 3120
gtcactgcct taagaacatt tgatgcaaga tggccagcac tgaacttttg agatatgac g 3180
gtgtacttac tgccttgtag caaaataaag atgtgccctt atttt 3225

```

<210> 356

<211> 369

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(369)

<223> 3' terminal sequence. zinc finger protein 9
(a cellular retroviral nucleic acid binding
protein) (ZNF9) gene.

<400> 356

```

gtagttaaat gcagaaagtc ggttttttcc cacccttttc ctctttttac acggcaagta 60
aagctcactg gcctgggagt tgcctctatc tgccaacctt tggccagtga agaggattca 1 20
gagaaaataa tacaaccatc aatcagaaaa aggaggggag acaaaggaaa ataattagga 180
tgtagctcaa ttgtgcattc ccgtgcaagg tgccttgact cgccacagcg gtaacagttg 240
acttcacttg tcttgctgca gttgatggct acatgaccag tttcaccaca cctatagcac 300
ttcacttttg tgagtccttt tttgaatgtg tcccgaattc tcccacaaga atancctttc 360
tgctcanct 369

```

<210> 357

<211> 1500

<212> DNA/RNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>
<221> misc_feature
<222> (1)..(1500)
<223> zinc finger protein 9 (a cellular retroviral
nucleic acid binding protein) (ZNF9) gene.

<400> 357
gaattccaaa cagcctctac cttgcgagcc gtcttcccca ggctgcgtc cgagtctccg 60
ccgctgcggg cccgctccga cgcggaagat ctgactgcag ccatgagcag caatgagtgc 120
ttcaagtgtg gacgatctgg ccactgggccc cgggaatgtc ctactgggtg aggcctgtgt 180
cgtggaatga gaagccgtgg cagaggtggt ttacctcgg atagaggttt ccagtttggt 240
tcctcgtctc ttccagatat ttgttatcgc tgtggtgagt ctgggtcatct tgccaaggat 300
tgtgatcttc aggaggatgc ctgctataac tgcggtagag gtg gccacat tgccaaggac 360
tgcaaggagc ccaagagaga gcgagagcaa tgctgctaca actgtggcaa accaggccat 420
ctggctcgtg actgcgacca tgcagatgag cagaaatgct attcttggtg agaattcgga 480
cacattcaaa aagactgcac caaagtgaag tgctataggt gtggtgaaac tgggtcatgta 540
gccatcaact gcagcaagac a agtgaagtc aactgttacc gctgtggcga gtcaggggcac 600
cttgacaggg aatgcacaat tgaggctaca gcctaattat ttcccttgt cgccctcct 660
ttttctgatt gatggttgta ttattttctc tgaatcctct tcaactggcca aaggttgga 720
gatagaggca actcccaggc cagtgcgtt tacttgccgt gtaaaaggag gaaaggggtg 780
gaaaaaaacc gactttctgc atttaactac aaaaaaagt tatgtttagt ttggtagagg 840
tgttatgtat aatgctttgt taaagaaccc ctttccgtg ccactggtga atagggattg 900
atgaatggga agagttgagt cagaccagta agcccgtcct gggttccttg aacatgttcc 960
catgtaggag gtaaaaccaa ttctggaagt gtctatgaac t tccataaat aactttaatt 1020
ttagtataat gatggtcttg gattgtctga cctcagtagc tattaataa catcaagtaa 1080
catctgtatc agccctaca tagaacatac agttgagtgg gagtaacaa aaagataaac 1140
atgcgtgtta atggctgttc gagagaaatc ggaataaaag cctaaacagg aacaacttca 1200
tcacagtgtt gatgtt ggac acatagatgg tgatggcaaa ggtttagaac acattatttt 1260
caaagactaa atctaaaacc cagagtaaac atcaatgctc agagtttagca taatttggag 1320
ctattcagga attgcagaga aatgcatttt cacagaaatc aagatgttat tttgtatatac 1380
tatatcactt agacaactgt gtttcatttg ctgtaatcag tttttaaag tcaga tggaa 1440
agagcaactg aagtactaga aaatagaaat gtaattttaa actattccaa taaagctgga 1500

<210> 358
<211> 425
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<220>
<221> misc_feature
<222> (1)..(425)
<223> 3' terminal sequence. camp responsive
element modulator (CREM) gene.

<400> 358
ttttttactt ctgcaagatc ttttatatta cacagtagag ttaaaaactg tagtaaatgt 60
tcagatatatt aaatgagcac caaacactac aaagtgcac caacatggtt ctattaaaaa 120
ctcncctttga ctatggcatt caaggacagc aatacaat ct tttttttttt taacaaagca 180
actaatataa aaatctgcaa atgcatata ttcatatcta ggctattctt cncatatagg 240
catgtcatta gatagacttt ctttctatc ttccngagg natTTTTTTT nggtttacnt 300
ttattgnact gctggatgca ttatttttga tcatcctttc ctaaaatgnt ttaaagacct 360
gcaataaatt ttattg cata ggacacnatt ggtgncacat agaatgggag cngcaagtat 420
gtggc 425

<210> 359

230/292

<211> 232
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<220>
<221> misc_feature
<222> (1)..(232)
<223> 5' terminal sequence. camp responsive
element modulator (CREM) gene.

<400> 359
ggatttagag ttaactagct caccactgcc tctgcctcca agctgccttt tagactgaat 60
agcttttctt gttagcccta ctttaacatt tcttttgaag tgggtgtctg cttgaagagg 120
gaaacacgtc atgaaactgt aatgcatgaa cagaactcag gagttgtctg gccagcttag 180
tgctgccact ggtgacatgc caacttacca gatccgagct cctantgnng ct 232

<210> 360
<211> 1431
<212> DNA/RNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:prime r

<220>
<221> misc_feature
<222> (1)..(1431)
<223> camp responsive element modulator (CREM)
gene.

<400> 360
atgaccatgg aaacagttga atcccagcat gatggaagta taacagcttc tttgacagag 60
agcaagtctg ctcatgtgca gactcagact gggcaaattt caatccctgc tttagctcag 120
tgcatgagc tgagatcagg caccagaaga ggctccccag ctgtaactct agtgcagtta 180
ccttcggggc aaactataca tgtccaggga gtaattcaga caccacagcc atgggttatt 240
cagtcacag aaatacacac cgttcaggta gcagcaattg cagagacaga tgaatctgca 300
gaatcagaag gtgtaattga ttctcataaa cgtagagaaa t cctttcacg aagaccctct 360
tataggaaaa tactgaatga actgtcctct gatgtgcctg gtgttcccaa gattgaagaa 420
gagagatcag aggaagaagg aacaccacct agtattgcta ccatggcagt accaactagc 480
atatatcaga ctacgacggg gcaatacatt gctatagccc aaggtggaac aatccagatt 540
tctaaccag gatctgatgg tgttcaggga ctgcaggcat taacaatgac aaattcagga 600
gctcctccac cagtgctac aattgtacag tacgcagcac aatcagctga tggcacacag 660
cagttctttg tcccaggcag ccagggtgtt gtccaagctg ccaactggtga catgccaact 720
taccagatcc gagtcctac tgcgtctttg ccacaggagg tgggtgatggc tgcacgccc 780
ggaagtttg acagtcccca gcagctggca gaagaagcaa cagcaaacg agagctgagg 840
ctaataaaaa acagagaagc tgcccgggag tgtcgcagga agaagaaaga atatgtcaaa 900
tgtcttgaat atcgtgtggc tgtgcttgaa aacaaaaaca agactctcat tgaggaaact 960
aaggccctca aagatcttta ttgccataaa gtagagtaac tgtctttgac ttggaccttg 1020
tttactctaa tcaaggcagg agatgcagca gtctactta ttgcatgtg gacttgtggg 1080
aaggacacgt gtgacctta agaatccagt ttggattagt gtttgaaatt gaattgggaa 1140
tgttgttcca ggatgtggaa tgcagcgtga tcacacttac cgagcttact ttgatctgtt 1200
tgtcaatagc atgcaaaaaa tgctttgttt gccctttgct tctgcttttt ttcagggaag 1260
ctgccaaga atgtcgacgt cgaagaaag aatatgtaaa atgcttgagg agccgagttg 1320
cagtgctgga agtccagaac aagaagctta tagaggaact tgaaaccttg aaagacattt 1380
gttctcccaa aactgattac tagaaatatt taactatgaa ctgattacag a 1431

231/292

<210> 361
<211> 457
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<220>
<221> misc_feature
<222> (1)..(457)
<223> 3' terminal sequence. cathepsin b (CTSB)
gene.

<400> 361
caagttggag aaacctttta ttggcacagg cattccttgt taacttgaca gggagaagct 60
gtaatttttc aaaaacagta aaagctggtt tctcctaaac tatcttcctt gtggtagtag 120
agatcagtg gtcagaaaca actcctgacc atttggttcc cttttgagcc gcgtcattag 180
gaggcaatct gtaaaactag cacagggtctc ccgctgttcc actggctcac ccacatg att 240
agcagagtg acgaaaaaat aaaacttcta ttaaagaatc atgctgagca caacatcaga 300
gaggttgatg cattgcaaac tcgatagatg cagggggcct gggagactgg cgttctccaa 360
agggtccca acaccatctc tcctctgatt tctgtgacaa atgtggaagc tacttgcttg 420
gaggtactgg ggggaactgat gggggaactt tcac cg 457

<210> 362
<211> 401
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<220>
<221> misc_feature
<222> (1)..(401)
<223> 3' terminal sequence. melan -a (MLANA) gene.

<400> 362
atcatgcatt gcaacattta ttgatggagt tttcccaatt taatatttct catcatttcc 60
tcacatgatt agtactgcta gcggacctac taaaatttta acactgactt attattagag 120
atggcttgca tttttcctac accattccaa aggagaacat tagatgtctg tattaaattc 180
aagcaaaagt gtgagagaaa taatttcagc atgtctcagg tgtctcgt g gcncttaagg 240
tgaataaggt ggtggtgact gttctgcaga gattttctca taagcagggt gagcattggg 300
aaccacaggt tcacagtttt tctcttgaag agacactttg ctgtcccgat gatcaaacc 360
ttcttgtggg catcttctg ttaaggcaca ttgaggccaa c 401

<210> 363
<211> 370
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<220>
<221> misc_feature
<222> (1)..(370)
<223> 5' terminal sequence. melan -a (MLANA) gene.

232/292

<400> 363

```
attaaggaag gtgtcctgtg ccctgaccct acaagatgcc aagagaagat gctcacttca 6 0
tctatggtta ccccaagaag gggcacggcc actcttacac cacggctgaa gaggccgctg 120
ggatcgcat cctgacagtg atcctgggag tcttactgct catcggtgt tggatttga 180
gaagacgaaa tggatacaga gccttgatgg ataaaagtct tcatgttggc actcaatgtg 240
cttaacaaga agatgccac aagaagggtt tgatcatcgg gacagcaaag tgtctcttca 300
agagaaaaac tgtgaacctg tggttcccaa tgctccacct gcttatggag aaactctctg 360
cagaacagtc                                     370
```

<210> 364

<211> 1524

<212> DNA/RNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(1524)

<223> melan-a (MLANA) gene.

<400> 364

```
agcagacaga ggacttcat taaggaaggt gtctgtgcc ctgaccctac aagatgcca 60
gagaagatgc tcaacttcac tatggttacc ccaagaaggg gcacggccac tcttacacca 120
cggctgaaga ggccgctggg atcggcatcc tgacagtgat cctgggagtc ttactgctca 180
tcggctgttg gtattgtaga agacgaaatg gatacagagc cttgatggat aaaagtcttc 240
atgttggcac tcaatgtgcc ttaacaagaa gatgccaca agaagggttt gatcatcggg 300
acagcaaagt gtctcttcaa gagaaaaact gtgaacctgt ggttccc aat gctccacctg 360
cttatgagaa actctctgca gaacagtcac caccacctta ttcacctta gagccagcga 420
gacacctgag acatgctgaa attatttctc tcacactttt gcttgaattt aatacagaca 480
tctaattgtc tcctttggaa tgggttagga aaaatgcaag ccatctctaa taataagtca 540
gtgttataat tttagtaggt ccgct agcag tactaatcat gtgaggaaat gatgagaaat 600
attaaattgg gaaaactcca tcaataaatg ttgcaatgca tgatactatc tgtgccagag 660
gtaattgttag taaatccatg gtgttatttt ctgagagaca gaattcaagt gggatttctg 720
gggccatcca attctctttt acttgaaatt tggctaataa caaactagtc aggttttctg 780
accttgaccg acatgaactg tacacagaat tgttcagta ctatggagtg ctcacaaagg 840
atacttttac aggttaagac aaagggttga ctggcctatt tatctgatca agaacatgtc 900
agcaatgtct ctttgtgctc taaaattcta ttatactaca ataatatatt gtaaagatcc 960
tatagctctt tttttttgag atggagtttc gcttttgttg ccag gctgg agtgcaatgg 1020
cgcgatcttg gctcaccata acctccgcct cccagggttca agcaattctc ctgccttagc 1080
ctctgagta gctgggatta caggcgtgcg ccactatgcc tgactaattt tgtagtttta 1140
gtagagacgg ggtttctcca tgttggtcag gctgggtctc aactcctgac ctcaggatgat 1200
ctgcccgcct cagcctccca aagtgtctga attacaggcg tgagccacca cgcctggctg 1260
gatcctatat cttaggtaag acatataacg cagtctaatt acatttcaact tcaaggctca 1320
atgctattct aactaatgac aagtattttc tactaaacca gaaattggta gaaggattta 1380
aataagtaaa agctactatg tactgcctta gtgctgatgc ctgtgtactg ccttaaatg t 1440
acctatggca atttagctct cttgggttcc caaatccctc tcacaagaat gtgcagaaga 1500
aatcataaag gatcagagat tctg                                     1524
```

<210> 365

<211> 556

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:p rimer

<220>

233/292

<221> misc_feature
<222> (1)..(556)
<223> 3' terminal sequence. apr -1 protein (APR-1)
gene.

<400> 365
actattcggtt aggccttttat ttttctctat gttctgcagt aactaaggaa aatcatggta 60
aatgtcaatc ttacacacaac agcagacaca aagggtttca gaaacgtcag atatgaag aa 120
atcctccatc cttcttcaac attttactgg gtatttcaac ttcaaaagaa cagcttattt 180
ctataagtgc tgtacaagat catagattat gatggaacga cttcatttta gaacgtagc 240
aaaactgtta tactaaatgt caatgacagg aaacaaagaa aaaaatttgt tcaattatat 300
ttttaaacat attgttattc tcaacaaacg gaattt taaa acgaatacaa ttttccatta 360
tcaaaaagca aacactctat ttgcgagttg aacaatgac actgacaca aatatacnaat 420
acagtgtccc cgcgccccaa tcgacatcat tttccactta gggaccctgg catccactcc 480
ctgggggtac ccgtgactcc ncctttacac cccccagggg ctggcctcag atctacctaa 540
gggnggggat aacccc 556

<210> 366
<211> 464
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<220>
<221> misc_feature
<222> (1)..(464)
<223> 5' terminal sequence. apr -1 protein (APR-1)
gene.

<400> 366
aacagcgcca aggaagctct ggtctggaaa gtgctgggga agtttagaat gcagcctgga 60
cgtcagcaca gcattcttgg agatccgaag aagatcgtca cagaagagtt tgtcgcgaga 120
gggtacctga ttataaacc ggtgccccgt agcagtcagg tggagtatga gttcttctgg 180
gggccccgag cacacgtgga atcgagcaaa ctgaaagtca tgcattttgt ggcaagggtt 240
cgtaaccgat gctctaaaga ctggccttgt aattatgact gggattcgga cgatgatgca 300
gaggttgagg ctatcctcaa ttcaggtgct aggggttatt cgcgccccta agtagatctg 360
gaggcagacc cttgggggtt gtaaaagaga gtnacaggta cccccaaagg agtagatg nc 420
aaggggccct aagttgcaaa atgatgtcga ttttggggcc gggg 464

<210> 367
<211> 1476
<212> DNA/RNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<220>
<221> misc_feature
<222> (1)..(1476)
<223> apr-1 protein (APR-1) gene.

<400> 367
ctggaagaat tcgcgtggca ggagaggcgg ggccaatttt gctgagcttt ctgcggggct 60
tgcagctgcg gcaagtgtcg gcggcggtcg ctgcgcgaag tcagctggcg tgggaactac 120
cctttgtagc tgagaacggc ttgtttattg ctacaaagac totattgaca ttggtagctt 180
cagcggcagc agcttcttac ggtataaagc tgttgcttcc tgaagaggct acaagcatcc 240

234/292

```

ttccctagga ctgctgtaag ctttgagcct ctagcaggag acatgcctcg gggacgaaag 300
agtcggcgcc gccgtaatgc gagagccgca gaagagaacc gcaacaatcg caaaatccag 360
gcctcagagg cctccgagac ccttatggcc gcctctgtgg tagcgagcac ccccgaaga c 420
gacctgagcg gccccgagga agacccgagc actccagagg aggcctctac caccctgaa 480
gaagcctcga gcaactgccca agcacaaaag ccttcagtgc cccggagcaa ttttcagggc 540
accaagaaaa gtctcctgat gtctatatta gcgctcatct tcatcatggg caacagcgcc 600
aaggaagctc tggctctgaa agtgctgggg aagttag gaa tgcagcctgg acgtcagcac 660
agcatccttg gagatccgaa gaagatcgct acagaagagt ttgtgcgcag aggttacctg 720
atttataaac cgggtgccccg tagcagtcgg gtggagtatg agttcttctg ggggccccga 780
gcacacgtgg aatcgagcaa actgaaagtc atgcattttg tggcaagggt tcgtaaccga 840
tgctctaaag actgg ccttg taattatgac tgggattcgg acgatgatgc agaggttgag 900
gctatcctca attcaggtgc taggggttat tccgccctt aagtagatct gaggcagacc 960
cttgggggtg taaaagagag tcacaggtac cccaaggagt agatgccagg gtcttaagtt 1020
gaaaatgatg tcgattgggg gcgggggaca ctgtatttga tatttgtgat cagtga tcat 1080
tgttcaactg cgaaatagag tgtttgcttt tgataatgga aaattgtatt cgttttaaaa 1140
ttccgtttgt tgagaataac aatatgttta aaaatataat tgaacaaatt tttttctttg 1200
tttctgtca ttgacattta gtataacagt tttgctaacg ttctaaaatg aagtcgttcc 1260
atcataatct atgatcttgt acagcactta tagaaataag ctgttctttt gaagttgaaa 1320
taccagtaa aatgttgaag aaggatggag gatttcttca tatctgacgt ttctgaaacc 1380
ctttgtgtct gctgttgtgt gaagattgac atttaccatg attttcctta gttacttgac 1440
gtcttgatc tctttttatt ttcgattgc ttatca 1476

```

<210> 368

<211> 436

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(436)

<223> 3' terminal sequence. ets variant gene 5
(ets-related molecule) (ETV5) gene.

<400> 368

```

cgtttttttg ctttaaatac caaaactaca aaaatcagtt tataaactgt ttttccaaaa 60
caaccaccaa aacaaaacaa tcccccaaat caggggcaaaa caaaatactg tcaaaagtgt 120
taatcgccct tctcctaaaa taaaagtcac ccacactcag ccacgtgatt ggaagagaa 180
agggggcttg ctctacttgg cgaccacatg gccgggtggg tcccaa gagt agccatgggt 240
tatgattttg agaaccacgg agngcgaaac agctgttctg actgcccccc tttttctaga 300
caaggggtaa tatttcagat tcagctagaa gagctttcca atgtttaaga tgtattttta 360
acccttaatg gtttgagcct cccaactta gcctacttac tttcnaagg gtttgtgatt 420
tttcaacaaa ttgtgc 436

```

<210> 369

<211> 414

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(414)

<223> 5' terminal sequence. ets variant gene 5
(ets-related molecule) (ETV5) gene.

<400> 369

```
ggttgctcgg cgctggggca tccagaagaa ccggccagcc atgaactatg acaagctgag 60
ccgctctctc cgctattact atgaaaaggg catcatgcag aagggtggctg gagagcgata 120
cgtctacaaa tttgtctgtg acccagatgc cctcttctcc atggctttcc cggataacca 180
gcgtccggtc ctgaaggcag agtccgagtg ccacctcagc gaggaggaca ccctgccgct 240
gacccacttt gaagacagcc ccgcttacct cctggacatg gaccgctgca gcagcctccc 300
ctatgccgaa ggtttgctta ctaagtttct gagtggcgga gtgnccaaac cctaggagct 360
agcagttccc attcagggca aacaagnngc agtggngttt gtt ttgtgtt tttt 414
```

<210> 370

<211> 249

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(249)

<223> 5' terminal sequence. cd69 antigen (p60,
early t-cell activation antigen) (CD69) gene.

<400> 370

```
ataataagga aacgtgttca cttattgact attatagaat ggaactcatg gaaatctgtg 60
tcagtggatg ctgctctgtg gtccgaagtc ttccatagag actttgtgaa aaaaaatttt 120
atagtgtctt gggaattttc ttccaaacag aactatggaa aaaaaggaag aaattccagg 180
aaaatctgca ctgtgggctt ttattgccat gagctagaag catcacaggg tgaccaataa 240
cccngacgc 249
```

<210> 371

<211> 1702

<212> DNA/RNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(1702)

<223> cd69 antigen (p60, early t-cell activation
antigen) (CD69) gene.

<400> 371

```
agactcaaca agagctccag caaagacttt cactgtagct tgacttgacc tgagattaac 60
tagggaatct tgagaataaa gatgagctct gaaaattgtt tcgtagcaga gaacagct ct 120
ttgcatccgg agagtggaca agaaaatgat gccaccagtc cccatttctc aacacgtcat 180
gaagggtcct tccaagttcc tgtcctgtgt gctgtaatga atgtgggtctt catcaccatt 240
ttaatcatag ctctcattgc cttatcagtg ggccaatata attgtccagg ccaatacaca 300
ttctcaatgc catcagacag ccatgtttct tcatgc tctg aggactgggt tggctaccag 360
aggaaatgct actttatttc tactgtgaag aggagctgga cttcagccca aaatgcttgt 420
tctgaacatg gtgctactct tgctgtcatt gattctgaaa aggacatgaa ctttctaaaa 480
cgatacgtag gtagagagga aacttggtt ggactgaaaa aggaacctgg tcacccatgg 540
aagtgggtcaa atggcaaaga atttaacaac tggttcaacg ttacagggtc tgacaagtgt 600
gtttttctga aaaacacaga ggtcagcagc atggaatgtg agaagaatct atactggata 660
tgaacaacac cttacaataa ataaggaaac atgttcactt attgactatt atagaatgga 720
actcaaggaa atctgtgtca gtggatgctg ctctgtggtc cgaagtcttc cataga gact 780
```

236/292

```
ttgtgaaaaa aaattttata gtgtcttggg aattttcttc caaacagaac tatggaaaaa 840
aaggaagaaa ttccaggaaa atctgcactg tgggctttta ttgccatgag ctagaagcat 900
cacaggttga ccaataacca tgccaagaa tgagaagaat gactatgcaa cctttggatg 960
cactttatat tattttgaat ccagaaataa tgaa ataact aggcgtggac ttactattta 1020
ttgctgaatg actaccaaca gtgagagccc ttcatgcatt tgcactactg gaaggagtta 1080
gatgttggtg ctagatactg aatgtaaaca aaggaattat ggctggtaac atagggtttt 1140
agtctaattg aatcccttaa actcaggag catttataaa tggacaaatg cttatgaaac 1200
taagatttgt aatatttctc tctttttaga gaaatttgcc aatttacttt gttatttttc 1260
cccaaaaaga atgggatgat cgtgtattta ttttttact tcctcagctg tagacaggtc 1320
cttttcgatg gtacatat ttttgccttt ataactttt atacagtgtc ttacagagaa 1380
aagacataag caaagactat gaggaatatt tgcaagacat agaatagt gt tggaaaatgt 1440
gcaatatgtg atgtggcaaa tctctattag gaaatattct gtaatcttca gacctagaat 1500
aatactagtc ttataatagg tttgtgactt tcctaaatca attctattac gtgcaatact 1560
tcaatacttc atttaaaata tttttatgtg caataaaatg tatttgtttg tattttgtgt 1620
tcagtacaat tataagctgt tt ttatatat gtgaaataaa agtagaataa acacaaaaaa 1680
aaaaaaaaa aaaaaaaaaa aa 1702
```

<210> 372

<211> 585

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(585)

<223> 3' terminal sequence. oncogene tc21 (TC21)
gene.

<400> 372

```
gtaggcagta tgattccaaa agttaaataa tatttcacaa cctgtagctt cagcttggca 60
aacagcttag attccaaaac tgattcatct ctattaaaat gtaagcactt aaaaaaagag 120
catgtctgtg tatatagaca tat attttta aggaatcaga taatctttga agcagcctta 180
gtgtttcctt taaatttgct tggaaatgac cattgtatta gcttcacaga aaggactagc 240
cagcttcttc gtctaaggct aacatggtga tcatttgtct aaggctagaa aggtaccaac 300
aagatgtaaa ctgaggagag aaagagaaga tgagggcctt tcctggccgt tggtagctaa 360
aactgaaggg attctagaaa atgacacaat ggcagccttt cntgtctttt tctttccgtg 420
ttggttcngg tgaaggagga cattcctggc cctggaaatt tccnggataa cccggacaag 480
ttcatgggaa agcttgatct acattcatcc taatccttgc cggatgcnc catgtatgtt 540
acctaagctg ccggcaacgg tngcctctnc cggggtaccg gcc ng 585
```

<210> 373

<211> 451

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(451)

<223> 5' terminal sequence. oncogene tc21 (TC21)
gene.

<400> 373

```
gattcttaca caaagcagtg tgtgatagat gacagagcag cccggctaga tattttggat 60
```

237/292

```

acagcaggac aagaagagtt tggagccatg agagaacagt atatgaggac tggcgaaggc 120
ttcctgttgg tcttttcagt cacagataga ggcagttttg aagaaatcta taagtttcaa 180
agacagattc tcagagtaaa ggatcgtgat gagttcccaa tgattt taat tggtataaaa 240
gcagatctgg atcatcaaag acaggtaaca caggaagaag gacaacagtt agcacggcag 300
cttaaggtaa catacatgga ggcacagca aagattagga tgaatgtaga tcaantttcc 360
atgaacttgt ccgggttatac aggaaatttc aagancagga atgtcctctt cacagaccac 420
acggaaagaa aagccagaaa gctg cattgt g
                                         451

```

<210> 374

<211> 425

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(425)

<223> 3' terminal sequence. cd44 antigen (homing
function and indian blood group system) (CD44)
gene.

<400> 374

```

gaagatcgaa gaagtacaga tatttattat gaatcagttt aaaccctttt gtgcctctga 60
caaagtaact ttaaaaaatt atactgatca aaggactgat ccagggttta atatttcaa 120
aacacagata aatagtttac tacagataaa tagcttcacc c ttgggtgc ctcccagaag 180
catctgaaaa atttctagag ggggtctgtt gaagatgtgt aactagtaca cccaacccc 240
caacctcagt ggaaagcaat gcccagggat taggctatgg aaggggcaaaa tggaccatt 300
caaatttcct cccagggaac aggccctatt aaccctggga aatgtcctta gctggtgggg 360
gaaagggttg cgattcagga atacatatgt gtagtttttg ttagaagcca tccatagcac 420
accgg
                                         425

```

<210> 375

<211> 478

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(478)

<223> 5' terminal sequence. cd44 antigen (homing
function and indian blood group system) (CD44)
gene.

<400> 375

```

ggcgttccag ttcccacttg gaggccttc atccctcggg tgtgctatgg atggcttcta 60
acaaaaacta cacatatgta ttctgatcg ccaacct ttc cccaccagc taaggacatt 120
tcccagggtt aatagggcct ggtccctggg aggaaatttg aatgggtcca tttgccctt 180
ccatagccta atccctgggc attgctttcc actgaggttg ggggttgggg tgtactagtt 240
acacatcttc aacagacccc ctctangaaa tttttcagat gcttctggga gacacccaaa 300
ggggaaagct atttatctgt agtaaaactat ttatctgtgt ttttgaaata ttaaaccctg 360
gatcagtcct ttgatcagta taaatttttt aaagttaact ttgtcagagg caccaaaggg 420
tttaaaactga ttcataaata aatatcngga cttcctcgtat cttccaaaaa aaaaaaaa 478

```

238/292

<210> 376
<211> 1794
<212> DNA/RNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<220>
<221> misc_feature
<222> (1)..(1794)
<223> cd44 antigen (homing function and indian
blood group system) (CD44) gene.

<400> 376
ccgcgcgcct ccgttcgctc cggacacccat ggacaagttt tgggtggcacg ca gcctgggg 60
actctgcctc gtgcgcgtga gcctggcgca gatcgatttg aatataacct gccgctttgc 120
aggtgtattc cactgtggaga aaaatggctg ctacagcatc tctoggacgg aggcgcgtga 180
cctctgcaag gctttcaata gcaccttgcc cacaatggcc cagatggaga aagctctgag 240
catcggattt gagacctgca ggtatgggtt c atagaaggg catgtgggtga ttccccggat 300
ccaccccaac tccatctgtg cagcaaacaa cacaggggtg tacatcctca catacaacac 360
ctcccagtat gacacatatt gcttcaatgc ttcagctcca cctgaagaag attgtacatc 420
agtcacagac ctgcccattg cctttgatgg accaattacc ataactattg ttaaccgtga 480
tggcaccgcg tatgtccaga aaggagaata cagaacgaat cctgaagaca tctaccccag 540
caaccctact gatgatgacg tgagcagcgg ctctccagt gaaaggagca gcacttcagg 600
aggttacatc ttttacacct tttctactgt acaccccatc ccagacgaag acagtccctg 660
gatcaccgac agcacagaca gaatccctgc taccagagac caagacacat t ccaccccag 720
tgggggggtc cataccactc atggatctga atcagatgga cactcacatg ggagtcaaga 780
aggtggagca aacacaacct ctggtcctat aaggacaccc caaattccag aatggctgat 840
catcttggca tccctcttgg ccttggcttt gattcttgca gtttgcattg cagtcaacag 900
tcgaagaagg tgtgggcaga agaaaaagct agtgatcaac agtggcaatg gagctgtgga 960
ggacagaaag ccaagtggac tcaacggaga ggccagcaag tctcaggaaa tgggtgcat 1020
ggtgaacaag gactcgctcag aaactccaga ccagtttatg acagctgatg agacaaggaa 1080
cctgcagaat gtggacatga agattgggtg gtaacaccta caccattatc ttggaaagaa 1140
acaaccgttg gaaacataac cattacaggg agctgggaca cttaacagat gcaatgtgct 1200
actgattgtt tcattgcgaa tcttttttag cataaaattt tctactcttt ttgttttttg 1260
tgttttgttc tttaaagtca ggtccaattt gtaaaaacag cattgctttg taaattaggg 1320
cccaattaat aatcagcaag aatttgatcg ttcagttcca cttg gaggcc ttcacccctg 1380
ggtgtgctat ggatggcttc taacaaaaac tacacatatg tattcctgat cgccaacctt 1440
tccccacca gctaaggaca tttcccaggg ttaatagggc ctgggtccctg ggaggaaatt 1500
tgaatgggtc cattttgccc ttcataagcc taatccctgg gcattgcttt ccactgaggt 1560
tgggggtgac tagttacac a tcttcaacag accccctcta gaaatttttc agatgcttct 1620
gggagacacc aaagggtgaa gctatttatc tgtagtaaac tatttatctg tgtttttgaa 1680
atattaaacc ctggatcagt cctttgatca gtataattt ttaaagttac tttgtcagag 1740
gcacaaaagg gtttaaactg attcataata aatatctgta cttcttcgat cttc 1794

<210> 377
<211> 452
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<220>
<221> misc_feature
<222> (1)..(452)
<223> 3' terminal sequence. cyclin-dependent
kinase inhibitor 3 (cdk2-associated dual
specificity phosphatase) (CDKN3) gene.

<400> 377

ttttgtcaat aaaacttttag gaatatctgc acatgtacat ttacattcaa gttgataaca 60
ctggtggttt catttcaata caaattatgc tagagaactg acatttcaga catggtcata 120
tatatgctat ttgaattcct ttatcttcga tacagatctt gattgtgaat ctc ttgatga 180
tagatgtgca gctaatttgt cccgaaactc atgaagataa ttgtattgct tgatggctctg 240
tattgccccg gatcctctta ggtctcgag gctgtctatg gcttgcctctg gtgatattgt 300
gtcagacagg tatagtagga gacaagcagc tacaagacaa gatctcccaa gtcctccata 360
gcagtgtatt aaggggttttc cggtaatttt t aaggcaggt tgtaagcncct tccattattt 420
cacagcagct ggccatgctn ggagtccccc ca 452

<210> 378

<211> 472

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(472)

<223> 5' terminal sequence. cyclin -dependent
kinase inhibitor 3 (cdk2 -associated dual
specificity phosphatase) (CDKN3) gene.

<400> 378

ggcacgagcg gcaactggtc tcgacgtggg gcggccanga ctgaagccca ngnttcaata 60
caaacaagtg agtttgactc atcagatg aa gagcctattg aagatgaaca gactccaatt 120
catatatcat ggctatcttt gtcacgagtg aattgttctc agtttctcgg tttatgtgct 180
cttccagggt gtaaatTTaa agatgttaga agaaatgtcc aaaaagatac agaagaacta 240
aagagctgtg gtatacaacg acatatttgt tttctgcacc agaggggaac tgtcaaaaata 300
tagagtccca aaccttctgg atctctacca gcaatgtgga attatcacc atcatcatcc 360
aatccgcaga tggagggact cctgacatag ccagctgctg tgaaataatg gaagagctta 420
caacctgcct taaaaattac cgaaaaacct taatacactg ctatggagga ct 472

<210> 379

<211> 639

<212> DNA/RNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(639)

<223> cyclin-dependent kinase inhibitor 3
(cdk2-associated dual specificity phosphatase)
(CDKN3) gene.

<400> 379

atggagccgc ccagttcaat acaacaagt gagtttgact catcagatga agagcctatt 60
gaagatgaac agactccaat tcatatatca tggctatctt tgtcacgagt gaattgttct 120
cagtttctcg gtttatgtgc tcttccagggt tgtaaatTTa aagatgttag aagaaatgtc 180
caaaaagata cagaagaact aaagagctgt ggtatacaag acatatttgt tttctgcacc 240
agaggggaac tgtcaaaaata tagagtccca aaccttctgg atctctacca gcaatgtgga 300
attatcacc atcatcatcc aatcgcatg ggagggactc ctgacatagc cagctgctgt 360
gaaataatgg aagagcttac aacctgcctt aaaaattacc gaaaaacctt aatacactgc 420

240/292

tatggaggac ttgggagatc ttgtcttgta gctgcttgt c tcctactata cctgtctgac 480
 acaatatcac cagagcaagc catagacagc ctgagagacc taagaggatc cggggcaata 540
 cagaccatca agcaatacaa ttatcttcat gagtttcggg acaaattagc tgcacatcta 600
 tcatcaagag attcacaatc aagatctgta tcaagataa 639

<210> 380

<211> 487

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(487)

<223> 5' terminal sequence. max-interacting
protein 1 (MXI1) gene.

<400> 380

aagtggcgac tggaacagct gcagggtcct caggagatgg aacgaatacg aatggacaga 60
 attggatcaa ctatttcttc agatcggttct gattcagagc gagaggagat tgaagtggat 120
 gttgaaagca cagagttctc ccatggagaa gtggacaata taagtaccac cagcatcagt 180
 gacattgatg accacagcag cctgccgagt attgggagtg acgagggtac tccagtgcc 240
 gtgtcaaaat ttcatctact tcatagaacc cagcatgaca taacagtgcg gggaaaatat 300
 tcaactgggc attcatacaa acaatctctt aaattgggtt catgatgcag tctcctcttt 360
 aaaacaaaac aaaacaaaac aaactatact tgaacaaaag ggtcagagga ctgttttaag 420
 caatacttag caaaagtggg cagctcccaa gagacaattt cagatttcat ttggaaatcc 480
 catttta 487

<210> 381

<211> 2416

<212> DNA/RNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(2416)

<223> max-interacting protein 1 (MXI1) gene.

<400> 381

agattatgat cgctgaggc ccctctccta cccagatacc gatgttatac tgatgtgttt 60
 ttcttttttt tttttttttt tttaagtaat taagggtagt taaattatth aaagtataca 120
 aagtccaaac agccaggggt aaggtctcca agaggccttc ccagggttaag ggagtgcgga 180
 gaggcccgcg tcgccaccgc cgggtcccat ggagcgggtg aagatgatca acgtgcagcg 240
 tctgtctggag gctgccgagt ttttgagcgc cggggagcga gagtgtgaac atggctacgc 300
 ctcttcattc cgtccatgc cgagccccc actgcagcat tcaaagcccc caccgagggtt 360
 gagccgggga cagaaacaca gcagcgggac gagcaacacc a gcactgcca acagatctac 420
 acacaatgag ctggaaaaga atcgacgagc tcatctgcgc ctttgtttag aacgcttaaa 480
 agttctgatt ccactaggac cagactgcac ccggcacaca acacttggtt tgctcaacaa 540
 agccaaagca cacatcaaga aacttgaaga agctgaaaga aaaagccagc accagctcga 600
 gaatttggaa cgagaacaga gatttttaaa gtggcgactg gaacagctgc agggctctca 660
 ggagatggaa cgaatacga tggacagcat tggatcaact atttcttcag atcgttctga 720
 ttacagagcga gaggagattg aagtggatgt tgaaagcaca gagttctccc atggagaagt 780
 ggacaatata agtaccacca gcatcagtga cattgatgac cacagcagcc tgccgagtat 840
 tgggagtgac gagggttact ccagtgccag tgtcaaactt tcattcactt catagaaccc 900

241/292

```

agcatgacat aacagtgcag ggcaaaatat tcaactgggc aattcaatac aaacaatctc 960
ttaaattggg ttcattgatgc agtctcctct ttaaaacaaa acaaaacaaa acaaaactat 1020
acttgaacaa aaggggcaga ggacctgtat ttaagcaaa t acttagcaaa aagtggggca 1080
gagctcccaa ggagaacaaa tattcagaat attcatattg gaaaaatcac aatttttaat 1140
ggcagcagaa aacttgtgtg aaattttctt gatttgagtt gattgagaag aggacattgg 1200
agatgccatc ctctttctct tttctcgttt gctcatacta cattgagtag acacatttaa 1260
ggatgggggtt atgaaccctt cctgagcttt atggtcctaa aagcaaaata aaaactattc 1320
gaatgaaaag acaagaaaat caggtattaa tcttgatag ctaataatga gctattaaaa 1380
ctcagcctgg gacagtttat catgaagcct gtggatgac aatcctttat tattattttt 1440
tttttttgaa aaaagctcat ttcattgctc gcaaaaggag agactcccat ga agcctttt 1500
gaaagggatc atcatgcagc tcaactttct gttggattcc atgctaagca agctaacctt 1560
atcctgcatt gtttagcata ggcaaccagc tgccacctct ccatcctgct gcccttaggc 1620
cacatgggag cagtcacatgc atgacagcct ctatcctaca aggcctatga gtatggattg 1680
ggggggccaa aaggaaaaag ctccatg tgc ctctttgtct gcgtgggtca gaagagttgt 1740
gcacgcagat tagcaggcca aggtctgagc cacagcagca tttttatttc agattttgat 1800
aactgtttat atgtgttgaa aacccaaatg acatcttttt aaagcttata cataaaaaaa 1860
aatagatgtc ttttatagtg gaaaaacaca tggggaaaaa aatcatctat tttgatgcag 1920
catttgataa tgataaaaca cctcacacct cactctttat agtgcacaaa atgaatgagg 1980
tctgggctag gtagaaaaag ggtcaatgct atttttgttt ttagaatcat tacctttttac 2040
cagcttttaa ccacttgata tctatagtag acacactatc atagttaaca tagttaagtt 2100
cagcacttgt acatttttaa tgtaaagatt tgcttcatt ttctacagg cagtctctct 2160
cttctcaca gtccactgt gcagggtgta ttgttactct tacgaatatt ttcagtaatg 2220
ttattttctt ctaagtgaag tttctagcct gcactttgat gtcattgtgt ccctttgtct 2280
ttcaaaactcc aagggtcccc tgtggccctc tcccttacct tgggaaggcc tcttgagac 2340
cttacccttg gctgt ttgga ctttgtatac ttaaataat ttaactacct ttaattactt 2400
aaaaaaaaa aaaaaa
2416

```

<210> 382

<211> 378

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(378)

<223> 3' terminal sequence. homeo box a5 (HOXA5) gene.

<400> 382

```

tttttttttt ttgttatagt tacttcaagt aacacagctt gcttcatata aataagttaa 60
aacatctatt ttttttcaag acaaagccat tcaggacaaa gagatgaaca gaaagcagat 120
ctacttatac aggcgc tata atggcaataa acaggctcat gattaaaaga tgaattaggg 180
caacgagaac agggcttctt cacagaagga acacaaggga gtttcagaaa gtcaccttag 240
tactgacact acgcgggacg cgctaaatac tgctcagtag tttaaacgct cagatactca 300
gggacggaag gccctccctt gcccgcggnc atnctccatg gcttttcagc ttattatc tt 360
ttttccactt caatcncc
378

```

<210> 383

<211> 439

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

242/292

<221> misc_feature
 <222> (1)..(439)
 <223> 5' terminal sequence. homeo box a5 (HOXA5) gene.

<400> 383
 aaatcaagca cacaatantan aaaacaaatg agctcttatt ttgtaaactc attttgcggt 60
 cgctatccaa atggcccgga ctaccagttg cataattatg gagatcatag ttccgtganc 120
 gagcaattca gggactcggc gagcatgcac tccggcaggt acggctacgg ctacaatggc 180
 atggatctca gcgtcggcng ctcgngctcc ngcacttttg ctccggagag cgcgcccgc 240
 gctacgtnc aagcgcacgc ggcncactcc aagcccaggt acagcnagcc ggccacgtcc 300
 acgcactctn cctcancncg atccgctgcn ctgctccgnc gtngggccct tcgcccngga 360
 ancgacanna ccaanggcgg gaaaaactcc cttaaggca a ctccagcngg cgcctcgggc 420
 cgacngccgg aagcaccca 439

<210> 384
 <211> 813
 <212> DNA/RNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:primer

<220>
 <221> misc_feature
 <222> (1)..(813)
 <223> homeo box a5 (HOXA5) gene.

<400> 384
 atgagctctt attttgtaaa ctcatthttgc ggtcgctatc caaatggccc ggactaccag 60
 ttgcataatt atggagatca cagttccgtg agcgagcaat tcagggactc ggcgagcatg 120
 cactccggca ggtacggcta cggtacaat ggcattggtc tcagcgtcgg ccgctcgggc 180
 tccggcact ttggtccgg agagcgcgc cgcagctacg ctgccagcgc cagcgcggcg 240
 ccgcccggag ccaggtacag ccagccggcc acgtccacgc actctcctca gcccgatccg 300
 ctgccctgct ccgcccgtggc cccctcgccc ggcagcgaca cgcaccacgg cgggaaaaac 360
 tccctaagca actccagcgg cgcctcggcc gacgcgggca gc accacat cagcagcaga 420
 gaggggggtg gcacggcgtc cggagccgag gaggacgccc ctgccagcag cgagcaggcg 480
 agtgcgcaga gcgagccgag cccggcgccg cccgcccac cccagatcta cccctggatg 540
 cgcaagctgc acataagtca tgacaacata ggcggcccgg aaggcaaaa ggcccggacg 600
 gcctacacgc gctaccagac cctggagctg gagaaggagt tccacttcaa ccgttacctg 660
 accgcagaa ggaggattga aatagcacat gctctttgcc tctccgagag acaaattaaa 720
 atctggtcc aaaaccggag aatgaagtgg aaaaaagata ataagctgaa aagcatgagc 780
 atggccgcgg caggaggggc cttccgtccc tga 81 3

<210> 385
 <211> 447
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:primer

<220>
 <221> misc_feature
 <222> (1)..(447)
 <223> 3' terminal sequence. x-box binding protein 1 (XBP1) gene.

<400> 385

243/292

gcattgtacc ttttaattgc atgggtagtt ttaaataaat ggagaaagca cctttcagaa 60
gctacactag caggaaaaaa ttccatcaag cattttacata gtaaatttct ataatttcac 120
aaaagattct tgatcttact tgaagtatac atgagggaaa gagccccctc agcaggtgtt 180
cccgttgctt acagaagcaa actaaaggac ctaaaactgg aggcaagcca ggatgc caaa 240
aagggggaag agaaatgata aagaaccatt cataaattcc atgtctactt caagacattt 300
gtctaatac ccttacataa taagtatttt agggaaaact accacccttt taagataaaa 360
gtacaatctt aaaagctgta gttctcaatt atagtaatat ttcntacttc cagtaatatg 420
tctcaatacc ttggactgct ggatgtc 447

<210> 386

<211> 462

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(462)

<223> 5' terminal sequence. x-box binding protein
1 (XBP1) gene.

<400> 386

aagaacctgt agaagatgac ctctgtccgg agctgggtat ctcaaactctg ctttcatcca 60
gccactgccc aaagccatct tccctgcctac tggatgctta cagtgactgt ggatacgggg 120
gttcccttcc cccattcagt gacatgtcct ctctgcttgg tgtaaaccat tcttgggagg 180
acacttttgc caatgaactc tttcccca gc tgattagtgt ctaaggaatg atccaatact 240
gttgcccttt tccctgacta ttacactgcc tggaggatag cagagaagcc tgtctgtact 300
tcattcaaaa agccaaaata gagagtatac agtcctagag aattcctcta tttgttcaga 360
tctcatagat gacccccagg tattgtcttt tgacatccca agcagtccaa ggtattggag 420
acatattact gggaagtaaa gaaatattac tnataattgg ag 462

<210> 387

<211> 1836

<212> DNA/RNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(1836)

<223> x-box binding protein 1 (XBP1) gene.

<400> 387

ggcgctgggc ggctgcggcg cgcggtgcmc ggtgcgtagt ctggagctat ggtgggtggtg 60
gcagccgcgc cgaaccgggc cgacgggacc cctaaagtcc tgcttctgtc ggggcagccc 120
gcctccgcgc cgggagcccc ggccggccag gccctgccgc tcatggtgcc agcccagaga 180
ggggccagcc cggagggcagc gagcgggggg ctgccccagg cgcgcaagcg acagcgcctc 240
acgcacctga gccccgagga gaaggcgctg aggaggaaac tgaaaaacag agtagcagct 300
cagactgcca gagatcgaaa gaaggctcga atgagtgcgc tggaacagca agtggtgatg 360
ttagaagaag agaaccaaaa acttttgcta gaaaatcagc ttttacgaga gaaaactcat 42 0
ggccttgtag ttgagaacca ggagttaaga cagcgcttgg ggatggatgc cctgggtgct 480
gaagaggagg cggaagccaa ggggaatgaa gtgaggccag tggccgggtc tgctgagtcc 540
gcagcactca gactacgtgc acctctgcag cagggtgcagg cccagttgtc acccctccag 600
aacatctccc catggattct ggcgggtatt actcttcaga ttcagagtct gatatcctgt 660
tgggcattct ggacaacttg gaccagtcga tgttcttcaa atgcccttcc ccagagcctg 720

244/292

```

ccagcctgga ggagctccca gaggtctacc cagaaggacc cagttcctta ccagcctccc 780
tttctctgtc agtggggacg tcatcagcca agctggaagc cattaatgaa ctaattcgtt 840
ttgaccacat atataccaa g cccctagtct tagagatacc ctctgagaca gagagccaag 900
ctaattgtgt agtgaaaatc gaggaagcac ctctcagccc ctgagagaat gatcaccctg 960
aattcattgt ctgagtgaag gaagaacctg tagaagatga cctcgttccg gagctgggta 1020
tctcaaatct gctttcatcc agccactgcc caaagccatc ttctgccta ctggatgctt 1080
acagtgaactg tggatacggg ggttcccttt cccattcag tgacatgtcc tctctgcttg 1140
gtgtaaacca ttcttgggag gacacttttg ccaatgaact ctttcccag ctgattagt 1200
tctaaggaat gatccaatac tgttgccctt ttcttgact attacactgc ctggaggata 1260
gcagagaagc ctgtctgtac ttcattcaaa aagc caaat agagagtata cagtcctaga 1320
gaattcctct atttgttcag atctcataga tgacccccag gtattgtctt ttgacatcca 1380
gcagtccaag gtattgagac atattactgg aagtaagaaa tattactata attgagaact 1440
acagctttta agattgtact tttatcttaa aagggtggta gttttcccta aaatacttat 1500
tatgtaaggg tcattagaca aatgtcttga agtagacatg gaatttatga atgggttctt 1560
atcatttctc ttcccccttt ttggcatcct ggcttgctc cagttttagg tcctttagtt 1620
tgcttctgta agcaacggga acacctgctg agggggctct ttocctcatg tatacttcaa 1680
gtaagatcaa gaatcttttg tgaattata gaaatttact atgtaaat gc ttgatggaat 1740
tttttctgc tagttagct tctgaaagg tctttctcca tttatttaa actacccatg 1800
caattaaaag gtacaatgca aaaaaaaaa aaaaaa 1836

```

<210> 388

<211> 433

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(433)

<223> 3' terminal sequence. tumor necrosis factor,
alpha-induced protein 3 (TNFAIP3) gene.

<400> 388

```

tttttcttaa ataatttatt ttttaagtgt gactcttggt aaaagttaca tttattttaga 60
aaaacttgaa gaaatccaac aaagaatagg tggctttcta ttagggacaa ttaaagtgtc 120
aaatttcaaa tactttttat aataagtata aataattact ttttttcaca ttaagaatgg 180
aaataatgat caacacaana tattaagata tcaactttta gagaattaga tgaaaacact 240
gaagtgttatt tgngtatcct tggaaangaa ttataaagat tcgtctggga aaaactt agg 300
gggctctaag gggaaagtig tgcctaatag tatgagtaaa ggctgtgtag agttatggat 360
cacaaatatt ttcaggccont aagtacagac cccnnaatg gcagcctta tcnccgggga 420
aatgcattt ccc 433

```

<210> 389

<211> 206

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(206)

<223> 5' terminal sequence. tumor necrosis factor,
alpha-induced protein 3 (TNFAIP3) gene.

<400> 389

245/292

ctcaaccagc tgccttttta aaggga gctc tagtcctttt tgtgtaattc actttattta 60
ttttattaca aacttcaaga ttatttaagt gaagatattt cttcagctct ggggaaaatg 120
ccacagtgtt ctctgagag aacatccttg ctttgagtca ggctgtgggc aagttcctga 180
ccacagggag taaatngnn cctctt 206

<210> 390

<211> 4426

<212> DNA/RNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(4426)

<223> tumor necrosis factor, alpha -induced protein
3 (TNFAIP3) gene.

<400> 390

tgccttgacc aggacttggg acttttgcga aggatcgagg ggcgcggaga ggtgttggag 60
agcacaatgg ctgaacaagt ccttcctcag gctttgtatt tgagcaatat gcggaaagct 120
gtgaagatac gggagagaac tccagaagac atttttaaac ctactaatgg gatcattcat 180
catttttaaaa ccatgcacccg atacacactg gaaatgttca gaacttgcca gtt ttgtcct 240
cagtttcggg agatcatcca caaagccctc atcgacagaa acatccaggc caccctggaa 300
agccagaaga aactcaactg gtgtcgagaa gtccggaagc ttgtggcgct gaaaacgaac 360
ggtgacggca attgcctcat gcatgccact tctcagtaca tgtggggcgt tcaggacaca 420
gaacttggtac tgaggaaggg gctgttcagc a cgctcaagg aaacagacac acgcaacttt 480
aaattccgct ggcaactgga gtctctcaaa tctcaggaat ttgttgaaac ggggctttgc 540
tatgatactc ggaactggaa tgatgaatgg gacaatctta tcaaaatggc ttccacagac 600
acacccatgg cccgaagtgg acttcagtac aactcactgg aagaaatata catatttgtc 660
ctttgcaaca tctcagaag gccaatcatt gtcatctcag acaaaatgct aagaagtgtg 720
gaatcaggtt ccaatttcgc ccctttgaaa gtgggtggaa tttacttgcc tctccactgg 780
cctgcccagg aatgctacag ataccccat gtctcggct atgacagcca tcattttgta 840
cccttggtga ccctgaagga cagtgggcct gaaatccgag ctgttccact t gtaacaga 900
gaccggggaa gatttgaaga cttaaaagtt cactttttga cagatcctga aaatgagatg 960
aaggagaagc tcttaaaaga gtacttaatg gtgatagaaa tccccgtcca aggcgtggac 1020
catggcaca ctcactcat caatgccgca aagttggatg aagctaactt accaaaagaa 1080
atcaatctgg tagatgatta ctttgaac tt gttcagcatg agtacaagaa atggcaggaa 1140
aacagcgagc aggggaggag agaggggcac gccagaatc ccatggaacc ttccgtgccc 1200
cagctttctc tcatggatgt aaaaatgtga acgcccact gcccttctt catgtctgtg 1260
aacaccagc ctttatgcca tgagtgtca gagaggcggc aaaagaatca aaacaaactc 1320
ccaaagctga actccaagcc gggccctgag gggctccctg gcatggcgct cggggcctct 1380
cggggagaag cctatgagcc cttggcggtg aaccctgagg agtccactgg ggggcctcat 1440
tcggccccc cagacagacc cagccctttt ctgttcagtg agaccactgc catgaagtgc 1500
aggagcccc gctgccctt cactgaat gtgcagcaca a cggtttttg tgaacgttgc 1560
cacaacgccc ggcaacttca cgccagccac gccccagacc acacaaggca cttggatccc 1620
gggaagtgcc aagcctgcct ccaggatgtt accaggacat ttaatgggat ctgcagtact 1680
tgcttcaaaa ggactacagc agaggcctcc tccagcctca gcaccagcct cctccttcc 1740
tgtcaccagc gttcca agtc agatccctcg cggctcgtcc ggagcccctc cccgcattct 1800
tgccacagag ctggaacga cgccctgct ggctgctgt ctcaagctgc acggactcct 1860
ggggacagga cggggacgag caagtgcaga aaagccggct cgtgtatatt tgggactcca 1920
gaaaacaagg gcttttgcac actgtgttc atcgagtaca gagaaaacaa acatt ttgct 1980
gctgcctcag ggaaagtca tcccacagc tccaggttcc agaaccat tccgtgcctg 2040
gggagggaat gcggcacct tggaagcacc atgtttgaag gatactgcca gaagtgttcc 2100
attgaagctc agaatcagag atttcatgag gccaaaagga cagaagagca actgagatcg 2160
agccagcgca gagatgtgcc tcgaaccaca caaagcacct caaggcccaa gtgcgcccgg 2220
gcctcctgca agaacatcct ggcctgccgc agcagaggag tctgcatgga gtgtcagcat 2280
cccaaccaga ggatgggccc tggggccccc cggggtgagc ctgccccga agaccccccc 2340
aagcagcggt gccgggcccc cgcctgtgat cattttggca atgccaagtgc caacggctac 2400

246/292

```

tgcaacgaat gctttcagtt caagcagatg tatggctaac cggaacaggg tgggtcacct 2460
cctgcaagaa gtggggcctc gagctgtcag tcatcatggg gctatcctct gaaccctca 2520
gctgccactg caacagtggg ctttaagggg tctgagcagg agaggaaaga taagctcttc 2580
gtgggtgccc cgatgctcag gtttgtaaac ccgggagtggt tcc caggtgg ccttagaaa 2640
caaagcttgt aactggcaag ggatgatgtc agattcagcc caaggttcct cctctcctac 2700
caagcaggag gccaggaaact tctttggact tggaagggtg gcggggactg gccgaggccc 2760
ctgcaccctg cgcatacagga ctgcttcacg gtcttggtcg agaaagggaa aagacacaca 2820
agtgcgctgg gttggaga ag ccagagccat tccacctccc cccccccagc atctctcaga 2880
gatgtgaagc cagatcctca tggcagcgag gccctctgca agaagctcaa ggaagctcag 2940
ggaaaatgga cgtattcaga gagggtttgt agttcatggg tttccctac ctgcccggtt 3000
cctttcctga ggaccgggca gaaatgcaga accatccatg gactgtgatt ctgaggc tgc 3060
tgagactgaa catgttcaca ttgacagaaa aacaagctgc tctttataat atgcaccttt 3120
taaaaaatta gaatatatta ctgggaagac gtgtaactct ttgggttatt actgtcttta 3180
cttctaaaga agttagcttg aactgaggag taaaagtgtg tacatatata atataccctt 3240
acattatgta tgaggatttt ttttaatta t attgaaatg ctgccctaga agtacaatag 3300
gaaggctaaa taataataac ctgttttctg gttgtgttg gggcatgagc ttgtgtatac 3360
actgcttgca taaactcaac cagctgcctt tttaaaggga gctctagtcc tttttgtgta 3420
attcacttta tttattttat tacaacttc aagattattt aagtgaagat atttcttcag 3480
ctctggggaa aatgccacag gtgtctcctg agagaacatc cttgctttga gtcaggctgt 3540
gggcaagttc ctgaccacag ggagtaaat ggctctcttg atacactttt gcttgccctc 3600
ccaggaaaag aggaattgca tccaaggtat acatacatat tcatogatgt ttctgtcttc 3660
tccttatgaa actccagcta tgtaataaaa aactatactc tgtgt tctgt taatgcctct 3720
gagtgctcta cctccttgga gatgagatag ggaaggagca gggatgagac tggcaatggg 3780
cacagggaag gatgtggcct tttgtgatgg ttttattttc tgtaaacact gtgtcctggg 3840
ggggctggga agtcccctgc atcccaggt accctggtat tgggacagca aaagccagta 3900
accatgagta tgaggaaatc tctttctgtt gctggcttac agtttctctg tgtgctttgt 3960
ggttgctgtc atatttgtc tagaagaaaa aaaaaaagg aggggaaatg cattttcccc 4020
agagataaag gctgccattt tgggggtctg tacttatggc ctgaaaatat ttgtgatcca 4080
taactctaca cagcctttac tcatactatt aggcacactt tccccttaga gccccctaa g 4140
tttttccag acgaatcttt ataatttctt ttccaaagat accaaataaa cttcagtgtt 4200
ttcatctaat tctcttaaag ttgatattt aatattttgt gttgatcatt atttccattc 4260
ttaatgtgaa aaaaagtaat tatttatact tattataaaa agtatttgaa atttgcacat 4320
ttaattgtcc ctaatagaaa gccacctatt ctt tgttgga tttcttcaag tttttctaaa 4380
taaattgaac ttttcacaag agtcaacatt aaaaaataaa ttattt 4426

```

<210> 391

<211> 440

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(440)

<223> 3' terminal sequence. serum response factor
(c-fos serum response element-binding
transcription factor) (SRF) gene.

<400> 391

```

ttttttgtg cacaaaaatg atacatttat tgaaagagta tttttttttt aatacaaaaag 60
aaagctctgt acataggact gtgaccatgt ccactattcc tgggtcagca tcccagggga 120
agtagaaaac actgacatac aactcacat tcaagcacac aactcactc aggcgcacac 180
accacacac acatacccga gagccacga ggaagggaaa caccaagggt cgctgcacat 240
aaaaatatca cctcaactca tccctgacac acgcatgtcc tcccaaggcc acgctcacac 300
aacacacatt ataagcatt tgctgattc actcactngg gtctgtcttt tgtgggaagg 360
agaggaagaa ttcatcaaag gtctcctccc catgggtngg gggagtgggg agtgagttag 420
tgatggtgga gtgaaacaag

```

440

<210> 392
<211> 471
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<220>
<221> misc_feature
<222> (1)..(471)
<223> 5' terminal sequence. serum response factor
(c-fos serum response element-binding
transcription factor) (SRF) gene.

<400> 392
aattcggcac gaaggcagga atgggggtca gaagaagtgg gagcagcttc ttgggctgag 60
tgcagcaaag gggagccaga aatgggcagt tctcccaggg agtgagcagc tactgtaact 120
tttttaaatt aagacaaaaa gccttgaaga aaatgacttt atttttctaa gtgtaacctc 180
agtatttatg taattttgtac agggggccatg ccacncccc tctccccct ttngtnaga 240
ccttgagggt gggccagcat aggggggagg gtcttttacc ctgtgtcaga gcctaccttc 300
accacctata tccagaaggg gagctttttc agaaacaggg cagcagtggg gtgaaathtt 360
cttaaccct aagactgcct tcagtaagga acaagctggc ttctgtgatt aggtgaaggg 420
atgggggaag attttaatgc acagccta gt tatcaagggg atgatttgcc g 471

<210> 393
<211> 4201
<212> DNA/RNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<220>
<221> misc_feature
<222> (1)..(4201)
<223> serum response factor (c-fos serum response
element-binding transcription factor) (SRF) gene.

<400> 393
ggtcggggga tccctccgcc gccagcgctt ggtcccgccc cctccaccc gcggtctcgg 60
ccgcggccag cagcccctgc ccccggggg acgctgacgg ccgcccggcg cgccgcccta 120
gcagacggac agggggcgct gcgcggggcc tggggcaacc cgggccac ag gggcaggaaa 180
gtgagggcc aggtcggccc gggcgtgcag gggccccggg ttgcagcgg cgcccgcggc 240
agcgatagcg gcactagcag cagcgggagt gccgggttga gccgggaagc cgatggcggc 300
ggctgcggcg gctccgattc ctgcgtgact gccgctccgc cctcctgcat cgagcgccat 360
gttaccgacc caagctgggg ccgcgg cggc tctgggcccgg ggtcggccc tggggggcag 420
cctgaaccgg accccgacgg ggcggccggg cggcgggcggc gggacacggc gggctaaccg 480
gggcccggtc cccgggaatg gcgcggggct cgggcccggc cgcctggagc gggaggctgc 540
ggcagcgggc gcaaccaccc cggcgcccac cgcggggggc ctctacagcg gcagcgagg 600
cgactcggag tcgggcgagg agggaggagct gggcgccgag cggcgcgccc tgaagcggag 660
cctgagcgag atggagatcg gtatgggtgt cgggtggccc gagcgctcgg cagcgccac 720
cgggggctac gggcgggtga gcggcgcggt gagcggggcc aagccgggta agaagaccg 780
gggcccgtg aagatcaaga tggagttcat cgacaacaag ctgcgg cgct acacgacctt 840
cagcaagagg aagacgggca tcatgaagaa ggcctatgag ctgtccacgc tgacagggac 900
acaggtgctg ttgctgggtg ccagtgcagc aggccatgtg tatacctttg ccaccgaaa 960
actgcagccc atgatcacca gtgagaccgg caaggcactg attcagacct gcctcaactc 1020
gccagactct ccaccctgt cag accccac aacagaccag agaatgagtg ccaactggctt 1080
tgaagagaca gatctcacct accaggtgtc ggagtctgac agcagtgggg agaccaagga 1140

248/292

```

cacactgaag ccggcggttca cagtcaccaa cctgccgggt acaacctcca ccatccaaac 1200
agcacctagc acctctacca ccatgcaagt cagcagcggc cctcctttc ccatcaccia 12 60
ctacctggca ccagtgtctg ctagtgtcag cccagtgct gtcagcagtg ccaatgggac 1320
tgtgtgaag agtacaggca gggccctgt ctcctctggg ggccttatgc agctgcctac 1380
cagcttcacc ctcatgcctg gtggggcagt ggcccagcag gtcccagtg aggccattca 1440
agtgcaccag gcccacagc aagcgtctcc ctcccg gac agcagcacag acctcacgca 1500
gacctcctcc agcgggacag tgacgtgcc cgccaccatc atgacgtcat ccgtgccac 1560
aactgtgggt ggccacatga tgtaccctag ccgcgatgcg gtgatgtatg cccccacctc 1620
gggcctgggt gatggcagcc tcaccgtgct gaatgccttc tcccaggcac catccaccat 1680
gcaggtgtca cacagccagg tccaggagcc aggtggcgtc cccaggtgt tctgacagc 1740
atcatctggg acagtgcaga tccctgtttc agcagttcag ctccaccaga tggctgtgat 1800
agggcagcag gccgggagca gcagcaacct caccgagcta caggtgtga acctggacac 1860
cgccacagc accaagagt aatgatccgc ccgcccct ggacagatgg cccaaggat 1920
ggcaccactt atttattgtt gccttttcac gttttcttta cacacagtt gacgggccgc 1980
aggaggagg cggggaggag gaacgggcag ccacaggact gagccctctc actccagcca 2040
aagaaatggg cctgcctgcc tccaccgctc ctccctcagc ctccctctct tcccgcacca 2100
cctccattt ctgttctg agggg ctgtc ctccctctg ggacccctc gccagcttg 2160
ctcgatgtt gccatgagta ttagcttacc caatgggacc gtgcccacc tcccacaca 2220
caggccttct gtgggctg gcaccgtgtc ctccctctgag gaagcagttg gggcctctt 2280
gccagcctc ttgtgaccc caggtcagcc ctgtgtctgt cacagctgg gtcaaaagag 2340
ccctgctct cccctcagg gggccagctg gggagatgg ggttctctcc tcacactgct 2400
gtcctctccc ccttcagctc ctgagtagct gggcctgtgc actgggcagg ttctggggc 2460
cgctgcct gccttgcgc tcccttgga cctccagggt ctctgggtt ggagggaacc 2520
accagcttc cttctcccc ctgtcttcc cccctctcc t cccagctgt ttacttaaag 2580
ttgatttga actttttatt tgaggagacg aagtgaac aaatctataa atatatatt 2640
ttaaaatatt taactttttt ttatggcgtt tttctctcc cctccctgc ccaaactccc 2700
cttccctggg gagccctcag gctccccaga actggctgg ccctgggga cagagccacc 2760
ccatgagctc ggggtccacc agtgtgtgg ggagattctg ggtttgccca gtcctggatt 2820
gtttccagga gaaagccggg ggaggggcc tcaggccatt ccccaacggg gtggggagg 2880
tgaccacag ctctgggcct ctttttgccc tttaggctg ttgctaggga gaggaagag 2940
ggagacaaa tctcggggtt ggggtgggag ggcgtcaggc agaggcaact ga ctctattt 3000
gtgccacag catgggcatt gcagccttgc gctgtcccag gcatgcagct gcctggggc 3060
caagtgcag tgagcagggt ggggtctgg aggggtgag aggcaggaat ggggtcaga 3120
agaagtggga gcagcttctt ggcctgagtg cagccaaagg ggagccagaa atgggcagtt 3180
ctccaggga gtgagcagct actgtaa ctt ttttaaatta agacaaaaag ccttgaagaa 3240
aatgacttta tttttctaag tgtaacctca gtatttatgt aatttgtaca ggggccatgc 3300
cccaccccc tctccccc ctggggtaga ccttgagggt gggccagcat aggggggagg 3360
gtcttttacc ctgtgtcaga gcctaccttc accacctata tccagaaggg gagcttttc 3420
agaaacaggg cagcagtggt gtgaaatttt cttaaccctc aagactgcct tcagtaggaa 3480
caagtggct tctgtgatta ggtgaaggga tgggggaaga ttttatgcac agcctagtta 3540
tcaaggggat gatttgccga catgtttgag aacccctaa cctctaacc tcattgctgt 3600
cttgcaccag tttggggtgc caagatggaa gtcaccttc tgggctttct cctggagact 3660
agctgggct tatgggtggc tttcaaggct ggggcattgc aaatcagggt ccagagagca 3720
ggggagctt ggactcaggt ctgtaactgc ccagccctt ttctctgctc ttgtttcact 3780
ccaccatcac tactcactc cccactcccc caccatggg gaggagacct ttgatgaatt 3840
cttctctcc tccccaaaa agacagacc agtgagtga tcaggcaaag tgcttataat 3900
gtgtgtgtg tgagcgtggc cttgggagga catgcgtgtg tcagggatga gttgaggta 3960
tatttttatg tgcagcacc cttggtgtt cccttctcgt gtggctctgg ggtatgtgtg 4020
tgtgggtgtg tgcgctgag tgagtgtgtg tgcctgaatg tgagtgtgta tgtc agtgg 4080
ttctacttcc cctgggatgc tgaccagga atagtggaca tggcacagt cctatgtaca 4140
gagctttctt ttgtattaaa aaaaaatact ctttcaataa atgtatcatt tttgtgcaca 4200
g 4201

```

<210> 394

<211> 563

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(563)

<223> 3' terminal sequence. sry (sex determining region y)-box 9 (campomelic dysplasia, autosomal sex-reversal) (SOX9) gene.

<400> 394

```
tttttaatgc aatgtatatt tattgtaaac aataatatac aaaaaaaaaa aagagaaaga 60
aaaagggaaa ggtaagtttc acggagagaa caaaagggtt ggggctggga gggaaacaag 120
tgaacaaaac aaaacacgaa cacaaaccaa agcttttacc taaagacaaa atatgattta 180
aatgccaggt ttcttaagtt acaga agtat ctttttaaaa agatctgctt ttatacagaa 240
attgaaggat gccatattat gagtgcttta agattttatt ctactgactt ctaaaactgt 300
taatatatct ttttttaaat aaaaaaaaaa gtttgctgtc ttttttaaaa agcaatcctc 360
aaactctcta gccacagcag taattaagat taaggctgtg cagtgaggctg atcccctcca 420
ggtagcctcc ctcaactcaa gagaagatgc ngagaaatat gggatggaca catgcctgca 480
tgtttttgtg nccaaacaca cacanacca nacacacnca caatataagg cngccccaag 540
gtctntggcc gaaancctgg caa                                     563
```

<210> 395

<211> 3936

<212> DNA/RNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(3936)

<223> sry (sex determining region y) -box 9
(campomelic dysplasia, autosomal sex -reversal)
(SOX9) gene.

<400> 395

```
ggagagccga aagcggagct cgaaactgac tggaacttc agtggcgcg agactcgcca 60
gtttcaaccc cggaacttt tctttgcagg aggagaagag aaggggtgca agcgccccc 120
cttttgctct ttttctccc ctctcctcc tctccaattc gctctccccc acttgagcgc 180
ggcagctgtg aactggccac ccgcgcctt cctaagtgtc cgccgcggtg gccggc cgac 240
gcgccagctt ccccgaggc cgcttgctcc gcatccgggc agccgagggg agaggagccc 300
gcgcctcgag tccccagacc gccgcggctt ctgcctttc ccggccacca gcccctgcc 360
ccgggcccgc gtatgaatct cctggacccc ttcatgaaga tgaccgacga gcaggagaag 420
ggcctgtccg gcgccccag cccaccatg tccg aggact ccgcgggctc gccctgccc 480
tcgggctccg gctcggacac cgagaacacg cgccccagg agaacacgtt cccaagggc 540
gagcccgatc tgaagaagga gagcgaggag gacaagtcc ccgtgtgcat ccgcgaggcg 600
gtcagccagg tgctcaaagg ctacgactgg acgctggtgc ccatgccggt gcgcgtcaac 660
ggctccagca agaacaagcc gcacgtcaag cggcccatga acgccttcat ggtgtggcg 720
caggcggcgc gcaggaagct gcgggaccag taccgcact tgcacaacgc cgagctcagc 780
aagacgctgg gcaagctctg gagacttctg aacgagagcg agaagcggcc ctctgtggag 840
gaggcgagc ggctgcgcgt gcagcacaag aaggaccacc cggattacaa gtac cagccg 900
cggcgaggga agtcggtgaa gaacgggcag gcggaggcag aggaggccac ggagcagacg 960
cacatctccc ccaacgccat cttcaaggcg ctgcaggccg actcgccaca ctctcctcc 1020
ggcatgagcg aggtgcactc ccccggcgag cactcgggc aatcccaggg cccaccgacc 1080
ccaccacca ccccaaaaac cgacgtgcag ccgggcaagg ctgacctgaa gcgagagggg 1140
cgcccttgc cagagggggg cagacagccc cctatcgact tccgcgacgt ggacatcggc 1200
gagctgagca gcgacgtcat ctccaacatc gagacctcg atgtcaacga gtttgaccag 1260
tacctgccgc ccaacggcca cccgggggtg ccggccacgc acggccaggt cacctacag 1320
ggcagctacg gcatcagcag caccgcggcc accccggcga gcgcgggcca cgtgtggatg 1380
tcaaagcagc aggcgcggcc gccacccccg cagcagcccc cacaggcccc gccggccccg 1440
```

250/292

```

caggcgcccc cgcagccgca ggcggcgccc ccacagcagc cggcggcacc cccgcagcag 1500
ccacagggcg acacgctgac cagcgtgagc agcgagccgg gccg gtccca gcgaacgcac 1560
atcaagacgg agcagctgag cccagccac tacagcgagc agcagcagca ctgcgcccaa 1620
cagatcgccct acagcccctt caacctccca cactacagcc cctcctaccc gcccatcacc 1680
cgctcacagt acgactacac cgaccaccag aactccagct cctactacag ccacgcgcca 1740
ggccaggcca ccggcctct a ctccaccttc acctacatga accccgctca gcgccccatg 1800
tacaccccca tcgccgacac ctctggggtc ccttccatcc cgcagaccca cagccccag 1860
cactgggaac aaccgctcta cacacagctc actcgacctt gaggaggcct cccacgaagg 1920
gcgacgatgg ccgagatgat cctaaaaata accgaagaaa gagaggacca accagaat tc 1980
cctttggaca ttgtgtttt ttgtttttt tattttgtt tgttttttt tcttcttctt 2040
cttccttaaa gacatttaag ctaaaggcaa ctctgaccca aatttccaag acacaaacat 2100
gacctatcca agcgcatlac ccacttgtgg ccaatcagtg gccaggccaa ccttggctaa 2160
atggagcagc gaaatcaacg agaaactgga ct ttttaaac cctcttcaga gcaagcgtgg 2220
aggatgatgg agaatcgtgt gatcagtggt cttaaactct ctgcctgttt ggactttgta 2280
attatttttt tagcagtaat taaagaaaaa agtcctctgt gaggaaatatt ctctatttta 2340
aatattttta gtatgtactg tgtatgattc attaccattt tgaggggatt tatacatatt 2400
tttagataaa attaaatgct cttatttttc caacagctaa actactctta gttgaacagt 2460
gtgccctagc tttcttgca accagagtat tttgtacag atttgctttc tcttcaaaaa 2520
agaaaaaaa aatcctgttg tattaacatt taaaaacaga attgtgttat gtgatcagtt 2580
ttgggggtta actttgctta attcctcagg ctttgcgatt taagga ggag ctgccttaaa 2640
aaaaataaaa ggccttattt tgcaattatg ggagtaaaca atagtctaga gaagcatttg 2700
gtaagcttta tgatatatat attttttaaa gaagagaaaa acaccttgag ccttaaaacg 2760
gtgctgtcgg gaaacatttg cactctttta gtgcatttcc tctgccttt gcttgttcac 2820
tgacgtctta agaaagaggt aaaaaggcaag caaaggagat gaaatctgtt ctgggaatgt 2880
ttcagcagcc aataagtgcg cgagcacact gcccccggtt gcctgcctgg gccccatgtg 2940
gaaggcagat gcctgctcgc tctgtcacct gtgcctctca gaacaccagc agttaacctt 3000
caagacattc cacttgctaa aattatttat tttgtaagga gaggttttaa ttaaaacaaa 3060
aaaaattct ttttttttt tttttttcca attttacctt ctttaaaata ggttgttgga 3120
gctttcctca aagggtatgg tcatctgttg ttaaattatg ttcttaactg taaccagttt 3180
tttttttatt atctctttaa tcttttttat tattaaaagc aagtttcttt gtattctca 3240
ccctagattt gtataaatgc cttttgttcc atcc cttttt tctttgttgt ttttgttgaa 3300
aacaactgg aaactgttt cttttttgt ataatgaga gattgcaaat gtagtgtatc 3360
actgagtcac ttgcagtggt ttctgccaca gaccttggg ctgccttata ttgtgtgtgt 3420
gtgtgggtgt gtgtgtgttt tgacacaaaa acaatgcaag catgtgcoat ccatatttct 3480
ctacatcttc tcttgagtg agggaggcta cctggagggg atcagcccac tgacagacct 3540
taatcttaat tactgctgtg gctagagagt ttgaggattg ctttttaaaa aagacagcaa 3600
actttttttt ttattttaaa aaagatatat taacagtttt agaagtcagt agaataaaat 3660
cttaaaagcac tcataatatg gcacacctca atttctgtat aaaagcag at ctttttaaaa 3720
aagatacttc tgtaacttaa gaaacctggc atttaaatca tattttgtct ttaggtaaaa 3780
gctttgggtt gtgttcgtgt tttgtttgt tcaactgttt cctcccagc cccaaacctt 3840
ttgttctctc cgtgaaactt acctttccct ttttctttct cttttttttt ttgtatatta 3900
ttgtttacaa taaatataga ttgcattaaa aagaaa 3936

```

<210> 396

<211> 204

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(204)

<223> 3' terminal sequence. cadherin 15,
m-cadherin (myotubule) (CDH15) gene.

<400> 396

```

tttttttttt tttttttttt tttttttttt ttttttttca ttcagattta cccaggaggt 60
tgctgtcttt canacaaaga tgaggttcac tggaggagg caaagggtggg actaggagg 120

```

251/292

tgaccgcgcat gggccagatn ggagagaaac tcttcccacc ccggcagaag gggcctcttc 180
ctggccgccc catccanact cagg 204

<210> 397
<211> 458
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<220>
<221> misc_feature
<222> (1)..(458)
<223> 5' terminal sequence. cadhe rin 15,
m-cadherin (myotubule) (CDH15) gene.

<400> 397
caggacgcct acgacatcag ccagctgcgt caccgcagag cgctgagcct gcctctggga 60
ccgccgccac ttcgcagaga tgccccgcag ncagcctgca ccccagcca ccccgagtgc 120
tgcccaccag ccccttgagc atcgccgact tcatcaatga tggcttga g gctgcagata 180
gtgacccag tgtgcgcct tacgacacag ccctcatcta tgactacgag ggtgacggct 240
cggtgccggg gacntgagct ccctcctgtc cagccagggc gatgaggacc aggactacga 300
ctacctcaga gactgggggc ccgcttcgc ccggctggca gacatgtatg ggcacccgtg 360
cgggttngga gttacggggc cagatgg gac caccaggcca gggagggtct ttctctggg 420
gcactgctac ccagacacag aggcgggaca gcctgan 458

<210> 398
<211> 2833
<212> DNA/RNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<220>
<221> misc_feature
<222> (1)..(2833)
<223> cadherin 15, m-cadherin (myotubule) (CDH15)
gene.

<400> 398
acttgcgctg tcaactcagcc tggacgcgct tcttcgggtc gcgggtgcac tccggcccgg 60
ctcccgcctc ggccccgatg gacgcgcgct tctcctcgt cctcgggctg ttggcccaga 120
gcctctgcct gtctttgggg gtt cctggat ggaggaggcc caccacctg taccctggc 180
gccgggcgcc tgccctgagc cgcgtgcgga gggcctgggt catcccccg atcagcgtat 240
ccgagaacca caagcgtctc ccctaccccc tggttcagat caagtccggac aagcagcagc 300
tgggcagcgt catctacagc atccagggac ccggcgtgga tgaggagccc cggggcgtct 360
tctctatcga caagttcaca gggaagggtct tctcaatgc catgctggac cgcgagaaga 420
ctgatcgtct caggctaaga gcgtttgccc tggacctggg aggatccacc ctggaggacc 480
ccacggacct ggagattgta gttgtggatc agaatgacaa ccggccagcc ttccctgcag 540
aggcgttcac tggccgcgtg ctggagggtg cagtcaccag cac ctatgtg accagggcag 600
aggccacaga tgccgacgac ccgagacgg acaacgcagc gctgcgggtc tccatcctgc 660
agcagggcag ccccgagctc ttcagcatcg acgagctcac aggagagatc cgcacagtgc 720
aagtggggct ggaccgcgag gtggtcgcgg tgtacaatct gacctgcag gtggcggaca 780
tgtctggaga cggcctcaca g ccaactgcct cagccatcat cacccttgat gacatcaatg 840
acaatgcccc cgagttcacc agggatgagt tcttcatgga ggccatagag gccgtcagcg 900
gagtggatgt gggacgcctg gaagtggagg acagggacct gccaggctcc ccaaactggg 960
tggccagggt caccatcctg gaaggcgacc ccgatgggca gttcaccatc cgcacggacc 102 0

252/292

```

ccaagaccaa cgagggtgtt ctgtccattg tgaaggccct ggactatgag agctgtgaac 1080
actacgaact caaagtgtcg gtgcagaatg agggcccgct gcaggcggct gcccttaggg 1140
ctgagcgggg ccaggccaag gtccgcgtgc atgtgcagga caccaacgag ccccccgtgt 1200
tccaggagaa cccacttcgg accagcctag cagagggg gc acccccaggc actctgggtg 1260
ccaccttctc tgcccgggac cctgacacag agcagctgca gaggtcagc tactccaagg 1320
actacgacc ggaagactgg ctgcaagtgg acgcagccac tggccggatc cagaccagc 1380
acgtgctcag cccggcgctc ccttctctca agggcggtg gtacagagcc atcgtcctgg 1440
cccaggatga cgctcccag ccccgaccg ccacggcac cctgtccatc gagatcctgg 1500
aggtgaacga ccatgcacct gtgtggccc cgccgcggc gggcagcctg tgcagcgagc 1560
cacaccaagg cccaggcctc ctctggggc ccacggatga ggacctgcc cccacgggg 1620
cccccttcca cttccagctg agccccaggc tcccagagct cggccggaac t ggagcctca 1680
gccaggtaaa cgtgagccac gcgcgcctgc ggccgcgaca ccaggtcccc gaaggcctgc 1740
accgctcag cctgtctctc cgggactcgg ggcagccgcc ccagcagcgc gagcagcctc 1800
tgaacgtgac cgtgtgcgc tgcggcaagg acggcgctct cctgccggg gccgcagcgc 1860
tgctggcggg gggcacaggc ctacgc ctgg gcgcactggt catcgtgctg gccagcgccc 1920
tctctgtctg ggtgtgtgct ctgtctgtgg cactccgggc gcggttcttg aagcagtctc 1980
ggggcaagg gctgtgtcac ggccccagg acgaccttc agacaatgtc ctcaactacg 2040
atgagcaagg agcgggggag gaggaccagg acgcctacga catcagccag ctgcgtcacc 2100
cgacagcgt gagcctgcct ctgggaccgc cgccacttc cagagatgcc ccgcagggcc 2160
gctgtcacc ccagccacc cgagtgtct ccacagccc cctggacatc gccgacttca 2220
tcaatgatgg cttggaggct gcagatagt accccagtgt gcgccttac gacacagccc 2280
tcatctatga ctacgagggt gacggctcgg tggcggggac gctgagctcc atcctgtcca 2340
gccagggcca tgaggaccag gactacgact acctcagaga ctggggggccc cgcttcgccc 2400
gggtggcaga catgtatggg caccogtgcg ggttgagta cggggccaga tgggaccacc 2460
aggccaagga ggtctttct cctggggcac tgctaccag acacagaggc cggacagcct 2520
gacctgggg cgcaactgga catgccact cccggcctcg tggcagtgat ggcccctgca 2580
gaggcagcct gaggtcaccg ggcccgacc cctgggcct ggggcagcct ccttctgtga 2640
ggcgagggcc caagtctggg ggcagaacct gagtgtgat gggcgggcca ggaagaggcc 2700
ccttctgcc ggggtgggaa gattttctct ccateggcc catgcgggtc acc tccctag 2760
tccaccttt gcctctacc agtgaacct atctttgtat gaaagacagc aacctcctgg 2820
gtaaacttga atg 2833

```

<210> 399

<211> 646

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: primer

<220>

<221> misc_feature

<222> (1)..(646)

<223> 3' terminal sequence. b-cell cl1/lymphoma 2
(BCL2) gene.

<400> 399

```

tatctcacac tgtactttat ttttcttcac aatattaact agacagacaa ggaaagttta 60
atggcaatgt gactttttcc aacaacacaa acaaagtgcc attata gcta atggtggcca 120
actggagact tactttacct taacctatgta aagtatcctt accgtatttt ttatgtgtac 180
agtgttgtag aatatcagcc acctcttaaa agtatcaatc ttaaaaaagag ccatggaagg 240
taaaagtatg aaaaatttga taacaaaagc tttcaataca aaaacactta ttgtacactt 300
atttttattt aaaaacaaaa taac cccagt aactcaaaac aaaagcaaac cttggttgaa 360
aacttaagaa ggtataataa acaaaaccac caaaagaaag cttcccaaaa agaaatgcaa 420
tccactgtca ctcttgcaaa ttctaccttg gagggaaaaa cttaatgaaa tgagctatct 480
ggaggggcca cgagatttt ccaaaagggt taggtgcatg gatttactca gtatctacnt 540
acagtcttat ttattaatag ctacagnttc ctgattgagc gagcctttcc atctccacca 600
gtgtcccccac ttctgtgcnc acttgggntg cagacaccct gtgttg 646

```

253/292

<210> 400
<211> 465
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<220>
<221> misc_feature
<222> (1)..(465)
<223> 5' terminal sequence. b-cell cll/lymphoma 2
(BCL2) gene.

<400> 400
ggtattttaa caataaatgt gcagttttta ctaacaggat atttaatgac aaccttcttg 60
ttggtaggga catctgtttc taaatgttta ttatgtacaa tacagaaaaa aattttataa 1 20
aattaagcaa tgtgaaactg aattggagag tgataatata agtccttttag tcttaccag 180
tgaatcattc tgttccatgt ctttggacaa ccatgacctt ggacaatcat gaaatatgca 240
tctcactgga tgcaaagaaa atcagatgga gcatgaatgg tactgtaccg gttcatctgg 300
actgccccag aaaaataact tcaagcaaac atcctatcaa caacaagggt gttctgcata 360
ccaagctgag cacagaagat gggaacactg gtggaggatg gaaaggctcg ctcaatcaag 420
aaaattctga gactattaat aaataagact gtagtgtaga tactg 465

<210> 401
<211> 419
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<220>
<221> misc_feature
<222> (1)..(419)
<223> 3' terminal sequence. ests (EST W73386)
gene.

<400> 401
gaaggtcatt cttgcgatgg gtttattgca ggagatgatg gaccaaagg ctctgacaca 60
tgcacacgct cctgggacag cctgctgcn gtncgcttcc catga cccc agggccctct 120
atgcctccc cccaggcac cctgcccact tgccccact tcatgtacca ccaagccctt 180
tccttttctg ggcaccactc ctgagcagcg tgaccagcgg cctccaagt catgtggctc 240
agaacataaa agcatcttca acattcgtca ttgagccaaa cgaaacacag tgtttggctc 300
aagagccggc gacactngca tcc ctatcca cacgtggaac ctgcccttgg gcttngttga 360
ccggaggatn ggccgctctt ccttgtcatc cagcancgg agcatgtatg tgcccaga 419

<210> 402
<211> 568
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<220>
<221> misc_feature
<222> (1)..(568)
<223> 3' terminal sequence. granzyme a (granzyme

254/292

1, cytotoxic t-lymphocyte-associated serine
esterase 3) (GZMA) gene.

<400> 402

```
tcatgcaaat tgattttatt tgtgaaaaga ttaagaagcc acagtanatg aaaggaaacg 60
gttatttaaa ctgctccctt gatagt cata attatccagt tgagggtgtt ctttgagaga 120
agaatataga caccaggccc acgaggggtct ccgcatttat tttcaaggcc aaaggaagtg 180
acccttcgga aaacaccctc gcacaacaaa gggcttcag aatctccatt gcacgagtct 240
cttccacctc ggaggtcttc agcacaacc atattcattc caatcacagg gttaaaatta 300
tagtgatttc gatcattgca gacttttctg tctatgatgg gtgatattga cttgcaactca 360
gagtatcggg acccaagatg cactattggg gagtcctgcc ccaccctggc aacttggcac 420
atggttctctg gntttcacat caatccccct ttttagggag atgaaggata gtcacatatn 480
tggtnathtt ggctttttcc ggtcagctgt aaagttttaa ggtccc ctnc gcgtttggtg 540
gggcctagcc tgggagggga aanccttt 568
```

<210> 403

<211> 878

<212> DNA/RNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(878)

<223> granzyme a (granzyme 1, cytotoxic
t-lymphocyte-associated serine esterase 3) (GZMA)
gene.

<400> 403

```
cagattttca ggttgattga tgtgggacag cagccacaat gaggaactcc tatagatttc 60
tggcatcctc tctctcagtt gtcgtttctc tcttgctaatt tcttgaagat gtctgtgaaa 120
aaattattgg aggaaatgaa gtaactcctc attcaagacc ctacatggtc ctacttagtc 180
ttgacagaaa aaccatctgt gctggggctt tgattgcaaa agactgggtg ttgactgcag 240
ctcactgtaa cttgaacaaa aggtcccagg tcattcttgg ggctcactca ataaccaggg 300
aagagccaac aaaacagata atgcttggtta agaaagagtt tcc ctatcca tgctatgacc 360
cagccacacg cgaagggtgac cttaaaacttt tacagctgac ggaaaaagca aaaattaaca 420
aatatgtgac tatccttcat ctacctaaaa agggggatga tgtgaaacca ggaaccatgt 480
gccaagtgc aggggtggggg aggactcaca atagtgcac ttggtccgat actctgagag 540
aagtcaatat caccatcata gacagaaaag tctgcaatga tcgaaatcac tataatttta 600
acctgtgat tggaaatgaat atggtttgtg ctggaagcct ccgaggtgga agagactcgt 660
gcaatggaga ttctggaagc cctttgttgt gcgagggtgt tttccgaggg gtcacttcct 720
ttggccttga aaataaatgc ggagaccctc gtgggcctgg tgtctatatt cttctotcaa 780
agaaacacct caactggata attatgacta tcaaggagc agtttaaata accgtttcct 840
ttcatttact gtggcttctt aatcttttca caaataaa 878
```

<210> 404

<211> 191

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(191)

<223> 3' terminal sequence. v-fos fbj murine

255/292

osteosarcoma viral oncogene homolog (FOS) gene.

<400> 404
gcagtgcacg tgctcctacc cagctctgct tcacagcgcc cacctgtctc cgccctcgg 60
ccctcgccc ggctttgcta accgccacga t gatgttctc gggcttcaac gcagactacg 120
aggcgtcatc ctcccgtgc agcagcgct cccggccgg gataantctc ctttattaca 180
attaatcanc g 191

<210> 405
<211> 245
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<220>
<221> misc_feature
<222> (1)..(245)
<223> 5' terminal sequence. v-fos fbj murine
osteosarcoma viral oncogene homolog (FOS) gene.

<400> 405
ttttcaactt aaatgctttt attgacaatg ttttgaaca ataagcaaac aatgcttaaa 60
tttttcattc aaattcactt tccacatgtc aaaagacctc aaggtagaaa aaaataaaat 120
aaaaatataa atatctgaga atccatctta ataaataaat taaaaacaca ataaaacgtt 180
ttcatggaaa actgttaatg tcngaacat tcagaccacc tcnacaatgn gtgntcngtn 240
anatt 245

<210> 406
<211> 489
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<220>
<221> misc_feature
<222> (1)..(489)
<223> 3' terminal sequence. interleukin enhancer
binding factor 1 (ILF1) gene.

<400> 406
gcgncgcgct caccgaagg ngnangtaga cagcgggtca gaggccgcct agagccggag 60
gacaccccaa atacaaacat accacggaga gacctgggat ctgagtttca aaagggcctg 120
tgataaaaaga ctgaatcttt ttccaaatga agtagaaatg gttctgtcgt tttaaacata 180
cacaatactt aggagacttg tt ttactcag agtggaaaat ttgtccaggg acaaagtcaa 240
cacaagaaaa caaacaacaa aaaatagcca gaaagagaac agttaagtgc agctcgggta 300
gtcccggcag ttccttcccg gcactggctc gtcctgggt tctcaagggt ccatgcggcc 360
acagcgtcg tccacctgtc cagcgagcc acatgctgaa atgggaggtg ggataaaatt 420
catcaggcag ctgctgtaac acggaaatgt gcagatgcca gagtagcttc gtctgaactt 480
gaacaagac 489

<210> 407
<211> 247
<212> DNA
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(247)

<223> 5' terminal sequence. interleukin enhancer
binding factor 1 (ILF1) gene.

<400> 407

```
tgttttcagc ctatggaatg atttcctttt gtctgtcttg ttcaagttca gacgaagcta 60
ctctggcacc tgcacatttc cgtgttacag cagctgcctg atgaa ttta tccacctcca 120
tttcagcatg tggctgcgct ggacaggtgg acggacgctg tggccgcatg gaaccttgag 180
aaccacagga cgagccagtg ccgggaagga actgccggga ctaccganc tgcncttaac 240
tgttctc                                     247
```

<210> 408

<211> 3059

<212> DNA/RNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(3059)

<223> interleukin enhancer binding factor 1 (ILF1)
gene.

<400> 408

```
gccccccccc cagcctcct cccctcctcc cgcccgcgcg tgctcccgcc cctcgccgcc 60
gctcgctcgc tcgcccggcg gcctcgcctc ggccccctcc ctacagctccg gtgcgcggcg 120
gccgacgacc cgcggccttg gcctcggcgc gccaccggcg ccgcgcgga gcggcccggg 180
ggccctcacc caggcccatg gcggcgcgcg gccgcgctct cgggcccggc accacgcggg 240
cgcgggggcg gggcgcgcg ggcggggggc ggtcccgcgc gcgctgggc cgtggggcgc 300
ctggaggggc gcgagttcga gtatctgat aagaagcgt cggtgacct cggccgcaac 360
tcgtcgcagg gctcggtgga cgtgagcat gcccactcga gttcatctc ccggcgccac 420
ctcgagatct tcacgcccc gggcggcgcg gccatggcgg ggccgctccg gagctgcgc 480
ccgcgcagcc caggcccgac gccggcgggc acttctacct gcgctgcttg ggcaagaacg 540
gggtattcgt ggacggcgtg ttccagaggc gcggggcgcc gccgctgag ctgccgcgcg 600
tgtgcacatt cagggtcccg agcacaaca tcaagataac gttcactgcc ctgtccagcg 660
agaagagaga gaagcaggag gcgtctgagt ctccagtga a ggccgtacag ccacacatct 720
cgccctgac catcaacatt ccagacacca tggcccacct catcagccct ctgccctccc 780
ccacgggaac catcagcgt gcaaactcct gccctccag ccccgggga gcggggtctt 840
cagggtacaa ggtgggcca gtgatgccat ctgacctcaa tttaatggct gacaactcac 900
agcctgaaaa tgaaaag gaa gttcagggtg gagacagccc gaaggatgat tcaaagccgc 960
cttactccta cgcgcagctg atagttcagg cgattacgat ggctcccgc aaacagctca 1020
ccctgaacgg gatttatata cacatcacta aaaattatcc ctactacagg actgcggaca 1080
agggtggcca gaattcaatt cgccacaatc tctctctgaa tcgttatttc atcaaag tgc 1140
cgcttccca ggaagaacca ggcaaaggct cgttctggag gatagacca gcctctgaaa 1200
gcaaatatga agaagagct tttaggaac cagcgcttag gggcgcgccc tgccttagaa 1260
ccctctggg accgtctct tctaggagt cccagcctc tcccaatcac gcgggagtgc 1320
tgtctgctca ctctagtggc gccagaccc c tgagagcct gtcgagggaa ggttcgccgg 1380
ccccctgga gcctgagcct ggcgctgcac agcccaaact cgctgtcatc cagggaagccc 1440
ggtttgccc gagcgcccc gggtcacctc tgtccagtca gccagtctta atcaccgtcc 1500
agcggcagct accacaggcc atcaagcctg tcacctaac tgtggccacc ccagtgaaca 1560
cctgcacctc ccagccaccc gtcgtgcaga cggttcacgt cgtccaccag atcccagcgg 1620
tgtcggtcac cagtgtggcc ggactggccc cagcgaacac gtacactgtc tctggacaag 1680
```

257/292

```

ctgtggtcac cccggcagcc gtgctggccc ctctaaggc agaggcccag gagaatggag 1740
accacaggga agtcaaagt aaagtagagc ctattcccgc cattg gccac gccacgctcg 1800
gcactgccag ccggatcatt cagacggcac agaccacccc ggtccagacg gtgaccatag 1860
tacaacaggc acctctaggt caacaccagc taccaataaa aactgtaaca caaaacggca 1920
ctcacgtggc atcagtcccc actgcggtcc acggccaggt gaacaatgcc gcggcgagtc 1980
ctttgcacat gttggcaaca cagcatccg catcggcctc cctgcccaca aagcgccaca 2040
acggtgacca gccggagcag ccggagctga agcggatcaa gacagaagac ggcgagggca 2100
tcgtcattgc cctgagcgtg gacacgccac cggcagccgt aagggaagag ggtgtccaga 2160
actagcgacc gggagagctt ttctttaacg atatcaactc tgtgttgcca aaaggagac g 2220
cggcctcccc ccagcactcg ggggtgcagg gccctgtggt tggacttcac ctctcagcac 2280
tgaaaaccca aaaccagct ggccttaaca ctccctaaag acagaagtca cacttgaaca 2340
aaaccacac acaacaaaac ctgatttggg agacggtgtc tccactgagc acctgctggg 2400
ctgagcttct acctacgagt gaaactctgt cct cccgcga ggaccaggca tcgctgtgtg 2460
aggacggcac gccagcgcg tgctgtgagt gggctctcca agactaggcc tcaggacgcg 2520
gggggagcca tccccgcgc cctcacagga cccaccagga agcggagaca tgtggaatta 2580
gagtattttg aggtgtcctt tctttacaaa ataatggggt cttgggcatt tcacatcact 2640
ccattttctac tgagactttc agaatcacac aggccctttc cgtggatttc atttggggca 2700
aagaacaac atagttttgt ttttgttttc agcctatgga atgatttcct tttgtctgtc 2760
ttgttcaagt tcagacgaag ctactctggc atctgcacat ttccgtgtta cagcagctgc 2820
ctgatgaatt ttatccacct ccatttcagc atgtggctcg cgtggac agg tggacggacg 2880
ctgtggccgc atggaacctt gagaacccag ggacgagcca gtgccgggaa ggaactgccg 2940
ggactcaccg agctgcactt aactgttctc tttctggcta tttttgttg tttgtttctt 3000
tgtgttgact ttgtccctgg caaaattttc cactctgagt aaaacaagtc tcggaattc 3059

```

<210> 409
 <211> 201
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:primer

<220>
 <221> misc_feature
 <222> (1)..(201)
 <223> 3' terminal sequence. rho gdp dissociation
 inhibitor (gdi) alpha (ARHGDI) gene.

```

<400> 409
tttttttttt tccttcaggg gcatttattt cccggtcaga aaagaagcag ggacaggcgc 60
ctctgcctga gcctggcaga cacaacacga agaccgggga tggggcgggg gaggcacagg 120
agacggtctc cagcaatgtg tgcacttggt cccttggttg ttcttggttg ggtcagggaa 180
ggcctgccgn ggtggtggc a
201

```

<210> 410
 <211> 297
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:primer

<220>
 <221> misc_feature
 <222> (1)..(297)
 <223> 5' terminal sequence. rho gdp dissociation
 inhibitor (gdi) alpha (ARHGDI) gene.

<400> 410

258/292

ggcctctgct gccctttctg tgccccccag gttctatctc cccgtcacac ccgaggcctg 60
gcttcaggag ggagcggana gccattctcc agggcccggtg gttgcccctg gacgtgtgcg 120
tgtgtgctc cggggtggan ctggggtgtg ggatgcacgg cctcgtgggg gccggggcgt 180
cctccagccc cgtgtctccc tggccagccc cc ttgtcgtc gtcggtcccg tctaaccatg 240
atgccttaac atgtggagtg tacctgtggg gcctcactaa gcctctaant cactgtg 297

<210> 411

<211> 1819

<212> DNA/RNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(1819)

<223> rho gdp dissociation inhibitor (gdi) alpha
(ARHGDI A) gene.

<400> 411

cctgaaccgc gcggccgaac cctccgggtg cccgacccag gctaagcttg agcatggctg 60
agcaggagcc cacagccgag cagctggccc agattgcagc ggagaacgag gaggatgagc 120
actcgggtcaa ctacaagccc ccggcccaga agagcatcca ggagatccag gagctggaca 180
aggacgacga gagcctgcga aagtacaagg agggccctgct gggcccgctg gccgtttccg 240
cagaccccaa cgtccccaac gtctgtgtga ctggcctgac cctgggtgtc agtcgggccc 300
cgggccccct ggagctggac ctgacgggag acctggagag cttcaagaag cagtcgtttg 36 0
tgttgaagga ggggtgtggag taccggataa aaatctcttt cggggttaac cgagagatag 420
tgtccggcat gaagtacatc cagcatacgt acaggaaagg cgtcaagatt gacaagactg 480
actacatggt aggcagctat gggccccggg ccgaggagta cgagttcctg acccccgtgg 540
aggaggcacc caagggtatg ctggccccgg gcagctacag catcaagtcc cgcttcacag 600
acgacgacaa gaccgaccac ctgtcctggg agtggaaatc caccatcaag aaggactgga 660
aggactgagc ccagccagag gcgggcaggg cagagtgatg gacggaagac ggacaggcgg 720
atgtgtcccc cccagcccct cccctcccca taccaagggtg ctgagcaggc cctccgtgcc 780
cctccaccct ggtccgctc cctggcctgg ctcaaccgag tgctccgac cccctcctc 840
agccctccc caccacagc cccagcctcc tcggtctcct gtctcgttgc tgcctctgcc 900
tgtgtgtggt gggagagagg ccgacgccag gcctctgctg ccctttctgt gccccccagg 960
ttctatctcc ccgtcacacc cgaggcctgg cttcaggagg gagcggagca gccattctcc 1020
agggcccggtg gttgccctg gacgtgtgct tctgtctc cggggtggag ctggggtgtg 1080
ggatgcacgg cctcgtgggg gccgggcgt cctccagccc cgtgctccc tggccagccc 1140
ccttgtcgtc gtcggtcccg tctaaccatg atgccttaac atgtggagtg taccgtgggg 1200
cctcactagc ctctactccc tgtgtctgca tgagc atgtg gcctcccgt cccttccccg 1260
gtggcgaaac cagtaccoca gggacacgtg ggggtgtgct gtgtgtctcc ccagcccacc 1320
aatgcctggc cagcctgccc ccttccctgg acagggtgtg ggagatggct ccggcggtt 1380
ggggaagcg aaattgccaa cactcaagtc acctcagta catccaggag gctgggtatt 1440
gtcctgcctc tgccttttct gtctcagcgg cagtgccag agcccacacc cccccaagag 1500
ccctcgtggt acaggcctga cccacccac ctggggccag ccaggagccc cgcctggggc 1560
atcagtatgt attgcctccg tccgtgccgt ccctgggcca ctggctggcg cctcttcccc 1620
cagcctctca gtgccaccac ccccggcagc cttccctgac ccagccagg a caaacaaggg 1680
accaagtga cacattgctg agagccgtct cctataggct ccccgcccca tccccgtgt 1740
tggtgtgtg tctgccaggc tcaggcagag gcgcctgtcc ctgcttcttt tctgaccggg 1800
aaataaatgc ccctgaagg 1819

<210> 412

<211> 306

<212> DNA

<213> Artificial Sequence

<220>

259/292

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(306)

<223> 3' terminal sequence. complement component
4a (C4A) gene.

<400> 412

```
gctgccaaaa gcctttaata tgccctggtc ccaggctgt g ttcattgaaag cggacacagc 60
agtgtctcca gcttcatggg tcccagggtc aggttcctcc cagcggaggt gggagggcag 120
ccctcacacc tggcaccctt gactgcatac tcttgaggga agtcgttgag ctgggcacag 180
gttgcccgtt ggcgggttgcn tccggcacag gcgttcagag ggcattctct cgatccagct 240
attcgagtc agcaagta ct ngggggggnc cctcccaggg gcataantng gncntccag 300
anccat 306
```

<210> 413

<211> 5417

<212> DNA/RNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(5417)

<223> complement component 4a (C4A) gene.

<400> 413

```
agaaggtagc agacagacag acggatctaa cctctcttgg atcctccagc catgaggctg 60
ctctgggggc tgatctgggc atccagcttc ttcacctat ctctgcagaa gccaggttg 120
ctcttggtct ctcttctgtt ggttcattct ggg gtcccc tatcgggtgg ggtgcagctc 180
caggatgtgc cccgaggaca ggtagtgaag ggatcagtg tcttgagaaa cccattctgt 240
aataatgtcc cctgctcccc aaaggtggac ttcacctta gctcagaaag agacttcgca 300
ctcctcagtc tccaggtgcc cttgaaagat gcgaagagct gtggcctcca tcaactctc 360
agaggccctg aggtccagct ggtggcccat tcgccatggc taaaggactc tctgtccaga 420
acgacaaaca tccaggggat caacctgtc ttctctctc gccgggggca cctctttttg 480
cagacgggac agcccattta caacctggc cagcgggttc ggtaccgggt ctttgcctg 540
gatcagaaga tgcgccgag cactgcacac atcacagtca tgggtgagaa ctc tcacggc 600
ctccgcgtgc ggaagaagga ggtgtacatg cctctgtcca tcttcagga tgactttgtg 660
atcccagaca tctcagagcc agggacctg aagatctcag cccgattctc agatggcctg 720
gaatccaaca gcagcaccga gtttgaggtg aagaaatatg tcttcccaa ctttgagggtg 780
aagatcaccc ctggaaagcc ctacatcctg a cggtgccag gccatcttga tgaaatgcag 840
ttagacatcc aggccaggtc catctatggg aagccagtgc agggggtggc atatgtgcgc 900
tttgggctcc tagatgagga tggtaagaag actttctttc gggggctgga gactcagacc 960
aagctggtga atggacagag ccacatttcc ctctcaaagg cagagttcca ggacgcctg 1020
gagaagctga atatgggcat tactgacctc caggggctgc gcctctacgt tgctgcagcc 1080
atcattgagt ctccaggtgg ggagatggag gaggcagagc tcacatcctg gtattttgtg 1140
tcattccctt tctccttgga tcttagcaag accaagcgac accttggtgc tggggcccc 1200
ttctgctgc aggccttggg cctgtagatg tcaggctccc cagcttct gg cattcctgtc 1260
aaagtttctg ccacgggtgc ttctcctggg tctgttctg aagcccagga cattcagcaa 1320
aacacagagc ggagcggcca agtcagcatt ccaataatta tccctcagac catctcagag 1380
ctgcagctct cagtattctg aggtcccca catccagcga tagccaggct cactgtggca 1440
gccccacctt caggaggccc cg ggtttctg tctattgagc ggccggatc tcgacctcct 1500
cgtgttgagg acactctgaa cctgaacttg cgagccgtgg gcagtggggc caccttttct 1560
cattactact acatgatcct atcccagggt cagatcgtgt tcatgaatcg agagcccaa 1620
aggaccctga cctcgtgtct ggtgtttgtg gaccatcacc tggcaccctc cttctacttt 1 680
gtggccttct actaccatgg agaccacca gtggccaact cctgcgagt ggatgtccag 1740
gctggggcct gcgagggcaa gctggagctc agcgtggacg gtgccaagca gtaccggaac 1800
```

260/292

ggggagtccg tgaagctcca cttagaaacc gactccctag ccctggtggc gctgggagcc 1860
ttggacacag ctctgtatgc tgcaggcagc aagtcc caca agccctcaa catgggcaag 1920
gtctttgaag ctatgaacag ctatgacctc ggctgtggtc ctgggggtgg ggacagtgcc 1980
cttcaggtgt tocaggcagc gggcctggcc ttttctgatg gagaccagtg gaccttatcc 2040
agaaagagac taagctgtcc caaggagaag acaaccgga aaaagagaaa cgtgaacttc 2100
caaaaggcga ttaatgagaa attgggtcag tatgcttccc cgacagccaa gcgctgctgc 2160
caggatgggg tgacacgtct gccatgatg cgttctctcg agcagcgggc agcccgctg 2220
cagcagccgg actgccggga gcccttccgt tctgctgcc aatttgctga gagtctgcgc 2280
aagaagagca gggacaaggg ccaggcgggc ctccaacgag ccctggagat cctgcaggag 2340
gaggacctga ttgatgagga tgacattccc gtgcgcagct tcttcccaga gaactggctc 2400
tgagagtggt aaacagtgga ccgctttcaa atattgacac tgtggctccc cgactctctg 2460
accacgtggg agatccatgg cctgagcctg tccaaaacca aaggcctatg tgtggccacc 2520
ccagtccagc tccgggtgtt ccgc gagtcc cacctgcacc tccgcctgcc catgtctgtc 2580
cgccgctttg agcagctgga gctgcggcct gtctctata actacctgga taaaaacctg 2640
actgtgagcg tccacgtgtc ccagtggag ggcctgtgcc tggctggggg cggagggctg 2700
gccagcagg tgctggtgcc tgcgggctct gcccgccctg ttgccttctc tgtggtgccc 276 0
acggcagccg ccgctgtgtc tctgaagggt gtggctcgag ggtccttcca attccctgtg 2820
ggagatgcgg tgtccaaggt tctgcagatt gagaaggaa gggccatcca tagagaggag 2880
ctggtctatg aactcaaccc cttggaccac cgaggccgga ccttggaat acctggcaac 2940
tctgatccca atatgatccc tgatggggac tttaacag ct acgtcagggt tacagcctca 3000
gatccatttg acacttttag ccttgagggg gccttctcac caggaggcgt gccctccctc 3060
ttgagccttc ctcgaggctg tggggagcaa accatgatct acttggctcc gacactggct 3120
gcttcccgct acctggacaa gacagagcag tggagcacac tgcctcccga gaccaaggac 3180
cacgccgtgg atctgatcca gaaaggctac atgcggatcc agcagtttcg gaaggcggat 3240
ggttccctat cggtctgtgt gtcacgggac agcagcacct ggctcacagc ctttgtgttg 3300
aaggctcctg gtttgcccca ggagcaggta ggaggctcgc ctgaaaaact gcaggagaca 3360
tctaactggc ttctgtccca gcagcaggct gacggctcgt tccaggacct c tgtccagt 3420
ttagacagga gcatgcaggt gggtttggtg ggcaatgatg agactgtggc actcacagcc 3480
tttgtgacca tgccttcca tcatggctg gccgtcttcc aggatgaggg tgcagagcca 3540
ttgaagcaga gagtggaaag ctccatctca aaggcaaact catttttggg ggagaaagca 3600
agtgtgggc tctgggtgc ccacgc agct gccatcacgg cctatgccct gtcactgacc 3660
aaggcgccgt tggacctgct cgggtgttgcc cacaacaacc tcatggcaat ggccaggag 3720
actggagata acctgtactg gggctcagtc actggttctc agagcaatgc cgtgtcgccc 3780
acccggctc ctcgcaaccc atccgacccc atgccccagg cccagccct gtggattgaa 3840
accacagcct acgccctgct gcacctcctg cttcaatgag gcaaagcaga gatggcagac 3900
caggcttcgg cctggctcac ccgtcagggc agcttccaag ggggattccg cagtacccaa 3960
gacacggtga ttgccctgga tgccctgtct gcctactgga ttgcctccca caccactgag 4020
gagaggggtc tcaatgtgac tctcagctcc acaggccgga atgggttcaa gtcccacgcg 4080
ctgcagctga acaaccgcca gatcgcggc ctggaggagg agctgcagtt ttcttgggc 4140
agcaagatca atgtgaaggt gggaggaaac agcaaaggaa cctgaagggt ccttcgtacc 4200
tacaatgtcc tggagatgaa gaacacgacc tgccaggacc tacagataga agtgacgtc 4260
aaaggccacg tcga gtacac gatggaagca aacaggact atgagtacga tgagcttcca 4320
gccaaggatg acccagatgc ccctctgcag ccgctgacac ccctgcagct gtttgagggt 4380
cggaggaacc gccgcaggag ggaggcggc aagggtgtgg aggagcagga gtccagggtg 4440
cactacaccg tgtgcatctg gcggaacggc aagggtgggc tgtctggcat ggc catcgcg 4500
gacgtcacc tctgagtgg attccacgcc ctgctgtctg acctggagaa gctgacctcc 4560
ctctctgacc gttacgtgag tcaatttgag accgaggggc cccacgtcct gctgtatttt 4620
gactcggtcc ccacctccg ggagtgcgtg ggccttgagg ctgtgcagga agtgccggtg 4680
gggctggtgc agccggccag cgcaaccc tg tacgactact acaacccga gcgcagatgt 4740
tctgtgtttt acggggcacc aagtaagagc agactcttg ccacctgtg ttctgctgaa 4800
gtctgccagt gtgctgagg gaagtgcct cgcagcgtc gcgcccagg gcggggtctg 4860
caggacgagg atggctacag gatgaagtt gcctgtact accccgtgt ggagtacggc 4920
ttccaggtta aggttctccg agaagacagc agagctgct tccgctctt tgagaccaag 4980
atcacccaag tctgtcact caccaaggat gtcaaggccg ctgtaataca gatgcgcaac 5040
ttctgtgttc gagcctcct cgccttccg ttggaacctg ggaaagaata ttgtatcatg 5100
ggtctggtg gggccacctg tgacctcgag ggacacccc a gtacctgt ggactcgaat 5160
agctggatgc aggagatgcc ctctgaacgc ctgtgccgga gcacccgcca gcgggcagcc 5220
tgtgccagc tcaacgact cctccaggag tatggcactc aggggtgcca ggtgtgagg 5280
ctgccctccc acctccgct ggaggaacct gaacctggga accatgaagc tggagcact 5340
gctgtgtccg ctttca tgaa cacagcctgg gaccagggca tattaaaggc ttttggcagc 5400
aaagtgtcag tgttggc 5417

<210> 414
<211> 408
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<220>
<221> misc_feature
<222> (1)..(408)
<223> 3' terminal sequence. cd3g antigen, gamma
polypeptide (tit3 complex) (CD3G) gene.

<400> 414
ttacaatttt ccccaatagg tggcgcttct gaaacacagt attgttttt atttttat 60
tatttgagaa acccccaa atgtctctgat ggcctttctt ctccatttgt catctctggg 120
aaccttgagt ctagatttag ggctgaaagt ctctctgcta ggagctttcc aaaatgcatt 180
gctttgattc tgggaactga ataggaggag aacacctgga ctactctgag tctgagttc 240
aattctctct caactgggtt ccttgaaggt ggctgtactg gtcatcttct cgatccttga 300
ggggtctgta gagctgtgta ttgggcaac a gactctgctt gtctgnaagc tctcgactgg 360
gcgaactcca tctgtgccag caatgaagta gaccccaaag gcaaggac 408

<210> 415
<211> 457
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<220>
<221> misc_feature
<222> (1)..(457)
<223> 5' terminal sequence. cd3g antigen, gamma
polypeptide (tit3 complex) (CD3G) gene.

<400> 415
aaccacttgg ttaaggtgta tgactatcaa gaagatgggt cggctacttct gacttgtgat 60
gcagaagcca aaaaatcac atggttttaa gatgggaaga tgatcggtt ctaactgaa 120
gataaaaaaa aatggaatct gggaagtaat gccaaggacc ctgagggat gtatcagtgt 180
aaaggatcac agaacaagtc aaaaccactc caagtgtatt acagaatgtg tcaganctgc 240
attgaactaa atgcagccac catatctggc tttctctttg ctgaaatcgt cagcattttc 300
gtccttgcct ttgggggtcta cttcattgct ggacaggatg gag ttcgcca gtcgagagct 360
tcagacaagc agactctgtt gcccaatgac cagctctacc agccctcaa ggatccgagg 420
aagatgacca gtacagccac cttcaagggn aaccagt 457

<210> 416
<211> 822
<212> DNA/RNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<220>
<221> misc_feature

262/292

<222> (1)..(822)

<223> cd3g antigen, gamma polypeptide (tit3 complex) (CD3G) gene.

<400> 416

```
gggctgctcc acgcttttgc cggagacaga gactgacatg gaacagggga agggcctggc 60
tgtctcatc ctggctatca ttcttcttca ag gtactttg gccagtcaa tcaaaggaaa 120
ccacttggtt aaggtgtatg actatcaaga agatggttcg gtacttttga cttgtgatgc 180
agaagccaaa aatatcacat ggttttaaga tgggaagatg atcggcttcc taactgaaga 240
taaaaaaaaa tggaatctgg gaagtaatgc caaggaccct cgagggatgt atcagtgtaa 300
aggatcacag aacaagtcaa aaccactcca agtgtattac agaatgtgtc agaactgcat 360
tgaactaaat gcagccacca tatctggctt tctctttgct gaaatcgtca gcattttcgt 420
ccttgctggt ggggtctact tcattgctgg acaggatgga gttcgccagt cgagagcttc 480
agacaagcag actctgttgc ccaatgacca gctctaccag cccctcaagg at cgagaaga 540
tgaccagtac agccaccttc aaggaaacca gttgaggagg aattgaactc aggactcaga 600
gtagtccagg tgttctcctc ctattcagtt ccagaaatca aagcaatgca ttttggaag 660
ctcctagcag agagacttcc agccctaaat ctagactcaa ggttccaga gatgacaaat 720
ggagaagaaa ggccatcaga gcaatttgg gggtttctca aataaaataa aaataaaaac 780
aaatactgtg ttccagaagc gccacctatt ggggaaaatt gt 822
```

<210> 417

<211> 439

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(439)

<223> 3' terminal sequence. v-rel avian
reticuloendotheliosis viral oncogene homolog b
(nuclear factor of kappa light polypeptide gene
enhancer in b-cells 3) (RELB) gene.

<400> 417

```
acatctttat tgggaagact ctgaacaacc aacctacccc c caccttcaa gtctggggaa 60
ggnagggcag gantctgccc cctcctccca tatgtacaat cttttccgaa toctactgga 120
gaaggtgccc ccacatgtgg aacagaggca gctgtaacaa gctagtgcac gggagccatg 180
tcccttttcc tctccggact cagtttcctc atctgtaaaa tgggctcaag gggaaacccg 240
tgcaacgagg cttctcgcca aggctganta tgtccacttc agaagcatga ggaagggcca 300
aggggatggg ggtgctagac atcctggggt gggattgcac ggctcctcca cctccctccc 360
caccagtgcc cctcctctg gcacgcggg gctacgtggc ttcaggcccg gggataggag 420
gccgccccca aaggccgct 43 9
```

<210> 418

<211> 234

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(234)

<223> 5' terminal sequence. v-rel avian
reticuloendotheliosis viral oncogene homolog b

263/292

(nuclear factor of kappa light polypeptide gene
enhancer in b-cells 3) (RELB) gene.

<400> 418
acgggggatg cccaacgtcc ttggggagct gaacagtctg gacccccatg gcacgagag 60
caaacggcgg aagaaaaagc cggccatcct ggaccacttc ctgcccacc acggctcagg 120
cccgttcctc ccgccgtcag cctgctgcc agacctgac ttcttctctg ggcaccgtgt 180
tcctgccccg gcngggaggc cctggggggc ctgnacctcc tgggacgatg gggt 234

<210> 419
<211> 2314
<212> DNA/RNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<220>
<221> misc_feature
<222> (1)..(2314)
<223> v-rel avian reticuloendotheliosis viral
oncogene homolog b (nuclear factor of kappa light
polypeptide gene enhancer in b-cells 3) (RELB)
gene.

<400> 419
ggaattcccc ccgggccccg ccccgcccc cgcagc ccgg ggccgcccgc gtcctgcccc 60
gcctgcccgc cagcccttgc gccgctcgtc cgaccgcgga tcgtccacca gaccgtgcct 120
cccggcccgc cgggccccgc gtgcatgctt cggctctggc cagcctcttg gccgtccgtc 180
cccactggcc gggccatgcc gagtcgccc gtccgagac ccgggctgc gccggagctg 240
ggggccttag ggtcc ccga cctctcctca ctctcgctcg ccgtttccag gacacagat 300
gaattggaga tcatcgacga gtacatcaag gagaacggct tcggcctgga cgggggacag 360
ccgggccccg gcgaggggct gccacgcctg gtgtctgcg gggctgcgtc cctgagcacg 420
gtcaccttg gccctgtggc gccccagcc acgcccgcg cttggggctg cccctg ggc 480
cgactagtgt cccagcgcc gggccgggg ccgcagccgc acctggtcat caggagcag 540
cccaagcagc gcggcatgcc gttccgctac gactgagagg gccgtcggc cggcagcatc 600
cttggggaga gcagaccga ggccagcaag acgtgcccg ccatcgagct ccgggattgt 660
ggagggctgc gggaggtgga ggtgactgcc tgcct ggtgt ggaaggactg gcctcaccga 720
gtccaccccc acagcctcgt ggggaaagac tgcaccgacg gcactctcag ggtgcggctc 780
cggcctcacg tcagccccg gcacagtgtt aacaacctgg gcattccagt tgtgaggaag 840
aaggagattg aggtgccat tgagcggaag attcaactgg gcattgacc ctacaacgct 900
gggtccctga aga accatca ggaagtagac atgaatgtgg tgaggatctg cttccaggcc 960
tcatatcggg accagcagg acagatgcg cggtggatc ctgtgcttcc cgagcccgtc 1020
tatgacaaga aatccacaaa cacatcagag ctgcccgttt gccgaattaa caaggaaagc 1080
gggcccgtgc ccggtggcga ggagctctac ttgctctgcg acaagggtgca gaa agaggac 1140
atatcagtgg tgttcagcag ggctcctgg gaaggtcggg ctgacttctc ccaggccgac 1200
gtgcaccgcc agattgccat tgtgttcaag acgcccgcct acgaggacct ggagattgtc 1260
gagcccgtga cagtcacagt cttcctgcag cggtcaccg atgggggtctg cagcgagcca 1320
ttgcctttca cgtacctgcc tcgcgacc at gacagctacg gcgtggacaa gaaggcgaaa 1380
cgggggatgc ccgacgtcct tggggagctg aacagctctg acccccatgg catcgagagc 1440
aaacggcggg aaaaaagcc ggccatcctg gaccacttcc tgcccaccca cggctcaggc 1500
ccgttcctcc ccgctcagc cctgctgcca gacctgact tcttctcttg caccgtgtcc 1560
ctgcccggcc tggagcccc tggcgggctt gacctcctgg acgatggctt tgcctacgac 1620
cctacggccc ccacactctt caccatgctg gacctgctgc ccccggcacc gccacacgct 1680
agcgtgttg tgtgcagcgg aggtgccggg gccgtggtt gggagacccc cggccctgaa 1740
ccactgacac tggactcgta ccaggccccg ggccccggg a tggaggcac cggcagcctt 1800
gtgggcagca acatgttccc caatcattac cgcgaggcgg cctttggggg cggcctccta 1860
tccccggggc ctgaagccac gtagccccgc gatgccagag gaggggcact ggggggggag 1920
ggaggtggag gagccgtgca atcccaacca ggatgtctag cacccccac ccttggccc 1980
ttcctcatgc ttctga agtg gacatattca gccttggcga gaagctccgt tgcacgggtt 2040

264/292

tccccttgag ccatttttac agatgaggaa actgagtccg gagaggaaaa gggacatggc 2100
tcccggtgcac tagcttggtta cagctgcctc tgcctccaca tgtgggggca ccttctccag 2160
taggattcgg aaaagattgt acatatggga ggagggggca gattcctggc cctcc ctccc 2220
cagacttgac ttgaagggtg ggggtagggt ggttggtcag agtcttccca ataaagatga 2280
gtttttgagc ctcaaaaaaa aaaaaaggaa ttcc 2314

<210> 420

<211> 214

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(214)

<223> 3' terminal sequence. estrogen receptor 1
(ESR1) gene.

<400> 420

tttagttgta attctttatt tgaacatcaa ataggttgag aaaattgttt acaggtgctc 60
gagcatcccg ctggattctt ttcaaagtg caaaagaggt ttacaagtgt gtttcattaa 120
acaaagcaaa gctgcgacaa aaccgagtca catcagtaat agtatgcatc ggcaaaaggg 180
catattaatc catcaaacac aatttgcat ttga 214

<210> 421

<211> 520

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(520)

<223> 5' terminal sequence. estrogen receptor 1
(ESR1) gene.

<400> 421

tgaaaactta ctctcaactg gagcaaatga actttggtcc caaatatcca tcttttcagt 60
agcgtaatt atgctctgtt tccaactgca ttctcttcc aattgaa tta aagtgtggcc 120
tcgtttttag tcatttaaaa ttgttttcta agtaattgct gcctctatta tggcacttca 180
attttgcact gtcttttgag attcaagaaa aatttctatt ctttttttg catccaattg 240
tgctgaact tttaaaatat gtaaagtctg ccatgttcca aaccatcgt cagtgtgtgt 300
gtttagagct gtcaccctag aaaca acata ttgtcccatg agcaggtgcc tgagacacag 360
accctttgc attcacagag aggtcattgg ttatagagac ttgaattaat aagtacatt 420
atgccagttt ctgttctctc acaggtgata aacaatgctt tttgtgact acatactctt 480
cagtgtagag ctcttgtttt atgggaaaag gctcaaatgc 520

<210> 422

<211> 6450

<212> DNA/RNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>
<221> misc_feature
<222> (1)..(6450)
<223> estrogen receptor 1 (ESR1) gene.

<400> 422
gagttgtgcc tggagtgatg ttttaagccaa tgtcagggca ag gcaacagt cctggccgt 60
cctccagcac ctttgaatg catatgagct cgggagacca gtacttaaag ttggaggccc 120
gggagcccag gagctggcgg agggcggttc tcttgggagc tgcacttgct ccgtcgggtc 180
gccggcttca ccggaccgca ggctcccggg gcagggccgg ggccagagct cgcgtgtcgg 240
cgggacatgc gctgcgtcgc c tctaacctc gggctgtgct ctttttccag gtggcccgcc 300
ggtttctgag cttctgccc tgcggggaca cggctctgcac cctgcccgg gccacggacc 360
atgacctga cctccacac caagcatct gggatggccc tactgcatca gatccaaggg 420
aacgagctgg agcccctgaa ccgtccgcag ctcaagatcc ccctggagcg gccctgggc 480
gaggtgtacc tggacagcag caagcccgcc gtgtacaact accccgaggg cgcgcctac 540
gagttcaacg ccgcggccgc cgccaacgcg caggtctacg gtcagaccgg cctcccctac 600
ggccccgggt ctgaggtgc ggcttcggc tccaacggcc tggggggttt cccccactc 660
aacagcgtgt ctccgagccc gctgatgcta ctgcaccgc c gccgcagct gtcgccttc 720
ctgcagccc ccggccagc ggtgcctac tacttgaga acgagcccag cggtacacg 780
gtgcgcgagg ccggcccgcc ggcattctac aggccaaatt cagataatcg acgccagggt 840
ggcagagaaa gattggccag taccaatgac aagggaagta tggctatgga atctgccaa 900
gagactcgct actgtgcagt gtgcaatgac tatgcttcag gctaccatta tggagtctgg 960
tctgtgagg gctgcaaggc cttcttcaag agaagtattc aaggacataa cgactatatg 1020
tgtccagcca ccaaccagt caccattgat aaaaacagga ggaagagctg ccaggcctgc 1080
cggctccgca aatgctacga agtgggaatg atgaaagggt ggatacgaag agaccgaaga 1140
ggaggggagaa tgttgaacaa caagcgccag agagatgatg gggagggcag ggggtgaagt 1200
gggtctgctg gagacatgag agctgccaac ctttgccaa gcccgctcat gatcaaacgc 1260
tctaagaaga acagcctggc cttgtccctg acggccgacc agatggtcag tgccttgtt 1320
gatgctgagc cccccatact ctattccgag tatg atccta ccagaccctt cagtgaagct 1380
tcgatgatgg gcttactgac caacctggca gacagggagc tggttcacat gatcaactgg 1440
gcgaagaggg tgccaggcct tgtggatttg acctccatg atcagggtcca ccttctagaa 1500
tgtgcctggc tagagatcct ctgtctcttg gacaggaacc agggaaaatg tgtagagggc 1620
aagctactgt ttgtccttaa gctgctggct acatcatctc ggttccgcat gatgaatctg 1680
atgggtggaga tcttcgacat gctgctggct attattttgc ttaattctgg agtgtacaca 1740
cagggagagg agtttgtgtg cctcaaatct attattttgc ttaattctgg agtgtacaca 1740
ttctgttcca gcacctgaa gtctctggaa gagaaggacc atatccac cg agtcctggac 1800
aagatcacag acactttgat ccacctgatg gccaggcag gcctgaccct gcagcagcag 1860
caccagcggc tggcccagct cctcctcatc ctctcccaca tcaggcacat gagtaacaaa 1920
ggcatggagc atctgtacag catgaagtgc aagaacgtgg tgcccctcta tgacctgctg 1980
ctggagatgc tggacgccc cc gctacat cgcgccacta gccgtggagg ggcacccgtg 2040
gaggagacgg accaaagcca cttggccact gcgggctcta cttcatcgca ttccttgcaa 2100
aagtattaca tcacggggga ggcagagggt ttccctgcca cagtctgaga gctccctggc 2160
tcccacacgg ttcagataat ccctgctgca ttttaccctc atcatgcacc actttagcca 2 220
aattctgtct cctgcataca ctccggcatg catccaacac caatggcttt ctatgatgag 2280
ggccattcat ttgcttgctc agttcttagt ggcacatctt ctgtcttctg ttgggaacag 2340
ccaaagggat tccaaggcta aatctttgta acagctctct tcccccttg ctatgttact 2400
aagcgtgagg attcccgtag ctcttcacag ctgaac tcag tctatgggtt ggggctcaga 2460
taactctgtg catttaagct acttgtagag acccaggcct ggagagtaga cattttgct 2520
ctgataagca ctttttaaag ggccttaaga ataagccaca gcaaagaatt taaagtggct 2580
cctttaattg gtgacttgga gaaagctagg tcaagggttt attatagcac cctcttgat 2640
tcctatggca atgcatcctt ttatgaaagt ggtacacctt aaagctttta tatgactgta 2700
gcagagtatc tgggtattgt caattcactt cccctatag gaatacaagg ggccacacag 2760
ggaaggcaga tcccctagtt ggccaagact tttttaact tgatacactg cagattcaga 2820
gtgtcctgaa gctctgcctc tggctttccg gtcattgggtt ccagttaatt catgcctccc 2880
atggacctat ggagagcaac aagttgatct tagttaagtc tccctatatg agggataagt 2940
tctgtatttt tgtttttatt tttgtgttac aaaagaaagc cctccctccc tgaacttgca 3000
gtaaggtcag cttcaggacc tgttccagtg ggcactgtac ttggatcttc ccggcgtgtg 3060
tgtgccttac acaggggtga actg ttcact gtgggtgatgc atgatgaggg taaatggtag 3120
ttgaaaggag caggggccct ggtgttgcat ttagccctgg ggcattggagc tgaacagtac 3180
ttgtgcagga ttgttgtggc tactagagaa caagaggga agtagggcag aaactggata 3240

266/292

```

cagttctgag cacagccaga cttgctcagg tggccctgca caggctgcag ctacctagga 330 0
acattccttg cagacccgcg attgcctttg ggggtgccct gggatccctg gggtagtcca 3360
gctcttattc atttccagc gtggccctgg ttggaagaag cagctgtcaa gttgtagaca 3420
gctgtgttcc tacaattggc ccagcaccct ggggcacggg agaaggggtg ggaccgttg 3480
tgtcactact caggctgact ggggcctggg cagattac gt atgcccttgg tggtttagag 3540
ataatccaaa atcaggggtt ggtttgggga agaaaatcct ccccttcct ccccgcccc 3600
gttccctacc gcctccactc ctgccagctc atttcttca atttctttg acctataggc 3660
taaaaaagaa aggtcattc cagccacagg gcagccttcc ctgggccttt gcttctctag 3720
cacaattatg ggttacttcc tttttcttaa caaaaaagaa tgtttgattt cctctgggtg 3780
acctatttgt ctgtaattga aacctattg agagggtgat tctgtgttag ccaatgacct 3840
aggtagctgc tcgggcttct cttgggtatgt cttgtttgga aaagtggatt tcattcattt 3900
ctgattgtcc agttaagtga tcaccaaagg actgagaatc tgggagggca a aaaaaaaaa 3960
aaaaagtttt tatgtgcact taaatttggg gacaatttta tgtatctgtg ttaaggatat 4020
gcttaagaac ataattcttt tgttgcgtgt tgtttaagaa gcaccttagt ttgtttaaga 4080
agcaccttat atagtataat atatatTTTT ttgaaattac attgcttgtt tatcagacaa 4140
ttgaatgtag taattctgtt ctggat ttaa tttgactggg ttaacatgca aaaaccaagg 4200
aaaaatattt agtttttttt tttttttttg tatacttttc aagctacctt gtcattgtata 4260
cagtcattta tgcctaaagc ctggtgatta ttcattttaa tgaagatcac atttcataatc 4320
aacttttgta tccacagtga acaaaatagc actaatccag atgcctattg ttggatattg 4380
aatgacagac aatcttctatg agcaaagatt atgcctgaaa aggaaaatta ttcaggggcag 4440
ctaattttgc ttttaccaaa atatcagtag taatattttt ggacagtagc taatgggtca 4500
gtgggttctt tttaatgttt atacttagat tttcttttaa aaaaattaaa ataaaacaaa 4560
aaaaatttct aggactagac gatgtaatac cagctaaagc caaacaatta tacagtggaa 4620
ggttttacat tattcatcca atgtgtttct attcatgtta agatactact acatttgaag 4680
tgggcagaga acatcagatg attgaaatgt tcggccaggg gtctccagca actttggaaa 4740
tctctttgta tttttacttg aagtgccact aatggacagc agatattttc tggctgatgt 4800
tggtattggg tgta ggaaca tgatttaaaa aaaaaactct tgctctgct tccccact 4860
ctgaggcaag ttaaaatgta aaagatgtga tttatctggg gggctcaggt atgggtgggga 4920
agtggattca ggaatctggg gaatggcaaa tatattaaga agagtattga aagtatttgg 4980
aggaaaatgg ttaattctgg gtgtgcacca aggttcagta gagtccactt ctg ccctgga 5040
gaccacaaat caactagctc catttacagc catttctaaa atggcagctt cagttctaga 5100
gaagaaagaa caacatcagc agtaaagtcc atggaatagc tagtggctctg tgtttctttt 5160
cgccattgcc tagcttgccg taatgattct ataatgccat catgcagcaa ttatgagagg 5220
ctaggctatc caaagagaag acctatc aa tgtaggttgc aaaatctaac ccctaaggaa 5280
gtgcagcttt tgatttgatt tccctagtaa ccttgcagat atgtttaacc aagccatagc 5340
ccatgccttt tgagggtctga acaataaagg gacttactga taatttactt ttgatcacat 5400
taagggtgtc tcaccttgaa atcttataca ctgaaatggc cattgattta ggccactggc 5460
ttagagtact cttccccctg catgacactg attacaaata ctttctatt catactttcc 5520
aatttagaga tggactgtgg gtactgggag gtactactaa caccatagta atgtctaata 5580
ttcacaggca gatctgcttg gggaagctag ttatgtgaaa ggcaaataaa gtcatacagt 5640
agctcaaaag gcaaccataa ttctcttttg tgcaagtctt g ggagcgtga tctagattac 5700
actgcacat tcccaagtta atccccgaa aacttactct caactggagc aaatgaactt 5760
tggtcccaa tatccatctt ttcagtagcg ttaattatgc tctgtttcca actgcatttc 5820
ctttccaatt gaattaaagt gtggcctcgt ttttagtcat ttaaaattgt tttctaagta 5880
attgctgctt ctatta tggc acttcaattt tgcactgtct tttgagattc aagaaaaatt 5940
tctattcatt tttttgcat caattgtgcc tgaactttta aaatatgtaa atgctgccat 6000
gttccaaacc catcgctcagt gtgtgtgttt agagctgtgc accctagaaa caacatactt 6060
gtcccatgag cagggtgcctg agacacagac ccctttgcat tcacagagag gtcatt tgggt 6120
atagagactt gaattaataa gtgacattat gccagtttct gttctctcac aggtgataaa 6180
caatgccttt tgtgcactac atactcttca gtgtagagct cttgttttat gggaaaaggc 6240
tcaaatgcca aattgtgttt gatggattaa tatgcccttt tgccgatgca tactattact 6300
gatgtgactc ggttttgtcg cagctttgct ttgtttaatg aaacacactt gtaaacctct 6360
tttgactttt gaaaaagaat ccagcgggat gctcgagcac ctgtaacaa ttttctcaac 6420
ctatttgatg ttcaataaaa gaattaaact 6450

```

<210> 423

<211> 580

<212> DNA

<213> Artificial Sequence

267/292

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(580)

<223> 3' terminal sequence. pre -b-cell leukemia
transcription factor 1 (PBX1) gene.

<400> 423

```
ttaaacgtac aaacactttt attattttct ttgtaatttt tttcctcttt aaattcctct 60
aattgttgaa aatatccttc agtgatatgc gagagggcgg gcacccggga gtctaggaca 120
gaggcacagg ggcaggggaag atgacgaaaa ccaggctgac agctggaggc agggaagggg 180
ggcttctacc cagaaaaaaaa aggggagaga gtataaagaa gtgtccagat tggctgaaat 240
agcatcccaa agaagagaag agaaggagac tcttattgtg tttgc tgatt gcttcgacct 300
ccagtctgac cgcttcaggn ttgggagaga aaccctccct tcctgcccct gcccactg 360
ggcgacaggg tcagccggga tgcgattgct gggagatcag ttggaggat cagagtgaac 420
actgccaggg ccttctgtag gggagggtcac tgatgaaggg gtagtagcat cctgcccaacc 480
tccattagca ctgatgccct gcg gactgta catctgactg gctgcgagtc catcactgta 540
tcctcctgtc tggctgataa catggcgaag ggtatccacc 580
```

<210> 424

<211> 503

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(503)

<223> 5' terminal sequence. pre -b-cell leukemia
transcription factor 1 (PBX1) gene.

<400> 424

```
gccaaagagg agttagccaa gaagtgtggc accacagtct cccaggtatc acaactgggt 60
tggaataaag cgaatccggt acaagaagaa cataggtaaa tttcaagagg aagccaatat 120
ttatgctgcc aaaacagctg tctgtgctac caatgtgtca gccatggaa gccaagctaa 180
ctcgccctca actcccaact cggctggtgg atacccttcg ccatgttatc agccagacag 240
gaggatacag tgatggactc gcagccagtc agatgtacag tccgcaggca tcagtgttaa 300
tggagggttg caggatgcta ctacccttc atcagtgacc tcccctacag aaggccctgg 360
cagtgttcac tctgatacct ccaactgata tcccagcaat cgcattccgg ctgacctgt 420
gcccagttg ggcaggggca ggaggaggg tttctctccc aacgtgaag cggtcagact 480
ggagggtcaaa cgattaggca aac 503
```

<210> 425

<211> 1819

<212> DNA/RNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(1819)

<223> pre-b-cell leukemia transcription factor 1
(PBX1) gene.

268/292

<400> 425

```

cttccctgtt taccctgaaa aggatttgaa g acaagcttg aaggataaaa agccttggtg 60
cttcccagga gccgagccga ggagcagaag aggaagagcc gggggctgcc gtagcctttg 120
gagatggacg agcagcccag gctgatgcat tcccatgctg gggctgggat ggccggacac 180
ccggcctgt cccagcactt gcaggatggg gccggaggga ccgaggggga gggcgggagg 240
aagcaggaca ttggagacat tttacagcaa attatgacca tcacagacca gagtttggat 300
gagcgcgagg ccagaaaaca tgctttaaac tgccacagaa tgaagcctgc cttgtttaat 360
gtgttgtgtg aaatcaaaga aaaaacagtt ttgagtatcc gaggagccca ggaggaggaa 420
cccacagacc cccagctgat gcggctggac aacatgctgt tagcggaagg cg tggcgggg 480
cctgagaagg gcggagggtc ggcggcagcg gcggcagcgg cggcggcttc tggaggggca 540
ggttcagaca actcagtgga gcattcagat tacagagcca aactctcaca gatcagacaa 600
atctaccata cggagctgga gaaatacagag caggcctgca acgagttcac caccacgtg 660
atgaatctcc tgcgagagca aagccggacc aggccatct ccccaaagga gattgagcgg 720
atggtcagca tcatccaccg caagttcagc tccatccaga tgcagctcaa gcagagcacg 780
tgcgaggcgg tgatgatcct gcgttccga tttctggatg cgcgcgga gagacggaat 840
ttcaacaagc aagcgacaga aatcctgaat gaatatttct attcccatct cagcaaccct 900
taccacagtg aggaagccaa agaggagtta gccagaagt gtggcatcac agtctcccag 960
gtatcaaact ggtttgaaa taagcgaatc cgttacaaga agaacatagg taaatttcaa 1020
gaggaagcca atatttatgc tgccaaaaca cgtgtcactg ctaccaatgt gtcagcccat 1080
ggaagccaag ctaactcgcc ctcaactccc aactcggctg gttcttcca g tctttttaac 1140
atgtcaaact ctggagattt gttcatgagc gtgcagtcac tcaatgggga ttcttaccaa 1200
ggggcccagg ttggagccaa cgtgcaatca cagggtggata cccttcgcca tggtatcagc 1260
cagacaggag gatacagtga tggactcgca gccagtcaga tgtacagtc gcagggcatc 1320
agtgtaatg gaggttggca gga tgctact accccttcat cagtgaacct ccctacagaa 1380
ggccctggca gtgttctact tgatacctcc aactgatctc ccagcaatcg catcccggct 1440
gaccctctgc cccagttggg gcaggggcag gagggagggt ttctctcca agctgaagcg 1500
gtcagactgg aggtcgaagc aatcagcaaa cacaataaga gtctccttct cttctcttct 15 60
ttgggatgct atttcagcca atctggacac ttctttatac tctcttccct ttttttctg 1620
ggtagaagcc acccttccct gcctccagct gtcagcctgg ttttcgtcat cttccctgcc 1680
cctgtgcctc tgccttagac ttcccggggg ccccgccctc tctcatatca ctgaaggata 1740
ttttcaacaa ttagaggaat ttaaagagga aaaaaat tac aaagaaaata ataaaagtgt 1800
ttgtacgttt tcaaaaaaa 1819

```

<210> 426

<211> 506

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(506)

<223> 3' terminal sequence. gli-kruppel family

member gli3 (greig cephalopolysyndactyly syndrome)
(GLI3) gene.

<400> 426

```

taaaaagagg gtggtttgag tgtaacaata ctgattcaaa actgaaatgg aagacagttt 60
ctccctagaa tactttaggg tttttcagag tccttttcca taaa aggaat ataattgaaa 120
cacatctcag ttaggtgaga tgagattgct aaaatacata cagaactaaa aaaacagcca 180
aaacaaaagc agtttaactc cttcaactcc taatgatttc cgttggttgc agtctttttt 240
tcctaaagcc tattgcataa ctgcaaggga attgctttct tccgctaggg aggtcagcaa 300
agaactcatg tccccgatag cc atgttggt ggtgctcatg gacagcgctg ggaatgggag 360
ggacgcccga gggctgggta aagccggaag aacctatgga aaaggtctca atgatacttg 420
ggctcagggc cccgacatca ggctcgagtg gtcccatct ctatgattgc atcgaagtca 480
atctggtacc ctccaggcc aggtcg 506

```

<210> 427
<211> 239
<212> DNA
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(239)

<223> 5' terminal sequence. gli-kruppel family
member gli3 (greig cephalopolysyndactyly syndr ome)
(GLI3) gene.

<400> 427

ggcagaagga tcacttgagg ccaggcattc aagaccagcc tatgcaagat aatgagacct 60
tgtctctatt taaaaaaciaa aaagcctggt gtggtggtgc atgcctgtag tctcagcctc 120
ctgagtagct gggactataa gcacgcacca ctatgtctgg ctaatttttg tatttttagt 180
agagacaggg ttccaccacg ttgcccaggg cagtcttgaa ctctgacct caagtgatc 239

<210> 428

<211> 5054

<212> DNA/RNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(5054)

<223> gli-kruppel family member gl i3 (greig
cephalopolysyndactyly syndrome) (GLI3) gene.

<400> 428

cgatactacg tgggcatttt tggtcgaaga gagctgaagt aatgagaaga catcatggag 60
gcccagtcac acagctccac gaccactgaa aagaaaaaag ttgagaattc catagtgaag 120
tgctccactc gaacagatgt gagcgagaaa gccgttgccct ccagcaccac ttctaattgag 180
gatgaaagtc ctggacagac ttatcacaga gagagaagaa acgcaatcac tatgcagcca 240
cagaatgtcc aggggctcag caaagtcagt gaggaacctt caacatcgag tgacgagagg 300
gcctcattga tcaagaaaga gatccatggg tccctgccac acgtggcgga gccctctgtg 360
ccgtaccgcg ggacgggtg tt tgccatggac cccaggaatg gttacatgga gcccactac 420
caccctcctc atcttttccc tgccttccat cctcctgtac caattgatgc cagacatcat 480
gagggccggt accattacga tccatctccg attcctc

cat tgcatatgac ttccgcctta 540

tctagtagcc ctacgtatcc ggacctgcc ttcattagga tctccccaca ccggaacc cc 600
gctgctgctt ccaggtctcc cttcagccct ccacatccct acattaatcc ctacatggac 660
tatatccgct ccttgccacag cagcccatcg ctctccatga tctcagcaac ccgtgggctg 720
agccctacag atgcgcccc a tgcaggagtc agccacgag aatactatca tcagatggcc 780
ctgctaactg gccagcgcag cccctatgca gacatt attc cctcagctgc caccgcggc 840
acgggggcca tccatgga atatcttcat gctatggata gcaccagatt ctccagcccc 900
aggctgtcag ccaggccgag ccgaaaacgt aactgtcca tatccacct ctccgatcat 960
agctttgacc ttcagacat gataaggacg tctcccaact ccttggtcac gattctcaat 1020
aattcccgta gca gctcttc agcaagtggc tcctatggtc acttatctgc aagtgcaatc 1080
agccctgctt tgagcttcac ctactctcc ggcggcgtct ctctccacat gcacagcag 1140
atcctaagcc gacaacagag cttaggttca gcctttggac acagccctcc actcatccac 1200
cctgccccaa cttttccaac acagaggcct attccaggga tccctacggt tc tgaacccc 1260

270/292

gtccagggtca gctccgggccc ttctgagttcc tcacagaaca agcccacgag tgagtctgca 1320
 gtgagcagca ctggtgaccc gatgcacaac aagagggtcca agatcaaacc cgatgaagac 1380
 ctccccagcc caggggctcg ggggcagcag gaacagcccg aaggaacaac ccttgtcaag 1440
 gaggaagggg acaaagatga aagcaaa cag gagcctgaag tcatctatga gacaaactgc 1500
 cactgggaag gctgcgcgag ggagttcgac acccaagagc agcttgtgca ccatataaat 1560
 aacgaccata ttcatggaga gaagaaggag ttctgtgtgca ggtggctgga ctgctcaaga 1620
 gagcagaaac ccttcaaagc ccagtatatg ttggttagtc atatgagaag acacacgggc 1680
 gagaagcctc acaaatgcac ttttgaaggt tgcacaaagg cctactcgag actagaaaac 1740
 ttgaaaacac acttgagatc tcacactgga gagaaacat acgtctgtga gcacgaaggt 1800
 tgcaacaagg ctttctcaaa tgctctgat cgcgccaaac accaaaacag aacgcattcc 1860
 aatgagaaac catatgtgtg caaaatccca ggctgcacta agcgttacac agaccaagc 1920
 tccctccgga aacatgtgaa gacagtgcac ggcccagagg ctcatgtcac caagaagcag 1980
 cgaggggaca tccactctcg gccgccaccc ccgagagatt ccggcagcca ttcacagtcc 2040
 aggtgcctcg ccgagccgac cttggttagc agcaggacct cagcaaacct 2100
 acctcaaagc ggaa gaatg cctccagggtg aaaaccgtca aggcagagaa gccaatgaca 2160
 tctcagccaa gccctgggtg tcagtcttca tgcagcagcc aacagtcccc catcagcaac 2220
 tattccaaca gtgggctcga gcttctctg accgatggag gtagtatagg agacctcagt 2280
 gccatcgatg aaaccccaat catggactca accatttcca ctgcaaccac agcc ctgtct 2340
 ttgcaagcca ggagaaaccc ggaggggacc aaatggatgg agcacgtaaa actagaadagg 2400
 ctaaaacaag tgaatggaat gttccgcga ctgaacccca tttaccctcc taaagcccct 2460
 gcggtctctc ctctcatagg aaatggcaca cagtccaaca acacctgcag cttgggtggg 2520
 cccatgacgc ttctcccggt cagaagcga c ctctctgggg tggacgtcac tatgtgtaac 2580
 atgtcaaca gaaggacag cagcgcagc accatcagct cggcctacct gagcagccgc 2640
 cgctctcag ggatctcgcc ctgcttctcc agcgcgcgt ccagcgaggc gtcacaggcc 2700
 gagggccggc cgcagaacgt gagcgtggcc gactcctacg accccatctc caccgacgcc 2760
 tcgcgcgcgt ccagcgaagc cagccagagc gagggcctgc ccagcctgct cagcctcagc 2820
 cccgccagc caatccgcct tacgcggctg ccacaggagg gccgcgccg 2880
 acgcccctgc ccaacatgga gaggatgagc ctgaagacgc gcctggcgt gctcggggat 2940
 gccctcgagc ctggcgtggc cctgcctcca gttcatgccc cg aggggtg cagcgacggg 3000
 ggagccacg gctacggcg gcgccacct cagccgcagc atgcgctggg ccacggcgtg 3060
 aggaggcca gcgacccggt gcggacaggc tccgagggcc tggccctgcc tegtgtgccg 3120
 cgcttcagca gctcagcag ctgcaacccc ccggcgatgg ccacgtccgc ggagaagcgc 3180
 agtctcgtgc ttcagaa tta cagcggccc gagggcgccc agtcccga aa cttccactcg 3240
 tccccctgct ccccagcat caccgagaac gtcaccctgg agtccctgac catggacgct 3300
 gatgccaacc tgaacgatga ggatttctct cgggacgagc tgggtgcagta tttaaattcc 3360
 cagaaccaag cagggtagca gcagcacttc cccagcgcgc tcccgagca cagcaa agtg 3420
 cccacgggc ccggtgactt tgacgcgcgc gggctgccag acagccacgc tggccagcag 3480
 ttccatgccc tcgagcagcc ctgccccgag ggcagcaaaa ccgacctgcc cattcagtgg 3540
 aacgaagtca gctccggaag cgcgcacctg tctctctcca agtcaagtg tgggcccgcg 3600
 cccgtgtgc cgagactcg cgcctttggg ttctgcaacg gcatggctgt ccaccgcag 3660
 aaccccttga ggcaggggct tgctgggggc tatcagaccc tcggggagaa cagcaacccc 3720
 tacggtggcc cagagcactt gatgtccac aacagccccc gaagtggcac cagtggaaac 3780
 gccttccatg aacagccctg taaggcccc cagtatggga actgtctcaa caggcagcca 3840
 gtggccctcg gtgactcga cgtgacctgt ggtgcggga ttcaagcctc aaagctgaag 3900
 agcaccacca tgcaaggag cgggggcccag ctgaatttcg gcctgccgt agcgcctaat 3960
 gagttagctg gcagcatgt gaatggcat cagaaccagg acccagtggg acagggtac 4020
 ctggtcacc agctcctcg cgacagcat cagcaccgg gggc aggcg ccccggtcag 4080
 cagatgcttg ggcagattag tgctacctca cacatcaaca tctaccaagg gccagagagc 4140
 tgctgccag gggctcagc catgggcagc cagccgtcaa gcttggcagt tgtcaggggc 4200
 taccagccat gtgccagctt tgggggcagc aggcgcagg ctatgccag ggacagcctt 4260
 gctctcagt caggacagc t cagtacaca agtcagacct gcagggtgaa tggatatcaag 4320
 atggagatga aagggcagcc ccatccgctg tgctctaate tgcagaatta ctctggtcag 4380
 ttcatgacc aaaccgtggg cttagtcag caagacaga aagctggttc attctctatt 4440
 ttagcggcca aggtctgct acaggggacc agcccaaaa actctgagtt actttccc ca 4500
 ggtgctaate aggtgacaag cacagtggac agcctcgaca gccatgacct ggaaggggta 4560
 cagattgact tcgatgccat catagacgat ggggaccact ccagcctgat gtcggggggc 4620
 ctgagcccaa gtatcattca gaacctttcc catagctcct cccgcctc acagcctcgg 4680
 gcgtccctcc cattcccagc gctgtccatg ag caccacca acatggctat cggggacatg 4740
 agttctttgc tgacctccct agcgggaagaa agcaaatcc ttgcagttat gcaataggct 4800
 ttaggaaaaa aagactgcaa ccaacggaaa tcaataggag ttgaagagat taaactgact 4860
 ttgttttggc tgttttttta gttctgtatg tatttttagca atctcatctc acctaaactga 4920

271/292

gatgtgtttc aattatattc cttttatgga aaaggactct gaaaaaccct aaagtattct 4980
aggagaaaac tgtcttccat ttcagttttg aatcagtatt gttacactca aaccaccctc 5040
tttttaaaaa aaaa 5054

<210> 429
<211> 271
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<220>
<221> misc_feature
<222> (1)..(271)
<223> 3' terminal sequence. interleukin enhancer
binding factor 1 (ILF1) gene.

<400> 429
aggagacttg ttttactcag agtggaaaat ttgcccaggg acaaagtc aa cacaaagaaa 60
caaacaacaa aaaatagcca gaaagagaac agttaagtgc agtcgggtga gtcccggcag 120
ttccttcccg gcactggctc gtccctgggt tctcaagggt ccatgcggcc acagcgtccg 180
tccacctgtc cagcgagcc acatgctgaa atggaggtgg ataaaattca tcaggcagct 240
gctgtaacac ggaaatgtgc agatgcc aga g 271

<210> 430
<211> 193
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<220>
<221> misc_feature
<222> (1)..(193)
<223> 5' terminal sequence. Similar to Retinoblastoma -like protein 2,
sw|Q08999|RBL2_HUMAN.

<400> 430
TGTCTACATT TNCCACATA AAAATGAAAC AATNNTTCT CCTCGNGAAA AGATTTTATA 60
TTACTTNAGC NAAAGTCCTT CAAAGNGACT GAGCGNANNT AATAGTNTGA TACGCATAGG 120
NGNAACTCCT ACTNNAANGN GCGGNNTTCT TNTNGNNGAT GGCNGTGAAT NCACTGCAAA 180
NAGCATTTGC CCN 193

<210> 431
<211> 184
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<220>
<221> misc_feature
<222> (1)..(184)
<223> 3' terminal sequence. Homo sapiens CD2 antigen (p50).

272/292

<400> 431
AGTCAAAGCT TTTATTTCAC TTTNACTCAC AGGATGGGGG GCAAGTNTCC ACCAGGGCAC 60
ATAAGAACT CCAGAGTCTC TTAAGCAGAT AGGCTGCTTG TAGNGAGACC CAGGNACACC 120
AATCACTGA TTTATCGCAT CTACACATGA CCNGAGAGGG GACAAGAAAT CTCTAAGTTT 180
TCTG 184

<210> 432
<211> 242
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<220>
<221> misc_feature
<222> (1)..(242)
<223> 5' terminal sequence. Similar to NM_022641 Homo sapiens
chorionic somatomammotropin hormone 1 (placental lactogen) (CSH1

<400> 432
ATTCGGCAGC ATGACTGGCC AGGTATAAA AAGGGCCCAC AAGAGACCGG CTCTAGGATC 60
CCAAGGCCCA ACTCCCGGAA CCACTCAGGG TCCTGTGGCA GCTCACCTAG TGGCAATGGC 120
TCCAGGCTCC CGGAACGTCC CTGATCCTGG NTTTTGNCCT NCTCTNACTG CCCTGGNTTN 180
AANAAGCTNG TGCCNTCCAA ANCGTTCGGT TATCCAGGGT TTTGACCAC GCTATGCTNC 240
AA 242

<210> 433
<211> 329
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<220>
<221> misc_feature
<222> (1)..(329)
<223> 5' terminal sequence. Homo sapiens plasminogen activator (PLAT)

<400> 433
AACAGTCACC GACAACATGC TGTGTGCTGG AGACACTCGG AGCGGCGGGC CCCAGGNAAA 60
CTTGACAGAC GCCTGCCAGG GNATTTCGGG AGGCCCCCTG GTGTGTCTGA ACGATGGCCG 120
CATGACTTTG GTGGGCATCA TCAGCTGGGG CCTGGGCTNT GGACAGAAGG ATGTCCCGGG 180
TGTGTACACC AAGGTTACCA ACTACCTAGA CTGGATTCTG GACAACATGC GACCGTGACC 240
AGGAACACCC GACTCCTCAA AAGNAAATGA GATCCCGNCT CTTCTTCTTC AG AAGACACT 300
GCAAGGCGC AGTGCTTCTC TACAGACTT 329

<210> 434
<211> 247
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<220>
<221> misc_feature

273/292

<222> (1)..(247)

<223> 3' terminal sequence. Homo sapiens plasminogen activator (PLAT)

<400> 434

```
AAATATATCT GAANNNTTA AGTACAGTNT AAAACAGGGT TNTGGCAACA GAAAGTAAAA 60
ACTAACATGG NTTGCTATAA ATATGCTGAA GCCTAGTTGT TCAAATGATA CAATTCTCTC 120
ATGCTACTCT AAAGTTTNTA AAGNAAAAGG GTTTACACTT TACACACT GT ACACAAAGGG 180
GNTACCTTCT GNGNGCCNGG GAGTGGGGAA AGGGGANGGN GACTTGACGT CAAGGGTGCT 240
TTTGAGG                                     247
```

<210> 435

<211> 63

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(63)

<223> 5' terminal sequence. Homo sapiens aminoacylase 1 (ACY1).

<400> 435

```
CCGCCAGNAC CTGCGTATCC GCACTGTTCA GCCCAAGCCT GACTATGGAG CTGCTGTGGC 60
TTT                                     63
```

<210> 436

<211> 190

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(190)

<223> 3' terminal sequence. Homo sapiens aminoacylase 1 (ACY1).

<400> 436

```
GAAGAGGAGG NCCTTGCCAC TGGTNGGGAN GGAAGCCCCA GGGGAAAAGG TTNAGGAGTC 60
CCAGGGCTCA GCTGTCCTG GGCAGGGCAG GCACACTGGC AGGGCCAGGC AGCAGGCNNG 120
TATATATGNC CACCCACGG AGGAACACAG CCTNATGCAG NCGTTNATCG TGGTNGTGCA 180
GNAGCACAGG                                     190
```

<210> 437

<211> 176

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(176)

274/292

<223> 3' terminal sequence. Homo sapiens E74 -like factor 1 (ets domain transcription factor) (ELF1)

<400> 437

CCCTTAGGCT GTTCTGGTGA TGAGGCTCCC GGTGAGTCTG CATATTTTNN TTGCACCTGC 60
TGTGTTTCCA TCACTTCAGG AATCCCATCT AATGTGACGG ACACATGGGT GACTGGGGCA 120
ACAACCATGT CATCTTCAGG NGAACATAAT ATATTATTAT TTATCCGGTT TTCATC 176

<210> 438

<211> 465

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(465)

<223> 5' terminal sequence. Homo sapiens selectin P, granule membrane protein CD62, SELP

<400> 438

NGGAACATAT GGAGTTTTTA CA AACGCTGC ATTTGACCCG AGTCCTTAAG AGACCTGTCC 60
TTTTCTGGT CTCCTCATTC AGCCTCCATA TGATCCTGTT GTGAACATCA AGTTTCCTGC 120
TACACTGGAC TTAACATAAA TGCAATTTGCT GCAGGTTTCC ATAAACACCC ATGANTCAAA 180
GACATGGAAT TACCTTAGAT TAGCTCTGGA CCAGCCTGTT GGACCCGCTC TGGACCAACC 240
CTGTTTCTCG AGTTTGGGAT TGTGGTACAA TCTCAAATTC TCAACCTACC ACCCCTTCCT 300
GTCCCACCTC TTCTCTTCCT GTAACACAAG CCACAGAAGC CAGGAGCAAA TGTTTCTGCA 360
GTAGTCTCTG TGCTTTGACT CACCTGTTAC TTGAAATACC AGTGAACCAA AGAGACTGGA 420
GCATCTGGAC TTNACAAGAA GACCAGACTT GTGGAGANAT TAA AA 465

<210> 439

<211> 396

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(396)

<223> 3' terminal sequence. Homo sapiens selectin P, granule membrane protein CD62, SELP

<400> 439

GAAAATCCTT TNAATTACGN ATTTNAANAT TGGNCTTTGG GNCATTTGAG GGACAGTGAC 60
TGGGGGCAGG AAGGCCACAG GNGACATGTG GCCTTCTAGC TTNATNCTTG GCCTTCTGCA 120
GCCTCTGGGG CCATCCAGAG GACTCTCTGG AAGCCTCAGA GCAGAGGNCC AAGAGGCCTC 180
ATCAACAGCA ACCANTGGAG ACTCCAGAAG ATGCTACAGG ANTTNCTCCC AATTAGAGAT 240
GCCACCTGTT TNCCAACAAA GTGGAGAAAA CCTTCCTNNA ATCAAAAANT AAAGAGGTNT 300
TTCNATTTCT CCACAGTTTG GCCTCCTTGT GAGTCAGATG NTCCAGTCTC TTTGGNNCAC 360
TGGTATTTCA AGTAACAGGT GAGNNAAGG ANAGAG 39 6

<210> 440

<211> 337

<212> DNA

275/292

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(337)

<223> 5' terminal sequence. Human interleukin 3 receptor (hIL -3Ra).

<400> 440

```
AAAGGCTCAG CAGTTGAC CT GGGACCTTAA CAGAAATGTG ACCGATATCG AGTGTGTTAA 60
AGACGCCGAC TATTCTATGC CGGCAGTGAA CAATAGCTAT TGCCAGTTTG GAGCAATTC 120
CTTATGTGAA GTGACCAACT ACACCGTCCG AGTGGCCAAC CCCCATTCT CCACGTGGAT 180
CCTCTCCCT GAGAACAGTG GGAAGCCTTT GGCAGGTGCG GAGAATCTGA CCTGCTNGAT 240
TCATGACGTT GATTTCTTGA GCTGCAGCTG GCGGGTAGGG CNCGGGGCCC CGCGGGACGT 300
CCAGTACGAC CTGTACTTGA ACGTTNCCAA CAGGNGT 337
```

<210> 441

<211> 104

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:prim er

<220>

<221> misc_feature

<222> (1)..(104)

<223> 3' terminal sequence. Human interleukin 3 receptor (hIL -3Ra).

<400> 441

```
TTCCCGCCTC CCAGACCACC AGNTTGNCGT TTTGGNAGNT NTNACCGANG GGGTNTTNCA 60
TGTNAGGGNT NCGGGNAAAN AGTTTNTGAA NCACCAGAAA CCTT 104
```

<210> 442

<211> 223

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(223)

<223> 5' terminal sequence. Human tumor protein p53 (Li -Fraumeni syndrome) (TP53)

<400> 442

```
AAGCAATGGA TGATTTGATG CTGTCCCCGG ACGATATTGA ACAATGGTTC ACTGAAGACC 60
CAGGTCCAGA TGAAGCTCCC AGAATGCCAG AGNTGNCTCC CCGCGTGGCC CCTGCACCAG 120
CAGCTCCTAC ACCGGCNGCC CCTGCACCAG CCCCTCCTG GCCCCTGTCA TCTTCTGTCC 180
CTTCCAGAN AACCTACCAG GGCAGCTACG GTTCCGTCT G GG 223
```

<210> 443

276/292

<211> 223
<212> ADN
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<220>
<221> misc_feature
<222> (1)..(223)
<223> 5' terminal sequence. Tumor protein p53
(Li-Fraumeni syndrome) (TP53) gene.

<400> 443
aagcaatgga tgatttgatg ctgtccccgg acgatattga acaatgggtc actgaagacc 60
caggtccaga tgaagctccc agaatgccag agntgnctcc ccgcgtggcc cctgcaccag 120
cagctcctac accggcngcc cctgcaccag cccctcctg gccctgtca tttctgtcc 180
cttccagaa aacctaccag ggcagctacg gttccgtct ggg

<210> 444
<211> 343
<212> ADN
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<220>
<221> misc_feature
<222> (1)..(343)
<223> 3' terminal sequence.

<220>
<221> misc_feature
<222> (1)..(343)
<223> v-erb-b2 avian erythroblastic leukemia viral
oncogene homolog 2 (neuro/glioblastoma derived
oncogene homolog) (ERBB2) gene.

<400> 444
caaggggctg caaactnncc cacacatgac cccagccctc tacagcggtc cagtgaggac 60
cccacagtac ccctgccctc tgagactgat ggctacgttg cccccctgac ctgcagcccc 120
cagcctgaat atgtgaacca gccagatgtt cggccccagc ccccttcgcc ccgagaggcc 180
ctctgcctgc tgcccagact gctgggtgcc ctctggaaag gcccaagact ctctccccag 240
ggaagaatgg ggtcgtcaaa gagtttttgc cttt gggggt gccgtgggag aaccccgagt 300
attgacaccc caggggaggg agcttgccct tcagccccac ctt 343

<210> 445
<211> 309
<212> ADN
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<220>
<221> misc_feature
<222> (1)..(309)
<223> 3' terminal séquence.

<220>

<221> misc_feature

<222> (1)..(309)

<223> zinc finger protein 144 (Mel -18) (ZNF144) gene.

<400> 445

```
ccgcccccca cccccaaggt gganagagct ggggaaagta gaagaggtgg aaaaaagggc 60
ccagaaaaag tggaaggagt ggagaggctt ag ctggaaga agggagaggg tccctggcct 120
caagttaagg ggggcacggg agcgccnttg acagtcatct tgcgccccct gctggtngaa 180
ganggtttct tcaggcagtt caagctaccc ccgttngcan ctttngnngc ccacttgct 240
ntcgaagggg ganttgggna ngtagggtn gtngettgan gcccatngga actnggaaaa 300
ccatnggat                                     309
```

<210> 446

<211> 268

<212> ADN

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(268)

<223> 3' terminal sequence.

<220>

<221> misc_feature

<222> (1)..(268)

<223> MAP/microtubule affinity-regulating kinase 3
(MARK3) gene.

<400> 446

```
attatcttgt gaatctactt agaaaaacac acacaagcaa tgttcacaac tataaattta 60
aaccttttgc actaaaaaaa cacaaaacaa caaacacaa accacaggca tgaactgtaa 120
acctgtatta actntgaact ggtcttaagg ttaattctta gcngtcattc agtattttcc 180
tccttggaac ctgtaatgtt ttngcaccgg ntgatctccc gcngggggta ctagtaatga 240
ctggctgccc gtgtaggagg atgcttcc                                     268
```

<210> 447

<211> 169

<212> ADN

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(169)

<223> 5' terminal sequence.

<220>

<221> misc_feature

<222> (1)..(169)

<223> MAP/microtubule affinity-regulating kinase 3
(MARK3) gene.

<400> 447

278/292

gaacactgat ggaaatgtat agaataatat ttaggcaata acgtctgcat cttctaaatc 60
atgaaattaa agtctgagga cgagagcacg nctgggngcg aaantntgcc tttttntac 120
ggatgcacta cantaaagan gtgcanccta tncgncccct gccctactt 169

<210> 448

<211> 393

<212> ADN

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(393)

<223> 3' terminal sequence.

<220>

<221> misc_feature

<222> (1)..(393)

<223> EST N68536 MAX-interacting protein 1 (MXI1) gene.

<400> 448

aagtaattaa gggtagttaa attattttaa gtatacaaag tccaaacagc caggggtaag 60
gtctccaaga ggccttccca gggtaaggga gagggccaca agggaacctt ggagtttgaa 120
agacaaaggg aacacatgac atcaaagtgc aggctagaaa tttcacttag aagaaaataa 1 80
cattactgaa aatattcgta agagtaacaa tagcacatgc acagtgggac tgtgaggaag 240
agagagactg cctgtaggaa aatggaagca aatctttaca ttaaaatgag acaagtgctg 300
aacttactat gttaactatg atagtgtgtc tacnatagat atnccgatgg ttaaaagctg 360
gtaaaaggta atggttctca aaaccnaaa a tag 393

<210> 449

<211> 217

<212> ADN

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(217)

<223> 5' terminal sequence.

<220>

<221> misc_feature

<222> (1)..(217)

<223> EST R81126 lymphotoxin beta receptor (LTBR) gene.

<400> 449

ttacntgggt atctcctact gtagtatgag gaagaatggc tgttaatgta ttttttgaat 60
tctggnetca cctttgtctc agctaaatgt agccgcaccc gggacacagt ttgtgccaca 120
tgtgccgaga attcctacaa cgagc actgg aactacctga ccatctgccca nctgtgccgc 180
ccctgtgacc cagtgtatgg cctcgnctga gantgcc 217

<210> 450

<211> 157

<212> ADN

279/292

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(157)

<223> 5' terminal sequence

<220>

<221> misc_feature

<222> (1)..(157)

<223> (POU2F2) gene.

<400> 450

nattcggcaa cngggaaagg aaagaaacta accaacaaaa gagaaaacca aaaataatca 60
caacagaaac cagctgcccc aaaggaggcc agtngtnggg acgcagaggg tcc tcagagc 120
aggagtnaca agggaggaaa gaccaaaaaa acaacca 157

<210> 451

<211> 282

<212> ADN

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(282)

<223> 5' terminal sequence.

<220>

<221> misc_feature

<222> (1)..(282)

<223> caspase 4, apoptosis -related cysteine protease
(CASP4) (ex CASP1)

<400> 451

gagaatctga cagccaggga tatggagtca gcgctgaggg catttgctac cagaccagag 60
cacaagtctc ctgacagcac attcttggtg ctcattgtct atggcatcct ggagggaatc 120
tgcggaactg tgcattgatg gaaaaaacca gatgtgctgc tttatgacac catcttccag 180
atattcaaca accgcaactt gcttcagtct ngaaggacaa acccaagggtc atcattgtnc 240
agggcttgca gagggtgcaa accttggggg aantttgggg tc 282

<210> 452

<211> 424

<212> ADN

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(424)

<223> 5' terminal sequence

<220>
<221> misc_feature
<222> (1)..(424)
<223> syndecan 1 (SDC1) (ex HRB)

<400> 452
ttgcttttng caaaactcta cttaatccaa tnggtttttc cctgtacagt agattttcca 60
aatgtaataa actttaatat aaagtagtcc tgtgaatgcc actgccttcg cttcttgect 120
ctgtgctgtg tgtgacgtga cgggactttt ctgcaaacac caacatgttg ggaaacttgg 180
ctcgaatctc tgtgccttcg tctttcccat ggggagggga ttctggttcc aggttcctc 240
tgtgtatttg cttttttgtt ttggctgaaa ttctcctgga ngtcggtagg ttcagccaag 300
gttttataag ggctgatgtc aatttctgt gtttgccaan ttccaagccc catcttncta 360
aatgggcaaa aggaaggttg gatgggcccc agcnacagct ttgnaccc ga gggctnttgg 420
gtca 424

<210> 453
<211> 435
<212> ADN
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<220>
<221> misc_feature
<222> (1)..(435)
<223> 5' terminal sequence

<220>
<221> misc_feature
<222> (1)..(435)
<223> Integrin, beta 2 (antigen CD18 (p95), lymphocyte
function-associated antigen 1; macrophage antigen
1 (mac-1) beta subunit) (ITGB2)

<400> 453
aggagtgcc cggctgcccc tcaccct gtg gcaagtacat ctctgcgcc gagtgccctga 60
agttcgaaaa gggccctnt ggaagaactg cagcgcgccg tgtccgggcc tgcagctgtc 120
gaacaacccc gtgaaggga ggacctgcaa ggagaggac tcagagggt gctgggtggc 180
ctacacgtg gagcagcagg acgggatgga cgcctacctc atctatgttg atgagagccg 240
agagtgtgtg gcaggcccga acatcgccgc catcgctcggg ggcaccgttg gcaggcatcg 300
tgctgatcgg cattctctg ctggatcatc gggaaggctc tgatccacct gacgacctc 360
cgggagttac aggcgttttg agnaggagaa gctcaagtc cagtnngaac aatgattatt 420
ccctttttca agagc 435

<210> 454
<211> 544
<212> ADN
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<220>
<221> misc_feature
<222> (1)..(544)

281/292

<223> 5' terminal sequence

<220>

<221> misc_feature

<222> (1)..(544)

<223> Protein phosphatase 1, catalytic subunit, alpha isoform (PPP1CA) (ex MGST1)

<400> 454

```
gtgtgaccag acatgcaacc gncatctatg gtttctacgn atgnagtgn aagcagnacg 60
nctnacaaca tcaaactgtg gnaaaacctt cactgnactg ncttcaactg ncctgnccca 1 20
tcgcggncca tagtggacgt aaaagatctt ctgnctgncc acggaggcct gttccccgga 180
cctgncagtt ctatggnagc agattcggcg ggatcatgcg gccacagat gtgtcctgta 240
ccaggggcct gctgtgtgac ctgctgtggt ctgaccctga caaggacgtg cagggctggg 300
gcgagaacga ccgtgggcgt ctcttttac c tttggagccg aggtggtggc caagttcctc 360
cacaagcacg acttggacct catctgccga gcacaccagg ttgtagaaga cggctacgag 420
ttctttgccg agcggcantt ggtgacactt ttctcagctt ccaactactg ttgcgagttt 480
nacaatgctt gcgccatgat gagtgtgacg agaccctatg tgcttttcag atcttaagcc 54 0
gccn                                     544
```

<210> 455

<211> 344

<212> ADN

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(344)

<223> 3' terminal sequence

<220>

<221> misc_feature

<222> (1)..(344)

<223> protein phosphatase 2 (formerly 2A), catalytic subunit, alpha isoform (PPP2CA)

<400> 455

```
actgcggtga gagccagcgg ccagcgccac cncaacagcc gccagaagna cagaggaac 60
cggcgcgggc gngtgcngt aggccgtg n gcggtgncgg cgcgggagga gccggannca 120
gccggcnggg gcggnggca ncanggacga gaaggngnnc accaaggagc tggaccagn 180
gaacgagcag cngaacgagn gcaagcagcn gnccgagncc caggnaaga gccncagcga 240
gaangcnaaa gaaanccnga caaagaanc caacngcaa gaggnncgan gnccaggnac 30 0
ngnccngnga gangngcang ggcaannnca ngaacccatg gaac 344
```

<210> 456

<211> 514

<212> ADN

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(514)

<223> 5' terminal sequence

<220>

<221> misc_feature

<222> (1)..(514)

<223> S100 calcium-binding protein A11 (calgizzarin)
(S100A11)

<400> 456

```
cagcctcccg cgcctcgtc agctccaaca tggcaaaaat ctccagccct acagagactg 60
agcgggtgcat cgagtccttg attgctgtct tccagaagta tgctggaa ag gatgggttata 120
actacactct ctccaagaca gagttcctaa gttcatgaa tacagaacta gctgccttca 180
caaagaacca gaaggaccct ggtgtccttg accgcatgat gaagaaactg gacaccaaca 240
gtgatggtca gctagatttc tcagaatttc ttaatctgat tgggtgccta gctatggctt 300
gccatggact ccttcctcaa ggctgtccct tcccagaagc gggacctgga gggacccctt 360
gggccctggg cctttcaaac ccacccctn ttcctttcca gcctttctgt tcatcatntt 420
ccacagccca cccttncctg gaggcacatt aaccacctna tggtagggtg ccaactggtc 480
attagttatt aaagznaatg tnaatttttt ttaa                               514
```

<210> 457

<211> 359

<212> ADN

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(359)

<223> 5' terminal sequence

<220>

<221> misc_feature

<222> (1)..(359)

<223> Granzyme A (granzyme 1, cytotoxic
T-lymphocyte-associated serine esterase 3) (GZMA)

<400> 457

```
gctggacgtc atcaacaagc attcattcaa caacttccgc ctgcgagtgg ggttgaacca 60
tggaccgcta gtagctggag ttattggggc ccagaagcog caatatgaca ttgggggcaa 120
cacagtgaac gtggccagcc gcatggagag tacaggagtc cttggcaaaa tccaagtgaac 180
tgaggagaca gcatgggccc tacagtcctt gggctacacc tgctacagcc nggggtgtca 240
tcanggtgaa aggcaaaggg cagctctgca cctacttcct gaacacagac ttgacacgaa 300
ctggacctcc ttcagctacc ctaggtctag attgactctg cct tnctaag aacctnaat 359
```

<210> 458

<211> 1251

<212> ADN

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(1251)

<223> 3' terminal sequence

<220>

283/292

<221> misc_feature
<222> (1)..(1251)
<223> endothelin 1 (EDN1)

<400> 458

```
ggagctgttt accccactc taataggggt tcaatataaa aagccggcag agagctgtcc 60
aagtcagacg cgctctgca tctgcccag gcgaacgggt cctgcgcctc ctgcagtcct 120
agctctccac caccgcccgc tgcgcctgca gacgtccgc tcgctgcctt ctctcctggc 180
aggcgctgcc ttttctcccc gttaaagggc acttgggctg aaggatcgct ttgagatctg 240
aggaaccgcg agcgctttga gggacctgaa gctgtttttc ttcgttttcc tttgggttca 300
gtttgaacgg gaggtttttg atcccttttt ttcagaatgg attatttgct catgattttc 360
tctctgctgt ttgtggcttg ccaaggagct cc agaaacag cagtcttagg cgctgagctc 420
agcgcggtgg gtgagaacgg cggggagaaa cccactccca gtccaccctg gcggctccgc 480
cggccaagc gctgctcctg ctctccctg atggataaag agtgtgtcta cttctgccac 540
ctggacatca tttgggtcaa cactcccgag cacgttggtc cgtatggact tggaagccct 600
aggtccaaga gagccttgga gaatttactt cccacaaagg caacagaccg tgagaataga 660
tgccaatgtg ctagccaaaa agacaagaag tgctggaatt tttgccaagc aggaaaagaa 720
ctcagggtcg aagacattat ggagaaagac tggataatc ataagaaagg aaaagactgt 780
tccaagcttg ggaaaaagtg tatttatcag cag ttagtga gaggaagaaa aatcagaaga 840
agttcagag aacacctaag acaaaccagg tcggagacca tgagaaacag cgtcaaatca 900
tcttttcatg atcccaagct gaaaggcaag cctccagag agcgttatgt gaccacacaac 960
cgagcacatt ggtgacagac ttcggggcct gtctgaagcc atagcctcca cgagagagccc 1020
tgtggccgac tctgcactct ccaccctggc tgggacaga gcaggagcat cctctgctgg 1080
ttcctgactg gcaaaggacc agcgtcctcg ttcaaaacat tccaagaaag gttaaggagt 1140
tcccccaacc atcttctact gcttccatca gtggttaact ctttggcttc ttctttcatc 1200
tggggatgac aatggacctc tcagcagaaa caca cagtca cattcgaatt c 1251
```

<210> 459
<211> 2145
<212> ADN
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<220>
<221> misc_feature
<222> (1)..(2145)
<223> 3' terminal séquence

<220>
<221> misc_feature
<222> (1)..(2145)
<223> Protein tyrosine phosphatase, non -receptor type 6
(PTPN6)

<400> 459

```
cggcagaact gggaccaccg ggggtggtga ggcggcccgc cactgggagc tgcattctgag 60
gcttagtccc tgagctctct gcctgcccag actagctgca cctcctcatt ccctgcgccc 120
ccttctcttc cggaa gccc caggatgggt aggtgggttc accgagacct cagtgggctg 180
gatgcagaga cctgctcaa gggccgaggt gtccacggta gcttctctgg tcggcccagt 240
cgcaagaacc aggggtgact ctgcctctcc gtcagggtgg gggatcaggt gacctatatt 300
cggatccaga actcagggga tttctatgac ctgtatggag gggagaagt t tgcgactctg 360
acagagctgg tggagtacta cactcagcag cagggtgtgg tgcaggaccg cgacggcacc 420
atcatccacc tcaagtaccc gctgaactgc tccgatccca ctagtgagag gtggtaccat 480
ggccacatgt ctggcgggca ggcagagacg ctgctgcagg ccaagggcga gccctggacg 540
ttctttgtgc gtgaga gcct cagccagcct ggagacttcg tgctttctgt gctcagtgac 600
cagcccaagg ctggcccagg ctcccgcctc agggtcaccc acatcaaggt catgtgcgag 660
ggtggacgct acacagtggg tggtttgag accttcgaca gcctcacgga cctggtggag 720
```

284/292

```

catttcaaga agacggggat tgaggaggcc tcaggcgcct ttgtctacct gcggcagccg 780
tactatgcc aaggggtgaa tgccggtgac attgagaacc gagggttgga actgaacaag 840
aagcaggagt ccgaggatac agccaaggct ggcttctggg aggagtttga gattttgcag 900
aagcaggagg tgaagaactt gcaccagcgt ctggaagggc aacggccaga gaacaagggc 960
aagaaccgct acaagaa cat tctccccctt gaccacagcc gaggatcct gcagggacgg 1020
gacagtaaca tccccgggtc cgactacatc aatgccaaact acatcaagaa ccagctgcta 1080
ggccctgatg agaacgctaa gacctacatc gccagccagg gctgtctgga ggccacggtc 1140
aatgacttct ggccagatggc gtggcaggag aacagccgtg tcactcgtcat gaccaccga 1200
gagggtggaga aaggccggaa caaatgcgtc ccatactggc ccgagggtggg catgcagcgt 1260
gcttatgggc cctactctgt gaccaactgc ggggagcatg acacaaccga atacaaactc 1320
cgtaccttac aggtctcccc gctggacaat ggagacctga ttcgggagat ctggcattac 1380
cagtacctga gctggccc ga ccatggggtc ccagtgagc ctgggggtgt cctcagcttc 1440
ctggaccaga tcaaccagcg gcaggaaagt ctgcctcagc cagggcccat catcgtgcac 1500
tgcagcgccg gactcggccg cacaggcacc atcattgtca tcgacatgct catggagaac 1560
atctccacca agggcctgga ctgtgacatt gacatccaga agaccatcca g atgggtcgg 1620
gcgcagcgtc cgggcatggt gcagacggag gcgcagtaca agttcatcta cgtggccatc 1680
gcccagttca ttgaaaccac taagaagaag ctggaggtcc tgcagtcgca gaagggccag 1740
gagtcggagt acgggaacat cacctatccc ccagccatga agaatgccca tgccaaggcc 1800
tcccgcacct cgtccaaac a caaggaggat gtgtatgaga acctgcacac taagaacaag 1860
agggaggaga aagtgaagaa gcagcgggtc gcagacaagg agaagagcaa gggttccctc 1920
aagaggaagt gagcgggtgt gtccctcagg ggccatgcct cagccctgac cctgtggaag 1980
catttcgcga tggacagact cacaacctga acctaggagt gccccattct tt tgtaattt 2040
aaatggctgc atccccccca cctctccctg acctgtata tagcccagcc aggccccag 2100
cagggccaac ccttctctc ttgtaaataa agccctggga tcaact 2145

```

<210> 460

<211> 2149

<212> ADN

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(2149)

<223> 3' terminal sequence

<220>

<221> misc_feature

<222> (1)..(2149)

<223> Transcription factor AP-4 (activating enhancer binding protein 4) (TFAP4)

<400> 460

```

gacctgcaaa cacacacaca cacacacaca cacacacaca cacacacaca catacacacg 60
caccagggca gccgagagac ctccctcccg cccctcccat gcccgccctc ctccctcgc 120
cgccgcccgc gccgccagca tctgggaccg gccgattctg cacctccgtc cggcgctgcc 180
ctttgattcg gatttccatc ttgcattctc cggctgatcg cgggacctgg ct cgtgcaga 240
ggaggggggc cgatcgctat ggagtatttc atgggtgccca ctcagaaggt gccctctttg 300
caacatttca ggaaaacaga gaaagaagt ataggagggc tctgtagcct tgccaacatt 360
ccactaacc cagagactca gcgggaccag gagcggcgga ttcggcgga gatcgccaac 420
agcaacgcagc gcagagcgc atcagcgggat tccagtcct caagaccctc 480
atccccaca cagacggaga gaagctcagc aaggcagcca ttctccagca gacagccgag 540
tacatcttct ccttgagca ggagaagacc aggtctttgc agcagaacac acagctcaag 600
cgcttcatcc aggagctgag cggctcgtcc cccaagcgac ggcgggcaga gga caaggac 660
gaaggcatag gctccccgga catctgggag gacgagaagg cggaggacct gcggcgggag 720
atgattgagc tgcggcagca gctggacaag gagcgctcgg tgcgcatgat gctggaggag 780
caggtcgct cgctggaggc ccacatgtac ccgaaaagc tcaaggtgat tgcgcagcag 840

```

285/292

gtgcagctgc agcagcagca ggaacaggtg aggctgctgc accaggagaa gctggagcgg 900
gaacagcagc agctgcggac ccagcttctg cccctccgg cccccacca ccacccacg 960
gtgatcgtgc cagcaccgcc tctctctccc tcccaccaca tcaatgtcgt caccatgggc 1020
ccctcctcgg tcatcaacte tgtttccaca tcccggcaaa atctggacac catc gtgcag 1080
gcaatccagc acatcgaggg caccagggaa aagcaggagc tggaggagga gcagcggcga 1140
gctgtcatcg tgaagcctgt ccgcagctgc ccggaggccc ccacctctga caccgcctcc 1200
gactccgagg cctcagacag tgacgccatg gaccagagcc gggaggagcc gtcgggggac 1260
ggggagcttc cctgactacc c cccagccc tctctccct tctgggggct ggaggagacc 1320
ggggcagcca caggagagaa catgggcgaa tgagtggaga atttttacaa aattacgatg 1380
tcatttgggt ctcttttatg acctcttttt caatactgta aatcgacctt tgaacgaagc 1440
cactcaaccc gaggtcccgg ggctgggggtg tcgcagagct gtgggagcat cggca cccca 1500
gggcgggggc tcggccccgg gggtggagg aagctgacac ggagatgcct ggctctctc 1560
tgccaaaaag cattttttcc ttttaaatg ttttttaaga acagggaata ttaaaaaaa 1620
ccccaggtta tttcttccct gccagagcc agcctgggat tgtcagcctt caatccctt 1680
tccttctct ttttgggttt tc ttttttct cttttaagca cttacatggt tgggggtaag 1740
actagctgg ggcattctgg ggcccccgg gtctccgtt cttcttggtt ggggtttgct 1800
gctgtctgtc cccctccccc ctcccccac tcggcactag aattcgccac tctccaccc 1860
cccagccccc acctctgcct ccaggtctca tctccaccc caaaaatgtc tgtctc tctc 1920
tttttgggtt gttgttggtt ggttttttat ttctttttgg tttgctttct gtttttgtt 1980
tgtttttctt ttttttcttt cttttttttt tttttacaat tttgaggtct tcgtgttcaa 2040
ggagaagcta ttatatattt ttaagaaagt ggggagaaaa aaaaccaaga ggccaccgtg 2100
cctttgtaaa gaaacaaaat aaa gtttgta ctttgttttt taaaaaaaaa 2149

<210> 461

<211> 6478

<212> ADN

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(6478)

<223> 3' terminal sequence

<220>

<221> misc_feature

<222> (1)..(6478)

<223> Cyclin D2 (CCND2)

<400> 461

agagcgagca ggggagagcg agaccagttt taaggggagg accggtgcga gtaaggcagc 60
cccagggctc tgctgcgcca ccaccaatc ctgcctccc ttctgtccca ccttctctc 120
ctgccctcac ctctcccccg aaaaccccct atttagccaa aggaagg agg tcaggggaaac 180
gtctctccct ccccttccaa aaaacaaaaa cagaaaaacc cttttccagg ccggggaaag 240
caggagggag aggggcccgc gggtggcca tggagctgct gtgccacgag gtggaccgg 300
tccgcagggc cgtgcgggac cgcaacctgc tccgagacga ccgcgtcctg cagaacctgc 360
tcaccatcga ggagcgctac cttccgcagt gctcctactt caagtgcgtg cagaaggaca 420
tccaacccta catgcgcaga atggtggcca cctggatgct ggaggtctgt gaggaacaga 480
agtgcgaaga agaggtcttc cctctggcca tgaattacct ggaccgttct ttggtgggg 540
tcccgactcc gaagtcccat ctgcaactcc tgggtgctgt ctgcatgt tc ctggcctcca 600
aactcaaaga gaccagcccg ctgaccggcg agaagctgtg catttacacc gacaactcca 660
tcaagcctca ggagctgctg gagggggaac tgggtggtgct ggggaagtgt aagtggaaac 720
tggcagctgt cactcctcat gacttcattg agcacatctt gcgcaagctg cccagcagc 780
gggagaagct gtctc tgatc cgcaagcatg ctccagacct cattgctctg tgtgccaccg 840
actttaagtt tcccatgtac ccaccgtcga tgatcgcaac tgggaagtgt ggagcagcca 900
tctgtgggct ccagcaggat gaggaagtga gctcgtcac ttgtgatgcc ctgactgagc 960
tgctggctaa gatcaccaac acagacgtgg attgtctcaa agcttgcca g gagcagattg 1020
aggcgggtgct cctcaatagc ctgcagcagt accgtcagga ccaacgtgac ggatccaagt 1080

286/292

cggaggatga actggacca gccagcacc ctacagacgt gcgggatatc gacctgtgag 1140
 gatgccagtt gggccgaaag agagagacgc gtccataatc tggctctctc ttctttctgg 1200
 ttgtttttgt tctttgtgt ttagggtgaa acttaaaaaa aaaattctgc cccacctag 1260
 atcatattta aagatctttt agaagtgaga gaaaaaggtc ctacgaaaac ggaataataa 1320
 aaagcatttg gtgcctattt gaagtacagc ataagggaat cccttgata tgcaacagt 1380
 tattgtttga ttatgtaaaa gtaatagtaa aatgcttaca ggaaaacctg cagagtagtt 1440
 agagaatatg tatgcctgca atatgggaac aaattagagg agactttttt ttcatgtta 1500
 tgagctagca catacaccoc cttgtagtat aatttcaagg aactgtgtac gccatttatg 1560
 gcatgattag attgcaaagc aatgaactca agaaggaatt gaaataagga gggacatgat 1620
 ggggaaggag tacaaaa caa tctctcaaca tgattgaacc atttgggatg gagaagcacc 1680
 tttgctctca gccacctgtt actaagtcag gagtgtagtt ggatctctac attaatgtcc 1740
 tcttgctgtc tacagtagct gtacacataa aaaagatgtt ttattttgcc agttggacac 1800
 aggtgattgg ctctggggtt tcatgttctg tgacatcctg cttcttcttc caaatgcagt 1860
 tcattgcaga caccaccata ttgctatcta atggggaaat gtactatgg gccataacca 1920
 aaactcacat gaaacggagg cagatggaga ccaagggtgg gatccagaat ggagtctttt 1980
 ctgttattgt atttaaaagg gtaatgtggc cttggcattt cttcttagaa aaaaactaat 2040
 ttttggtgct gattggca tg tctggtcac agtttagcat tgtataaac cattocattc 2100
 gaaaagcact ttgaaaaatt gttcccgagc gatagatggg atgggttatg caagtcatgc 2160
 tgaatactcc tcccctcttc tcttttgccc cctcccttcc tgccccagt ctgggttact 2220
 ctctgcttct ggtatctggc gttctttggt acacagttct ggtgttcta c caggactca 2280
 agagacaccc ctctctgctg acattcccat cacaacattc ctacagaaag cctgtaaaact 2340
 aaaatctgtt accatctgat ggacagaag gatcttaatt cccatctcta tacttctcct 2400
 ttggacatgg aaagaaaagt tattgctggt gcaaagatag atggctgaac atcagggtgt 2460
 ggcattttgt tcccttttc c gtttttttt tttttattgt tgtgttaat ttattgcaa 2520
 agttgtatc agcgtacttg aatttttctt cctctccact tcttagaggc attcagttag 2580
 caaagaggtt ggagcaaca cttttttttt tttttttgc acaattgtaa ttgacaggta 2640
 atgaagctat ttgttaaaat atttgctttt ttaagtaaaa aagaaaaatc ag aacagggc 2700
 tatttgaaga attattttat acacagattc tgccttggtt catagtatga gggttgaaga 2760
 cggaaaacaa tctaagggtc tctcattttt ttaattttgt ttgttcagt ttggtttttt 2820
 ttttttttg cgtgctaag aagctaaagt catccatcct tattcacgtt gacagtacct 2880
 agctgtaatg tttcacagag tgtgctgcta ttttataaac atttttataa tatattattt 2940
 tactgcttaa attccaagtc ctgaagtaga tggttgagat atgagttctt cgtactggaa 3000
 aagcccttc gtagtttgtt ttcttctggt agcatattca tggttgtttt ttttttctt 3060
 ttttggtttt ttggtttttt ttttttctc tgaacacatt ctcaaagac gga gtattct 3120
 tacctcaggt ttactggaca aaatcaataa ctacaaaagg caatgattca cgttttgtt 3180
 ttcataatac ctcaaacccg tacagtttct gcttgggagc ccattcgcat gaggaataca 3240
 gaagcagtgat gagcagggct gactccctct caggtggaag gcaggcggt ctcactcca 3300
 gggacctttt tggcatgga ggccatcggg ctcccagtta gacctggta tcctcatcat 3360
 gatggaaaaa atacattgaa ccaagggatc ctccctcccc ttcaaggcag acgttcagta 3420
 caaacattta tgcgtaggc tcagatgtcg taatttgcac ttaggtaaca ggtgtcagga 3480
 aacagactaa aaagaattcc accaggtgtt ttggagatcc tcatcttga gctt tttcaa 3540
 aagcggggct tcatctgcaa agggcccttt catottgaag tttttccct cgtctttcc 3600
 cctcccttg catggacacc ttgtgttag gatcatctct gcaggtttcc taggtctgaa 3660
 tctgcagta gatgaacctg cagcaagcag cgtttatggt gcttctctct ccctcctctg 3720
 tctcaaacctg cgcaggcaag c actatgcaa gcccaggccc tctgctgagc ggtactaaac 3780
 ggtcggttt tcaatcacac tgaattggca ggataagaaa aataggtcag ataagtatgg 3840
 gatgatagtt gaaggaggt gaagaggctg ctctcttaca gaggtgaaat tccagatgag 3900
 tcagctctt gggaagtgtg tttagaaggg ttcaggactt tgtgagttag catga cccta 3960
 aaattctagg ggatttctgg tgggacaatg ggtggtgaat tttgaagttt tggagaggga 4020
 agtggagcag ccagcaagta agctagccag agttttctca agagccagct ttgctcagca 4080
 cactctctg ggcccaagg agtcccacgg aatggggaaa gtgggaacc tggagtctt 4140
 gggaatcttg gagcctaaag ag aaaccgag gtgcaaattc atttcatggt gactgacct 4200
 ttagcttaaa cagaagcagc aaatgaaaga accggacaaa taaggaagg cacaagccta 4260
 ccgactcta ttacagctg gtaactttcc actcttctg tagtcccgag gccctgggt 4320
 ccttctagct tttctcttc ccatccttg ggccttggt gatgatgggt gtggg ctgc 4380
 cgatgggaaa gtcgggggtt gttaggcttt tctgctgct cctgcttaa cacaagaagg 4440
 aatcctggat ttgcccctc ctttagctct tagtctctt ggtaggagt ttgtccaga 4500
 ggagctctcc cccttggtt tgaacttgct ctttttggt ttgtgttct ttctctctt 4560
 tttcttacct ccactaaag ggg ttccaaa ttatcctggt cttttctac cttgttgtgt 4620
 ttctatctog tcttacttc catctgtttg ttttttctc catcagtggt ggccgagttg 4680
 ttccccagc ctgccaatt ttgatcttc cctcttttg gccaaatcct agggggaaga 4740

287/292

aatcctagta tgccaaaaat atatgctaag cataattaaa ctccatgagg gtccata aca 4800
gccaaagaagc ctgcaggaga aagccaaggg cagttccctc cgcagaacac cccatgctg 4860
ctgagaggcg agctccttga agaaggggct gttcttccag gaggccttat tttgaactgc 4920
ctcaggaccc cactggagag cacagcatgc cttactactg ggtcatcctt ggtctatgtg 4980
ctctgtactg gaggctctgt tctg cctctt atcagccagg tcaggggcac acatggctta 5040
agtgacaaaag ccagaggaga agacaaccct gacagcatca cgctgcatcc cattgctagc 5100
aggattggca actcttcaga cggagctgcg cttccctgca gtctagcacc tctagggcct 5160
ctccagactg tgccctggga gctctgggac tgaaagggtta agaacataag gcaggatc ag 5220
atgactctct ccaagagggc aggggaattt tctctccatg ggccacaggg gacagggctg 5280
ggagaagaaa tagacttgca ccttatgtca tgtaataat tgattttcta gttcaagaag 5340
ataatattgg tagtgtggga attggaggta ggaaggggag gaagtctgag taagccagt 5400
ggcttctaag ccaaaaggat tctc tttgt ttatctctga gacagtccaa ccttgagaat 5460
agcttttaaaa gggaaattaa tgctgagatg ataaagtccc cttagccaa caaacctct 5520
gtagctatag aatgagtgcg ggtttctatt ggtgtggact cagagcaatt tacaagagct 5580
gttcatgcag ccatccattt gtgcaaaata gggtaagaag attcaagagg atatttatt a 5640
cttcctcata ccacatggct tttgatgatt ctggattcta aacaaccag aatggctatt 5700
tcaggcacia cgatactaca ttctgtgtg tctgctttta aacttggtg ggctatcaga 5760
ccctattctc ggctcagggt ttgagaagcc atcagcaaat gtgtacgtgc atgctgtagc 5820
tgacgcctgc atccctcgc ctgcag ccta ctttggggaa ataaagtgc ttactgactg 5880
tagcattac agtatccaat gtcttttgac aggtgcctgt ccttgaaaaa caaagtttct 5940
atttttattt ttaattgggt tagttcttaa ctgctggcca actcttacat cccagcaaa 6000
tcacggggcc attggatttt ttccattatg ttcatcacc ttatatcatg tacctcagat 6060
ctctctctct ctctctctc tcagttatat agttcttgt cttggacttt ttttttcttt 6120
tctttttctt ttttttttg ctttaaaaca agtgtgatgc catatcaagt ccatgttatt 6180
ctctcacagt gtactctata agaggtgtgg gtgtctgtt ggtcaggatg ttagaaaagt 6240
ctgataagta gcatgatcag tgatgc gaa aaggttttta ggaagtatg caaaaatgtt 6300
gtattggcta tgatggtag atgatatag cagctgcctt ttaagaggtc ttatctgttc 6360
agtgttaagt gatttaaaaa aataataacc tgttttctga ctagtttaaa gatggatttg 6420
aaaatgggtt tgaatgcaat taggttatgc tatttggaca ataaactcac cttgacct 6478

<210> 462

<211> 3490

<212> ADN

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(3490)

<223> 3' terminal sequence

<220>

<221> misc_feature

<222> (1)..(3490)

<223> Junction plakoglobin (JUP)

<400> 462

cgccagagtc cggagcagcc gccgcccgc cgcgcgcagc tcagttcgct gtccgcgcgc 60
gtccaccacc cggcccgacc ccgaccgcgc cgggtcaggc cccatactca gtagccacga 120
tgagggtgat gaacctgatg gagcagccta tcaaggtgac tgagtggcag cagacataca 180
cctacgactc gggatccac tcgggcgcga acacctgcgt gccctccgtc agcagcaagg 240
gcatcatgga ggaggatgag gctgcgggc gccagtacac gctcaagaaa accaccactt 300
acaccagggt ggtgcccccc agccaagggt acctggagta ccagatgtcc acaacagcca 360
gggccaacg ggtgcgggag gccatgtgcc ctgggtgtgc ag gcaggac agctcgcttc 420
tgctggccac ccagggtgag gggcaggcca ccaacctgca gcgactggcc gagccgtccc 480
agctgctcaa gtcggccatt gtgcattca tcaactacca ggacgatgcc gagctggcca 540
ctcgcgcct gcccgagctc accaaactgc tcaacgacga ggaccgggtg gtggtgacca 600

288/292

```

aggcggccat gattgtgaac cagctgtcga agaaggaggc gtcgcgggcg gccctgatgg 660
gctcgcccca gctgggtggc gctgtcgtgc gtaccatgca gaataccagc gacctggaca 720
cagcccgtcg caccaccagc atcctgcaca acctctccca ccaccgggag gggctgctcg 780
ccatcttcaa gtcggtggc atccctgtct tggctcgcag gct cagctcc cctgtggagt 840
cggctcctgt ctatgccatc accacgtctg acaacctgct cctgtaccag gagggcgcca 900
agatggccgt gcgcctggcc gacgggctgc aaaagatggg gccctgtct aacaagaaca 960
acccaagtt cctggccatc accacogact gcctgcagct cctggcctac ggcaaccagg 1020
agagcaagct gatcatcctg gccaatgggt ggcccaggc cctcgtgcag atcatgcgt 1080
actacagtta tgaaggctg ctctggacca ccagtcgtgt gctcaagggt ctatccgtgt 1140
gtcccagcaa taagcctgcc attgtggagg ctggtgggat gcaggccctg ggcaagcacc 1200
tgaccagcaa cagccccgc ctggtgcaga actgcctgtg gacc ctgcgc aacctctcag 1260
atgtggccac caagcaggag ggctggaga gtgtgctgaa gattctggtg aatcagctga 1320
gtgtggatga cgtcaacgtc ctacacctgt ccacgggcac actctccaac ctgacatgca 1380
acaacagcaa gaacaagac gtggtgacac agaacagcg tgtggaggct ctcatccatg 1440
ccatcctgcg tgctggtgac aaggacgaca tcacggagcc tgccgtctgc gctctgcgcc 1500
acctactag ccgccacct gagggcgaga tggcccagaa ctctgtgct ctcaactatg 1560
gcateccagc catcgtgaag ctgtcaacc agcccaacca gtggccactg gtcaaggcaa 1620
ccatcggtt gatcaggaat ctggccctgt gccagccaa catg ccccg ctgcaggagg 1680
cagcgtcat ccccgctc gtccaactgc tggtaaggc ccaccaggat gccagcgcc 1740
acgtagctgc aggcacacag cagccctaca cggatgggtg gaggatggag gagattgtg 1800
aggctgcac cggagcactg cacatcctcg cccgggacc catgaaccg atggagatct 1860
tccggtcaa caccattccc ctgtttgtgc agctcctgta ctcgtcgtg gagaacatcc 1920
agcgcgtggc tgccgggtg ctgtgtgagc tggcccagga caaggaggcg gccgacgcca 1980
ttgatgcaga gggggcctcg gcccactca tggagttgct gcaactccgc aacgagggca 2040
ctgccaccta cgtgctgccc gtctgttcc gcatctccga ggacaa gaac ccagactacc 2100
ggaagcgcgt gtccgtggag ctcaaccaact cctcttcaa gcatgaccg gctgcctggg 2160
aggctgcca gagcatgatt ccctcaatg agcctatgg agatgacatg gatgccacct 2220
accgcccac gtactccagc gatgtgcccc ttgaccgct ggagatgcac atggacatg 2280
atggagacta ccccatcgac acctacagcg acggcctcag gcccccgta cccactgcag 2340
accacatgct ggcctaggcg gcctggcccc agtgacggcc cctctttgc aggttttcc 2400
tctctctag aacctcctc tgttgaggc cctcccatct ccccgctgaa acctgcgctc 2460
cttttttggg gggatcctt gctgctgagc ttcccaagc acggtgt gcc ctggcctgcc 2520
ttcttctgt gtctttggtg gggatgggga ggctattcc tgetggcccc ttctgggggt 2580
ggtgggagc tgacacggag tggcttgagc ttctgggat gcaggccac cgagccctg 2640
acccctgtct gtcccgcctc cctaacagg tcggttccat catctgagag gctctccgtg 2700
caggcgatgg ggcaagacag aaaagtgcct gagctgggga agccgggggt taacttctg 2760
ctgcaccctg cgcctccaga ggtcctcct aggtctttc ttgggatagt gttctgctc 2820
tgcttttctg tctgggcat ggtccaggg cctgacaccc cctccccgc cctgtggccc 2880
tggccactaa agcttcagac tcaagtaccc attctgttt cccccagc aa cgccccctca 2940
aacctccagc ctccctgtct ccagctgct gggccggaa gggctttgt tcttctctg 3000
ggtctgattt tctcactgaa ctccacogac caactgccct aagccccag ggcctccag 3060
gccaggttc gagacccaaa ccccaaaaat ccaaaacttc tcttgaagag ttcagggacc 3120
gtccagggga gatggggagg agatatggag tgagtcacct gctccagaag atgccagctt 3180
ctctctccag ggtgcttagt tggctttgcc caccctcac tcccaggga gctccgggga 3240
cagcttctc acaccctgt cccaccaca cagctgcct agctgacccc gagaagtgt 3300
cttggctgac cctctggtg tgtggtgagg gctttctct tccccttc t gtttcagacc 3360
ccccatttc ccgacatgg tgtggggggc tggggagggt ccaagcagag tgttttatta 3420
ttatcgcttt atgtttttg ttattggtt tttgtatag accaaagcaa agaaaataaa 3480
aataacacag                                     3490

```

<210> 463

<211> 1355

<212> ADN

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: primer

<220>

<221> misc_feature
<222> (1)..(1355)
<223> 3' terminal sequence

<220>
<221> misc_feature
<222> (1)..(1355)
<223> Growth arrest and DNA -damage-inducible, alpha
(GADD45A)

<400> 463
cagtggctgg taggcagtg ctgggaggca gcggcccaat tagtgtcgtg cggcccgtgg 60
cgaggcgagg tccggggagc gagcgagcaa gcaaggcggg aggggtggcc ggagctgcgg 120
cggtggcac aggaggagga gcccgggcgg gcgaggggagc gccagggcct 180
gagctgccgg agcgggcgct gtgagtgagt gcagaaagca ggcggccgag cgctagccgt 240
ggcaggagca gcccgcacgc cgcgctctct ccctgggaga cctgcagttt gcaatatgac 300
tttgaggagaa ttctcggctg gagagcagaa gaccgaaagg atggataagg tgggggatgc 360
cctggaggaa gtgctcagca aagccctgag tc agcgcacg atcactgtcg ggggtgtacga 420
agcggcccaag ctgctcaacg tcgacccaga taacgtggtg ttgtgcctgc tggcggcgga 480
cgaggacgac gacagagatg tggctctgca gatccacttc accctgatcc aggcgttttg 540
ctgcgagaac gacatcaaca tcctgcgctg cagcaaccgc ggccggctgg cggagctcct 600
gctcttgagg accgacgctg gccccgcggc gagcgagggc gccgagcagc ccccgacact 660
gcaactgcgt ctgggtgacga atccacattc atctcaatgg aaggatcctg ccttaagtca 720
acttatttgt ttttgccggg aaagtgcgta catggatcaa tgggttccag tgattaatct 780
ccctgaacgg tgatggcatc tgaatgaaa taa ctgaacc aaattgcact gaagtttttg 840
aaataccttt gtagttactc aagcagttac tcctacact gatgcaagga ttacagaaac 900
tgatgccaa gggctgagtg agttcaacta catgttctgg gggcccgag atagatgact 960
ttgcagatgg aaagaggtga aaatgaagaa ggaagctgtg ttgaaacaga aaaataagtc 1020
aaaaggaaca aaaattacaa agaaccatgc aggaaggaaa actatgtatt aatttagaat 1080
ggttgagtta cattaaaaata aaccaaatat gttaaagttt aagtgtgcag ccatagtttg 1140
ggtatttttg gtttatatgc cctcaagtaa aagaaaagcc gaaagggtta atcatatttg 1200
aaaaccatat tttattgtat tttgatgaga tatt aaattc tcaaagtttt attataaatt 1260
ctactaagtt attttatgac atgaaaagtt atttatgcta taaatttttt gaaacacaat 1320
acctacaata aactggtatg aataattgca tcatt 1355

<210> 464
<211> 732
<212> ADN
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<220>
<221> misc_feature
<222> (1)..(732)
<223> 3' terminal sequence

<220>
<221> misc_feature
<222> (1)..(732)
<223> Non-metastatic cells 1, protein (NM23A) expressed
in (NME1)

<400> 464
tgctgcgaac cacgtgggtc ccgggcgcgt ttcgggtgct ggcggtgca gccggagtgc 60
aacctaagc agctggaagg aaccatggcc aactgtgagc gtaccttcat tgcgatcaaa 120
ccagatgggg tccagcgggg tctgtgga gagattatca agcgttttga gcagaaagga 180
ttccgccttg ttggtctgaa attcatgcaa gcttccgaag atcttctcaa ggaacactac 240
gttgacctga aggaccgtcc attctttgcc ggcctggtga aatacatgca ctcagggccg 300

290/292

gtagttgcc a tggtctggga ggggctgaat gtggtgaaga cgggccgagt catgctcggg 360
 gagaccaacc ctgcagactc caagcctggg accatccgtg gagacttctg catacaagtt 420
 ggcaggaaca ttatacat gg cagtgattct gtggagagtg cagagaagga gatcggcttg 480
 tggtttcacc ctgaggaact ggtagattac acgagctgtg ctcagaactg gatctatgaa 540
 tgacaggagg gcagaccaca ttgcttttca catccatttc cctccttcc catgggcaga 600
 ggaccaggct gtaggaaatc tagttattta caggaacttc atcataattt g gagggaagc 660
 tcttgagct gtgagttctc cctgtacagt gttaccatcc ccgaccatct gattaaaatg 720
 cttctccca gc

<210> 465

<211> 942

<212> ADN

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(942)

<223> 3' terminal sequence

<220>

<221> misc_feature

<222> (1)..(942)

<223> Ribosomal protein L13 (RPL13) (ex BBC1)

<400> 465

ctttccgctc ggctgttttc ctgcgcagga gccgcagggc cgtaggcagc catggcgccc 60
 agccggaatg gcatgggtctt gaagcccccac ttccacaagg actggcagcg gcgcgtggcc 120
 acgtgggtca accagccggc ccgtaagatc cgcagacgta aggcccgga agccaaggcg 180
 cgccgcatcg ccccgcgccc cgctcggtt cccatccggc ccatcgtgcg ctgccccacg 240
 gtccggtacc acacgaaggt gcgcgcggc cgcggttca gcctggagga gtcagggtg 300
 gccggcattc acaagaaggt ggcccgacc atcggcattt ctgtggatcc gaggaggcgg 360
 aacaagtcca cggagtccct gcagaccaac gtgcagcggc tgaaggagta ccgctccaaa 420
 ctcatcctct tccccaggaa gccctcgcc cccaagaagg gagacagttc tgctgaagaa 480
 ctgaaactgg ccaccagct gaccggaccg gtcatgccc tccggaacgt ctataagaag 540
 gagaaagctc gagtcatcac tgaggaagag aagaatttca aagccttcgc tagtctcgt 600
 atggcccgtg ccaacgccc gctcttcggc atacgggcaa aaagagccaa ggaagccgca 660
 gaacaggatg ttgaaaagaa aaaataaagc cctcctggg acttgaatc agtcgggcag 720
 tcatgctggg tctccacgtg gtgtgtttcg tgggaacaac tgggcctgg atggggcttc 780
 actgctgtga cttcctcctg ccaggggatt tggggctttc ttgaaagaca gtccaagccc 840
 tggataatgc tttactttct gtgttgaagc actgttggtt gtttggttag tgactgatgt 900
 aaaacggttt tcttgtggg aggttacaga ggctgacttc ag 942

<210> 466

<211> 755

<212> ADN

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(755)

<223> 3' terminal sequence

<220>
<221> misc_feature
<222> (1)..(755)
<223> vascular endothelial growth factor B (VEGFB)m

<400> 466
caccatgagc cctctgctcc gccgcctgct gctcgcgcga ctcttgacgc tggccccccg 60
ccaggccctt gtctccacgc ctgatgcccc tggccaccag aggaagtgg tgcatggat 120
agatgtgtat actcgcgcta cctgccagcc ccgggaggtg gtggtgccct tgactgtgga 180
gctcatgggc accgtggcca aacagctggt gccagctgc gtgactgtgc agcgtgtgg 240
tggtgtgtgc cctgacgatg gcctggagtg tgtgccact ggcagcacc aagtcggat 300
gcagatcctc atgatccgtt acccgagcag t cagctgggg gagatgtccc tggaagaaca 360
cagccagtgt gaatgcagac ctaaaaaaaaa ggacagtgtc gtgaagccag acagggtgc 420
cactccccac caccgtcccc agccccgttc tgttcggggc tgggactctg cccccggagc 480
accctcccca gctgacatca cccatccac tccagcccca ggccccctctg cccacgtgc 540
accagcacc accagcgccc tgacccccgg acctgcggcc gccgtgccc acgcccagc 600
ttcctccgtt gccaaaggcg gggcttagag ctcaaccag acacctgcag gtgcccgaag 660
ctgcgaaggt gacacatggc ttttcagact cagcaggtg acttgctca gaggctatat 720
cccagtgggg gaacaaagag ggcctggta aa aaa 755

<210> 467
<211> 1039
<212> ADN
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<220>
<221> misc_feature
<222> (1)..(1039)
<223> 3' terminal sequence

<220>
<221> misc_feature
<222> (1)..(1039)
<223> Laminin receptor 1 (67kD, ribosomal protein SA)
(LAMR1)

<400> 467
tgctgtctt ttccgtgcta cctgcagagg ggtccatacg gcgttgttct ggattcccg 60
cgtaacttaa agggaaactt tcacaatgtc cggagccctt gatgtcctgc aaatgaagga 120
ggaggatgtc cttaa gttcc ttgcagcagg aaccactta ggtggacca atcttgactt 180
ccagatggaa cagtacatct ataaaaggaa aagtgatggc atctatatca taaatctcaa 240
gaggacctgg gagaagcttc tgctggcagc tegtgcatt gttgccattg aaaacctgc 300
tgatgtcagt gttatctcct ccaggaatac tggccagagg gctgtgtg a agtttgctgc 360
tgccactgga gccactccaa ttgctggccg ctccactcct ggaaccttca ctaaccagat 420
ccaggcagcc ttccgggagc caaggcttct tgtggttact gacccagggt ctgaccacca 480
gcctctcacg gaggcattct atgttaacct acctaccatt gcgtgtgtga acacagattc 540
tcctctgcgc tatgtg gaca ttgccatccc atgcaacaac aaggagctc actcagtggg 600
tttaatgtgg tggatgctgg ctcggaagt tctgcgcag cgtggacca tttcccgta 660
acacccatgg gaggtcatgc ctgatctgta ctctacaga gatcctgaag agattgaaa 720
agaagagcag gctgctgctg agaaggcagt gaccaaggag gaatttcagg gtgaatggac 780
tgctcccgct cctgagttca ctgactca gcctgaggtt gcagactggg ctgaaggtgt 840
acaggtgcc tctgtgcta ttcagcaatt ccctactgaa gactggagcg ctcagcctgc 900
cacggaagac tggctgcag ctcccactgc tcaggccact gaattggtag gagcaaccac 960
tgactggtct taagctg ttc ttgcataggc tcttaagcag catggaaaaa tggttgatgg 1020
aaaataaaca tcagtttct 1039

<210> 468
<211> 240
<212> ADN
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<220>
<221> misc_feature
<222> (1)..(240)
<223> 3' terminal sequence

<220>
<221> misc_feature
<222> (1)..(240)
<223> Chorionic somatomammotropin hormone 1 (placental
lactogen) = LACTOGEN Precursor

<400> 468
attcggcagc atgactggcc aggggtataaa aaggggccac aagagac cgg ctctaggatc 60
ccaaggccca actccccgaa ccactcaggg tcctgtggca gtcacctag tggcaatggc 120
tccaggctcc cggaaagctc ctgactctgg nttttgnoct nctctnactg ccctggnttn 180
aanaagctng tgccttccaa ancgttcctg tatccagggt ttttgaccac gctatgctnc 240

THIS PAGE BLANK (USPTO)

**This Page is Inserted by IFW Indexing and Scanning
Operations and is not part of the Official Record**

BEST AVAILABLE IMAGES

Defective images within this document are accurate representations of the original documents submitted by the applicant.

Defects in the images include but are not limited to the items checked:

- ☐ BLACK BORDERS
- ☐ IMAGE CUT OFF AT TOP, BOTTOM OR SIDES
- ☒ FADED TEXT OR DRAWING
- ☒ BLURRED OR ILLEGIBLE TEXT OR DRAWING
- ☐ SKEWED/SLANTED IMAGES
- ☐ COLOR OR BLACK AND WHITE PHOTOGRAPHS
- ☐ GRAY SCALE DOCUMENTS
- ☐ LINES OR MARKS ON ORIGINAL DOCUMENT
- ☐ REFERENCE(S) OR EXHIBIT(S) SUBMITTED ARE POOR QUALITY
- ☐ OTHER: _____

IMAGES ARE BEST AVAILABLE COPY.

As rescanning these documents will not correct the image problems checked, please do not report these problems to the IFW Image Problem Mailbox.

THIS PAGE BLANK (USPTO)